

Db	2093	GTGCTGGGCTTGACGATATCCAGAGGCGCTGGCGCACCTTCGTGCTGCGTGGCGGC	2152
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Db	2153	CAGGACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGACGGGCGGTACGACACC	2212
QY	2161	ATCCCCCAGGACAGGCTCACGAGGTATCGCCAGCATCATCAACCCAGAACAGTAC	2220
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QY	2221	TGCGTGCGTGGTATGCGGTGTCAGAAAGCGCCCATGGGCAAGTCCGCAAGGCTTC	2280
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QY	2281	AAGAGCCAGTCTCTACTTGAACAGCCTCCAGCCGTACATGCCAGAGTTCGTGGTCA	2340
Db	2333	AAGAGCCAGTCTCTACTTGAACAGCCTCCAGCCGTACATGCCAGAGTTCGTGGTCA	2392
QY	2341	CTGACGAGACCAAGCCCGCTGAGGGATGCCGTGTCATCGACAGAGCTCCTCCCTGAT	2400
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QY	2461	ATCAGGGGCAAGTCTCTACGTCAGTGCACAGGGGATCCCGCAGGGCTCCATCTCTCACG	2520
Db	2513	ATCAGGGGCAAGTCTCTACGTCAGTGCACAGGGGATCCCGCAGGGCTCCATCTCTCACG	2572
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QY	2581	GACGGGCTGCTCCTGCGTTGGTGATGATTTCTTGTGTGAACACTCACTCACTCAACCAC	2640
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QY	2641	GCGAAAAACCTTCTCTCAGAACCCCTGGTCCGAGGTGTCCTGATATGGGTGCGTGAAC	2700
Db	2693	GCGAAAAACCTTCTCTCAGAACCCCTGGTCCGAGGTGTCCTGATATGGGTGCGTGAAC	2752
QY	2701	TGCGGAAAGACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGACAGGCTTTT	2760
Db	2753	TGCGGAAAGACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGACAGGCTTTT	2812
QY	2761	GTTCAGATGCGGCGCCACGGCCTATTCCTGCTGTCGCGGCTGCTGTGATACCCGGAAC	2820
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QY	2821	CTGGAGGTGACAGAGCACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCAC	2880
Db	2873	CTGGAGGTGACAGAGCACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCAC	2932
QY	2881	TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGG	2940
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QY	2941	CTGAAGTGTACAGCGCTGTTCTGGATTTGACAGGTGAACAGCCTCCAGACGGTGTGCACC	3000
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Db 3413 AACCCGGCACTGCCCTCAGACTTCAAGACCATCTGGACTGATGGCACC 3463

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RESULT 2
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LOCUS      ARI175848      4015 bp      DNA
DEFINITION Sequence 224 from patent US 6309867.
ACCESSION  ARI175848
VERSION     ARI175848.1  GI:17917147
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 4015)
AUTHORS     Cech,T.R. and Nakamura,T.
TITLE       Telomerase
JOURNAL      Patent: US 6309867-A 224 30-OCT-2001;
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ORIGIN

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QY	61	GAGGTGCTGCCGCTGCGCCACAGTTGCTGCGCGCGCTGCGGCCCCCAGGAGCTGCGCGCTGCTG	120		
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QY	121	CAGCGCGGAGACCCGCGCGCTTTCGCGCGCGCTGCTGAGCCACAGTGCCCTGCTGCTGCTGCCC	180		
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QY	181	TGGGACGACACGCGCGCGCCCCCGCGCGCCCCCTCTCTCCGCCAGGTGTCTGCTGTAAGAG	240		
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QY	241	CTGTGCGCCCGAGTGTCTGCAGAGGCTGTGCGAGCGCGCGCGGAGAAAGAGTGTGCTGCGCTTC	300		
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QY	301	GCGCTTGGCGCTGTGGAACGGGGCCCCGCGGGGGCCCCCCCCGAGGCTTCAACCAACAGCGTG	360		
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QY	361	CGCAGCTACCTGCCCCAACACGGGTGACCGCAGCACTGCGGGGGAGCGGGGCGTGGGGGCTG	420		
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RESULT 10
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DEFINITION Sequence 224 from patent US 6093809. *6,261,836*
ACCESSION ARI04587
VERSION ARI04587.1 GI:12817295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech, T.R. and Lingner, J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 224 25-JUL-2000;
FEATURES
Location/Qualifiers
Source 1. 4015
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Query Match 82.4%; Score 3306.6; DB 6; Length 4015;
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Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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DB 61 GCGCGCTCCCGCTGCTGCGCAGCGGCTCTCTGCTGCGCAGCGCACTACCGGAGTGTCT 120
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QY 248 ACGCGCGCGGCTTCTGCTGCGCAGCGGCTCTCTGCTGCGCAGCGCACTACCGGAGTGTCT 307
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QY 308 CCGAGTGTCTGAGAGGCTGTGCGCAGCGGCTCTCTGCTGCGCAGCGCACTACCGGAGTGTCT 367
DB 301 CCGAGTGTCTGAGAGGCTGTGCGCAGCGGCTCTCTGCTGCGCAGCGCACTACCGGAGTGTCT 360
QY 368 GCTGCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
DB 361 GCTGCTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 428 CCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
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QY 548 GCGTCCCGAGCTGCGCTACCGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
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DB 1681 CAAGTTCTCTGCACTGGCTGATGAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 1740
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QY	1868	GGAAGCAGAGGTCAAGGCAGCATCGGGAAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1927
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QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTCTGTGGAGC	1987
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QY	2168	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGCTACGACACCATCCCCCA	2227
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QY	2348	CGTCTCTACCTTGACAGAGCTCCAGCCGTACATGCGACAGTTGCTGAGCTACCTGCAGGA	2407
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QY	2828	GCCGCGCCACAGGCTTATTCCTCTGTGTGCGGCTGCTGCTGGAATCCCGAACCTGAGGT	2887
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QY	3068	CAAGATCCTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGTGAGCTCCCATTTCA		3127
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QY	3810	TTTCTGTGTGTGAGAGCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTGGAGTGACCA		3865
Db	3833	CACCATCCAGGTGAGAGCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTGGAGTGACCA		3892
QY	3870	AAAGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA		3929
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QY 3421 GGGAGCTGCCATCTTCCCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
DB 3421 GGGAGCTGCCATCTTCCCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3481 CCTGTTTGGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
DB 3481 CCTGTTTGGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
QY 3541 ATTGGCTGCTCTCCGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
DB 3541 ATTGGCTGCTCTCCGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
QY 3601 AGGAGGAGCCAGGCCCCAGGCTACCCCACTCTCAAGAGCAGAGGCGCGTATCAACA 3660
DB 3601 AGGAGGAGCCAGGCCCCAGGCTACCCCACTCTCAAGAGCAGAGGCGCGTATCAACA 3660
QY 3661 CGACAGAGCCCCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
DB 3661 CGACAGAGCCCCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
QY 3721 GTCCAGATCAGGAGGTTTCTGATCCCTCTGAATTCAGACCATGTGAACCTGCGGTC 3780
DB 3721 GTCCAGATCAGGAGGTTTCTGATCCCTCTGAATTCAGACCATGTGAACCTGCGGTC 3780
QY 3781 CTGAGCTTAACAGCTTCTACTTCTGTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTT 3840
DB 3781 CTGAGCTTAACAGCTTCTACTTCTGTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTT 3840
QY 3841 CTGGAAGCTCTGGAATTTGGAATTCAGCAAAAGTGTGCTGTACACAGGCGAGACCT 3900
DB 3841 CTGGAAGCTCTGGAATTTGGAATTCAGCAAAAGTGTGCTGTACACAGGCGAGACCT 3900
QY 3901 GCACCTGATGGGGTCCCTGCTGCTCAAAATTGGGGGAGTGTGTGAGTAATAATAC 3960
DB 3901 GCACCTGATGGGGTCCCTGCTGCTCAAAATTGGGGGAGTGTGTGAGTAATAATAC 3960
QY 3961 TGAATATATAGTTTTCAGTTTGAATAAAAAAAAAAAAAAAAAAAAAA 4012
DB 3961 TGAATATATAGTTTTCAGTTTGAATAAAAAAAAAAAAAAAAAAAAAA 4012

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RESULT 2

US-09-424-686B-1

; Sequence 1, Application US/09424686B

; GENERAL INFORMATION:

; APPLICANT: Hagen, Gustav

; APPLICANT: Siegmund, Hans-Ulrich

; APPLICANT: Weichelt, Walter

; APPLICANT: Wick, Maresa

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; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; FILE REFERENCE: Bayer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686B
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/EP98/03468
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-686B-1

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Query Match

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Best Local Similarity 83.1%; Score 3333.6; DB 20; Length 4042;
Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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QY 1 GTTTCAGGACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 1 GTTTCAGGACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 61 CGATGCGCGCGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 61 CGATGCGCGCGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 AGGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
DB 121 AGGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 AGCGCGGAGACCCGCGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 AGCGCGGAGACCCGCGCTTCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 241 GGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 TGTGCGCCGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 TGTGCGCCGAGTGTCTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 GCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 GCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 GCAGTACTTGCACACAGGTGACCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GCAGTACTTGCACACAGGTGACCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 TGTGCGCGCGCGCTGCGCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 TGTGCGCGCGCGCTGCGCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CTGCACTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 601 CTGCACTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 661 AACGGGCTGGAACATAGCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 661 AACGGGCTGGAACATAGCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 GTGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 721 GTGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 781 GTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840

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Db	781	GTGGCGCTGCCCCCTGAGCCCGGAGCGGACGCCCGCTTGGGCAAGGGGTCTCGGGCCCAACCCGG	840
QY	841	GCAGGACGCGTGGACCGAGTGAACCGTGGTTCTGTGTGTGTAACCTGCCAGAACCCGCCG	900
Db	841	GCAGGACGCGTGGACCGAGTGAACCGTGGTTCTGTGTGTGTAACCTGCCAGAACCCGCCG	900
QY	901	AAGAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTTCCACCCATCCGTGG	960
Db	901	AAGAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCACGCGCCACTTCCACCCATCCGTGG	960
QY	961	GCCGCGAGCACCAACGCGGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGC	1020
Db	961	GCCGCGAGCACCAACGCGGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACGC	1020
QY	1021	CTTGTCCCCCGGTGTACGCGCCGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAGAGAGC	1080
Db	1021	CTTGTCCCCCGGTGTACGCGCCGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAGAGAGC	1080
QY	1081	AGCTGCGGGCCCTCCTTCTCTACTCAGCTCTCTGAGGCCCGACCTGACTGGCGCTCGAGGC	1140
Db	1081	AGCTGCGGGCCCTCCTTCTCTACTCAGCTCTCTGAGGCCCGACCTGACTGGCGCTCGAGGC	1140
QY	1141	TGCTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGAACTCCCGCAGGTTGC	1200
Db	1141	TGCTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGAACTCCCGCAGGTTGC	1200
QY	1201	CCCGCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCGTAAGCTGCTTGGGAACC	1260
Db	1201	CCCGCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCGTAAGCTGCTTGGGAACC	1260
QY	1261	ACGCGCAGTGCCCCCTACGCGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA	1320
Db	1261	ACGCGCAGTGCCCCCTACGCGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA	1320
QY	1321	CCCCAGCAGCCGGTGTCTGTGCCCGGAGAAAGCCCCCAGGGCTGTGGCGGCCCCCGAGG	1380
Db	1321	CCCCAGCAGCCGGTGTCTGTGCCCGGAGAAAGCCCCCAGGGCTGTGGCGGCCCCCGAGG	1380
QY	1381	AGGAGGACACAGACCCCCCGTCCCTGGTGCACTGTCTCCGCCAGCACAGACGCCCTGGC	1440
Db	1381	AGGAGGACACAGACCCCCCGTCCCTGGTGCACTGTCTCCGCCAGCACAGACGCCCTGGC	1440
QY	1441	AGGTGTACGGCTTCTGTGCGGGCTGCTGCCGCCGCTGGTGTGCCGCCAGGCTCTGGGGCT	1500
Db	1441	AGGTGTACGGCTTCTGTGCGGGCTGCTGCCGCCGCTGGTGTGCCGCCAGGCTCTGGGGCT	1500
QY	1501	CCAGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAACTTCACTCCCTGGGGAGAC	1560
Db	1501	CCAGGCACAACGAACGCCGCTTCTCAGGAACACCAAGAACTTCACTCCCTGGGGAGAC	1560
QY	1561	ATGCCAAGCTCTCGCTGCAGGACCTGACGTGGAAGATGAGCGTCCGGACTGCGCTTGGC	1620
Db	1561	ATGCCAAGCTCTCGCTGCAGGACCTGACGTGGAAGATGAGCGTCCGGACTGCGCTTGGC	1620
QY	1621	TGCGCAGGAGCCCAAGGGTGGCTGTTCGCGCCGACAGACACCGTCTGCGTGAGGAGA	1680
Db	1621	TGCGCAGGAGCCCAAGGGTGGCTGTTCGCGCCGACAGACACCGTCTGCGTGAGGAGA	1680
QY	1681	TCCTGGCCCAAGTTCCTGCACTGGCTGATGAGTGTACGTGTCAGAGCTGTCAAGTCTT	1740
Db	1681	TCCTGGCCCAAGTTCCTGCACTGGCTGATGAGTGTACGTGTCAGAGCTGTCAAGTCTT	1740
QY	1741	TCTTTATGTCAAGGAGACCAAGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGTG	1800
Db	1741	TCTTTATGTCAAGGAGACCAAGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGTG	1800
QY	1801	TCTGAGCAAGTTGCAAGCAATTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGG	1860
Db	1801	TCTGAGCAAGTTGCAAGCAATTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGG	1860
QY	1861	AGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCGCCCTGTGACGTCCA	1920

Db	1861	AGCTGTGGAAGACAGAGGTCAAGCAGCATCGGGAAGCCAGGCCGCCCTGTGACTGCCA	1920
QY	1921	GACTCCGCTTCATCCCCAAGCCTGACGGGCTGGGCCGATTGTGAACATGACTACGTGG	1980
Db	1921	GACTCCGCTTCATCCCCAAGCCTGACGGGCTGGGCCGATTGTGAACATGACTACGTGG	1980
QY	1981	TGGAGCCAGAACGTTCCGACAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAG	2040
Db	1981	TGGAGCCAGAACGTTCCGACAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAG	2040
QY	2041	CACTGTTACGCGTGTCACTACGAGCGGGCGCGGCCGCCCTCCTGTGGCGCTCTG	2100
Db	2041	CACTGTTACGCGTGTCACTACGAGCGGGCGCGGCCGCCCTCCTGTGGCGCTCTG	2100
QY	2101	TGCTGGGCTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGGGGCC	2160
Db	2101	TGCTGGGCTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGGGGCC	2160
QY	2161	AGGACCCGCGCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTAACACCA	2220
Db	2161	AGGACCCGCGCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTAACACCA	2220
QY	2221	TCCCCAGGACAGGCTCACGGAGTCAATGCGCAGCATCATCAAACCCAGAACGTA	2280
Db	2221	TCCCCAGGACAGGCTCACGGAGTCAATGCGCAGCATCATCAAACCCAGAACGTA	2280
QY	2281	GCGTGCCTCGGTATGCCGTGGTTCAGAAAGCGCCCATGGGCACGTCCGCAAGCCTTCA	2340
Db	2281	GCGTGCCTCGGTATGCCGTGGTTCAGAAAGCGCCCATGGGCACGTCCGCAAGCCTTCA	2340
QY	2341	AGAGCCACGTTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGACTCAC	2400
Db	2341	AGAGCCACGTTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGACTCAC	2400
QY	2401	TGCAGAGACCAAGCCGCTGAGGGATGCCGTGTATCGAGCAGAGCTCCTCCCTGAATG	2460
Db	2401	TGCAGAGACCAAGCCGCTGAGGGATGCCGTGTATCGAGCAGAGCTCCTCCCTGAATG	2460
QY	2461	AGGCAGCAGTGGCCTCTTCGACGCTTCTTCAAGCTTCATGTGCCAACAGCGGTGCCA	2520
Db	2461	AGGCAGCAGTGGCCTCTTCGACGCTTCTTCAAGCTTCATGTGCCAACAGCGGTGCCA	2520
QY	2521	TCAGGGGCAAGTCCATCGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCCACGC	2580
Db	2521	TCAGGGGCAAGTCCATCGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCCACGC	2580
QY	2581	TGCTCTGACGCTGTGCTACGGGACATGGAGAACAAAGCTGTTGGCGGGAATCCGGCGG	2640
Db	2581	TGCTCTGACGCTGTGCTACGGGACATGGAGAACAAAGCTGTTGGCGGGAATCCGGCGG	2640
QY	2641	ACGGGCTGCTCCTGCGTTTGTGTGATGATTTCTTGTGTGACACCTCACTCACCCACG	2700
Db	2641	ACGGGCTGCTCCTGCGTTTGTGTGATGATTTCTTGTGTGACACCTCACTCACCCACG	2700
QY	2701	CGAAACCTTCTCAGGACCCCTGTCCGAGGTGCCCTGAGTATGGCTGCGTGTGA	2760
Db	2701	CGAAACCTTCTCAGGACCCCTGTCCGAGGTGCCCTGAGTATGGCTGCGTGTGA	2760
QY	2761	TGCGGAGACAGTGTGTAATTTCCCTGTGTAAGAAGCAGAGCCCTGGGTGGCA	2820
Db	2761	TGCGGAGACAGTGTGTAATTTCCCTGTGTAAGAAGCAGAGCCCTGGGTGGCA	2820
QY	2821	TTCAGATGCGGCGCCCAAGGCTATTTCCCTGTGTGCGGCTGTGCTGATACCCGGA	2880
Db	2821	TTCAGATGCGGCGCCCAAGGCTATTTCCCTGTGTGCGGCTGTGCTGATACCCGGA	2880
QY	2881	TGGAGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCA	2940
Db	2881	TGGAGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCA	2940
QY	2941	TCAACCGCGGCTTCAAGGCTGGGAGGAATGCGTCGCAAACTCTTTGGGGTCTTGCGG	3000
Db	2941	TCAACCGCGGCTTCAAGGCTGGGAGGAATGCGTCGCAAACTCTTTGGGGTCTTGCGG	3000

Db 3061 TTCAAGCATGTGTGCTGAGCTCCCATTTTCATGACGAAGTTTGAAGAAGCCCAATTTT 3120
QY 3121 TCCTGCGGCTCATCTGTGACACGCGCTCCCTGCTACTTCCATCTGAAAGCCAGAAGC 3180
Db 3121 TCCTGCGGCTCATCTGTGACACGCGCTCCCTGCTACTTCCATCTGAAAGCCAGAAGC 3180
QY 3181 CAGGATGTGCTGGGGCCAAAGGGCGCGCGCCCTCTGCTCCGAGGGCCGTGAGT 3240
Db 3181 CAGGATGTGCTGGGGCCAAAGGGCGCGCGCCCTCTGCTCCGAGGGCCGTGAGT 3240
QY 3241 GGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTGACACCCGTGTCACTAAGTCCAC 3300
Db 3241 GGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTGACACCCGTGTCACTAAGTCCAC 3300
QY 3301 TCCTGGGGTCACTCAGACAGCCCAAGAGCCAGCTGAGTCCGGAAGCTCCCGGGGACGACGC 3360
Db 3301 TCCTGGGGTCACTCAGACAGCCCAAGAGCCAGCTGAGTCCGGAAGCTCCCGGGGACGACGC 3360
QY 3361 TGAATGCTGAGAGGGCCGACCAACCCGCTGCTGCTCAGACTTCAAGACCATCTCTGG 3420
Db 3361 TGAATGCTGAGAGGGCCGACCAACCCGCTGCTGCTCAGACTTCAAGACCATCTCTGG 3420
QY 3421 ACTGATGGCCACCCGCCCCACAGCCAGGCGGAGACAGACACAGAGCCCTGTACAGCCG 3480
Db 3421 ACTGATGGCCACCCGCCCCACAGCCAGGCGGAGACAGACACAGAGCCCTGTACAGCCG 3480
QY 3481 GGCTCTACGTCCCAAGGAGGAGGGGGCGGCCCCACACCCAGGCGCGCTGGAGTCT 3540
Db 3481 GGCTCTACGTCCCAAGGAGGAGGGGGCGGCCCCACACCCAGGCGCGCTGGAGTCT 3540
QY 3541 GAGGCTGAGTGTGTTGGCCGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
Db 3541 GAGGCTGAGTGTGTTGGCCGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
QY 3601 TGAGGCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
Db 3601 TGAGGCTGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
QY 3661 TCCCAACAGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
Db 3661 TCCCAACAGGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
QY 3721 CTTCACCTCCCAACATAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
Db 3721 CTTCACCTCCCAACATAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
QY 3781 TGCCCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
Db 3781 TGCCCTCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
QY 3841 GCTCTGGGAATTTGAGTGAACCAAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3900
Db 3841 GCTCTGGGAATTTGAGTGAACCAAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3900
QY 3901 GGATGGGGGTCCCTGTGGGTCAAAATTGGGGGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 3960
Db 3901 GGATGGGGGTCCCTGTGGGTCAAAATTGGGGGAGGTGCTGCTGCTGCTGCTGCTGCTGCT 3960
QY 3961 TATGAGTTTTCAGTTTGAAGAAAAA 4006
Db 3961 TATGAGTTTTCAGTTTGAAGAAAAA 4006

RESULT 2

US-09-424-686B-1

; Sequence 1, Application US/09424686B

; GENERAL INFORMATION:

; APPLICANT: Hagen, Gustav

; APPLICANT: Siegmund, Hans-Ulrich

; APPLICANT: Weichel, Walter

; APPLICANT: Wick, Marese

; APPLICANT: Zubov, Dmitry

; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
; FILE OF INVENTION: Therapeutic Use
; FILE REFERENCE: Bayer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686B
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/EP98/03468
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-424-686B-1

Query Match 98.9%; Score 3960; DB 20; Length 4042;

Best Local Similarity 99.1%; Pred. No. 0; Mismatches 0; Indels 36; Gaps 1;

Matches 4006; Conservative 0; Mismatches 0; Indels 36; Gaps 1;

QY 1 GTTTCAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 GTTTCAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 61 CGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 CGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 121 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
Db 121 AGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 181 AGCGCGGGGACCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 181 AGCGCGGGGACCGCGCGCTTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GAGAGCAGCG 300
Db 241 GAGAGCAGCG 300
QY 301 TGGTGGCGCGAGTGTGAGAGGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 301 TGGTGGCGCGAGTGTGAGAGGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 GCTTGGCGCTGCTGAGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 361 GCTTGGCGCTGCTGAGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 GAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GAGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 TGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 481 TGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
QY 541 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 CTGCACTCAGCG 660
Db 601 CTGCACTCAGCG 660
QY 661 AACGGGCTGGAACCTAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db 661 AACGGGCTGGAACCTAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 GTGCGAGAGCG 780
Db 721 GTGCGAGAGCG 780
QY 781 GTGGCGCTGCTGAGCGCGAGCG 840

Db 781 GTGGCGCTGCCCCCTGAGCCGGAGCGCCCGTTGGGCAAGGGCTCTTGGGCCACCCGG 840
QY 841 GCAGAGCGCTGGAGACCGAGTGAACCTGGGTTTCTGTGTGTCTGCTGCACTGCGACAGCCCGCG 900
Db 841 GCAGAGCGCTGGAGACCGAGTGAACCTGGGTTTCTGTGTGTCTGCTGCACTGCGACAGCCCGCG 900
QY 901 AAGAGCCACTCTTTTGGAGGGTGGCTCTCTGGACCGCGCACTCCACCCATCCGTGG 960
Db 901 AAGAGCCACTCTTTTGGAGGGTGGCTCTCTGGACCGCGCACTCCACCCATCCGTGG 960
QY 961 GCCCGCAGACCAACGCGGGCCCCCATCCATCGCGGCAACAGTCCCTGGGACACGC 1020
Db 961 GCCCGCAGACCAACGCGGGCCCCCATCCATCGCGGCAACAGTCCCTGGGACACGC 1020
QY 1021 CTTGTCCCCGGGTGACGCGCGAGCAACCACTTCTCTACTCTCAGGCGACAGAGC 1080
Db 1021 CTTGTCCCCGGGTGACGCGCGAGCAACCACTTCTCTACTCTCAGGCGACAGAGC 1080
QY 1081 AGCTGGGCGCTCTCTCTACTCTCTGAGGCGCGAGCTGAGCTGGCGTGGAGGC 1140
Db 1081 AGCTGGGCGCTCTCTCTACTCTCTGAGGCGCGAGCTGAGCTGGCGTGGAGGC 1140
QY 1141 TCGTGAGAACCATCTTTCTGGGTTCCAGGCGCTGATGCGAGGACTCCCGCAGGTTGC 1200
Db 1141 TCGTGAGAACCATCTTTCTGGGTTCCAGGCGCTGATGCGAGGACTCCCGCAGGTTGC 1200
QY 1201 CCCGCTGCCCCAGCGCTACTGSCAAATGCGGCCCTGTTTCTGAGCTGCTGGGAAC 1260
Db 1201 CCCGCTGCCCCAGCGCTACTGSCAAATGCGGCCCTGTTTCTGAGCTGCTGGGAAC 1260
QY 1261 ACGGCAAGTGCCTCTACGCGGTGCTCTCAAGACGCACTGCGCGCTGCGAGTGGCTCA 1320
Db 1261 ACGGCAAGTGCCTCTACGCGGTGCTCTCAAGACGCACTGCGCGCTGCGAGTGGCTCA 1320
QY 1321 CCCAGCAGCGCGGTGCTGTCGCGCGGAGAGAGCCCGAGGCTCTGTGGCGGCCCGAGG 1380
Db 1321 CCCAGCAGCGCGGTGCTGTCGCGCGGAGAGAGCCCGAGGCTCTGTGTGGCGGCCCGAGG 1380
QY 1381 AGGAGGACACAGACCCCGCTGCTGCTGAGCTGCTCCGCGAGCAGACAGACCCCTGGC 1440
Db 1381 AGGAGGACACAGACCCCGCTGCTGCTGAGCTGCTCCGCGAGCAGACAGACCCCTGGC 1440
QY 1441 AGGTGTAAGGCTTCTGTCGCGGCTGCTGCGCGGCTGCTGCGCGGCTTGGGCT 1500
Db 1441 AGGTGTAAGGCTTCTGTCGCGGCTGCTGCGCGGCTGCTGCGCGGCTTGGGCT 1500
QY 1501 CCAGGACACAGACCGCGCTTCTCAAGAACACCAAGAGTCACTCTCCCTGGGGAAGC 1560
Db 1501 CCAGGACACAGACCGCGCTTCTCAAGAACACCAAGAGTCACTCTCCCTGGGGAAGC 1560
QY 1561 ATGCCAAGCTCTGCTGCGAGAGCTGACGTGAAGATGAGCGTGGCGGACTGCGCTTGGC 1620
Db 1561 ATGCCAAGCTCTGCTGCGAGAGCTGACGTGAAGATGAGCGTGGCGGACTGCGCTTGGC 1620
QY 1621 TGGCGAAGAGCCCGAGGGGTGGCTGTGTTCCGCGCGAGAGCAGCCGTGCGTGAAGAGA 1680
Db 1621 TGGCGAAGAGCCCGAGGGGTGGCTGTGTTCCGCGCGAGAGCAGCCGTGCGTGAAGAGA 1680
QY 1681 TCCTGGCCAAAGTCTGCACTGCGTGAAGTGTGTAAGTGTGCAAGCTGCTCAGGCTTT 1740
Db 1681 TCCTGGCCAAAGTCTGCACTGCGTGAAGTGTGTAAGTGTGCAAGCTGCTCAGGCTTT 1740
QY 1741 TCTTTATGTCAAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCAACCGAAGAGTG 1800
Db 1741 TCTTTATGTCAAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCAACCGAAGAGTG 1800
QY 1801 TCTGAGCAAGTGTCAAGACATTTGAATCAGACACTTGAAGAGGGTGAAGTGGCGG 1860
Db 1801 TCTGAGCAAGTGTCAAGACATTTGAATCAGACACTTGAAGAGGGTGAAGTGGCGG 1860
QY 1861 AGCTGTGGAAGCAAGGTCAAGGAGCATGCGGAAGCCAGGCCGCTGCTGACGTCCA 1920
Db 1861 AGCTGTGGAAGCAAGGTCAAGGAGCATGCGGAAGCCAGGCCGCTGCTGACGTCCA 1920

QY 1921 GACTCCGCTTCAATCCCAAGCTGACGGGCTGCGCGCGATTTGAAATGACTACGTG 1980
Db 1921 GACTCCGCTTCAATCCCAAGCTGACGGGCTGCGCGCGATTTGAAATGACTACGTG 1980
QY 1981 TGGAGCCAGAACGTTCCGCAAGAAAAGAGGGCCGAGGCTCTCACTGAGGGTGAAG 2040
Db 1981 TGGAGCCAGAACGTTCCGCAAGAAAAGAGGGCCGAGGCTCTCACTGAGGGTGAAG 2040
QY 2041 CACTGTTAGGCTGCTCAACTACAGAGCGGGCGCGCGCGCTCTCTGGCGGCTTG 2100
Db 2041 CACTGTTAGGCTGCTCAACTACAGAGCGGGCGCGCGCGCTCTCTGGCGGCTTG 2100
QY 2101 TGTGGGCTTGAAGATATCAAGAGGCTGCGCACCTTGTGCTGCTGCGGGGCC 2160
Db 2101 TGTGGGCTTGAAGATATCAAGAGGCTGCGCACCTTGTGCTGCTGCGGGGCC 2160
QY 2161 AGGACCGCGCGCTGAGCTGTA 2183 2218
Db 2161 AGGACCGCGCGCTGAGCTGTA 2183 2218
QY 2185 TCCCGCAGGACAGGCTCAGGAGGTATCGCCAGCATCAAAACCCAGAACAGTACT 2244
Db 2185 TCCCGCAGGACAGGCTCAGGAGGTATCGCCAGCATCAAAACCCAGAACAGTACT 2244
QY 2221 TCCCGCAGGACAGGCTCAGGAGGTATCGCCAGCATCAAAACCCAGAACAGTACT 2280
Db 2221 TCCCGCAGGACAGGCTCAGGAGGTATCGCCAGCATCAAAACCCAGAACAGTACT 2280
QY 2245 GCGTGGCTGGATATGCGGTGTCAGAGAGCGCGCCCATGGGCACGTCCGCAAGGCTTCA 2304
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VERSION AX001446.1 GI:7241612
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SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4042)
AUTHORS Wick, M. and Hagen, G.
TITLE HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC AND THERAPEUTIC USE
JOURNAL Patent: WO 9859040-A 1 30-DEC-1998;
WICK MARESA (DE); BAYER AG (DE)
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2543 TGCGAAGACAGTGTGAATTTCCCTGTAGAGACAGAGCCCTGGGTGGCAAGGCTTTTG 2602
2543 TGCGAAGACAGTGTGAATTTCCCTGTAGAGACAGAGCCCTGGGTGGCAAGGCTTTTG 2602
2761 TGCGAAGACAGTGTGAATTTCCCTGTAGAGACAGAGCCCTGGGTGGCAAGGCTTTTG 2820
2761 TGCGAAGACAGTGTGAATTTCCCTGTAGAGACAGAGCCCTGGGTGGCAAGGCTTTTG 2820
2603 TTCAGATGCGCGCCCAAGGCTATTTCCCTGTGCTGCGGCTGCTGATACCCGAGACC 2662
2603 TTCAGATGCGCGCCCAAGGCTATTTCCCTGTGCTGCGGCTGCTGATACCCGAGACC 2662
2821 TTCAGATGCGCGCCCAAGGCTATTTCCCTGTGCTGCGGCTGCTGATACCCGAGACC 2880
2821 TTCAGATGCGCGCCCAAGGCTATTTCCCTGTGCTGCGGCTGCTGATACCCGAGACC 2880
2663 TGGAGTGCAGAGGCTACTATTCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACT 2722
2663 TGGAGTGCAGAGGCTACTATTCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACT 2722
2881 TGGAGTGCAGAGGCTACTATTCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACT 2940
2881 TGGAGTGCAGAGGCTACTATTCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACT 2940
2723 TCAACCGCGGCTTCAAGGCTGGAGAGAAACATGCTGCGCAAACTTTTGGGGTCTTGGCG 2782
2723 TCAACCGCGGCTTCAAGGCTGGAGAGAAACATGCTGCGCAAACTTTTGGGGTCTTGGCG 2782
2941 TCAACCGCGGCTTCAAGGCTGGAGAGAAACATGCTGCGCAAACTTTTGGGGTCTTGGCG 3000
2941 TCAACCGCGGCTTCAAGGCTGGAGAGAAACATGCTGCGCAAACTTTTGGGGTCTTGGCG 3000
2783 TGAAGTGTCAAGGCTGCTTCTGATTTGAGGTGAACAGCTCCAGAGCGGTGCAACA 2842
2783 TGAAGTGTCAAGGCTGCTTCTGATTTGAGGTGAACAGCTCCAGAGCGGTGCAACA 2842
3001 TGAAGTGTCAAGGCTGCTTCTGATTTGAGGTGAACAGCTCCAGAGCGGTGCAACA 3060
3001 TGAAGTGTCAAGGCTGCTTCTGATTTGAGGTGAACAGCTCCAGAGCGGTGCAACA 3060
2843 ACATCTCAAGATCTCTCTGCTGCAAGGCTGCAAGGCTTCAAGCATGTGTGCTGAGCTCC 2902
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2903 CATTTCACTAGCAAGTGTGAAGAAACCCCAATTTTCTGCGGCTCATCTGACACAG 2962
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3181 CTTCCTCTGCTACTCATCTCTGAAAGCCCAAGAACGAGAGTGTGCTGCGGCGCAAG 3240
3181 CTTCCTCTGCTACTCATCTCTGAAAGCCCAAGAACGAGAGTGTGCTGCGGCGCAAG 3240
3023 GCGCGCGCGGCTCTGCTGCTGCAAGGCGGCTGAGTGTGCTGCAAGCATTCCTGC 3082
3023 GCGCGCGCGGCTCTGCTGCTGCAAGGCGGCTGAGTGTGCTGCAAGCATTCCTGC 3082
3241 GCGCGCGCGGCTCTGCTGCTGCAAGGCGGCTGAGTGTGCTGCAAGCATTCCTGC 3300
3241 GCGCGCGCGGCTCTGCTGCTGCAAGGCGGCTGAGTGTGCTGCAAGCATTCCTGC 3300
3083 TCAAGCTGACTGACACCGGTGTCAACCTAGTGCCTCTGCGGCTCATCTGACACAG 3142
3083 TCAAGCTGACTGACACCGGTGTCAACCTAGTGCCTCTGCGGCTCATCTGACACAG 3142
3301 TCAAGCTGACTGACACCGGTGTCAACCTAGTGCCTCTGCGGCTCATCTGACACAG 3360
3301 TCAAGCTGACTGACACCGGTGTCAACCTAGTGCCTCTGCGGCTCATCTGACACAG 3360
3143 AGAGCAGCTGAGTGAAGAGCTCCCGGAGAGAGCTGACTGCTGCTGAGAGCGGAGCA 3202
3143 AGAGCAGCTGAGTGAAGAGCTCCCGGAGAGAGCTGACTGCTGCTGAGAGCGGAGCA 3202
3361 AGAGCAGCTGAGTGAAGAGCTCCCGGAGAGAGCTGACTGCTGCTGAGAGCGGAGCA 3420
3361 AGAGCAGCTGAGTGAAGAGCTCCCGGAGAGAGCTGACTGCTGCTGAGAGCGGAGCA 3420
3203 ACCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3262
3203 ACCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3262
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3421 ACCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
3263 AGCGGAGAGCAGACACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3322
3263 AGCGGAGAGCAGACACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3322
3481 AGCGGAGAGCAGACACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3481 AGCGGAGAGCAGACACAGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
3323 GCGCGGCGCACACAGAGCGCGCAGCGCTGAGAGTGTGAGGCTGAGTGTGCTGCTGCTG 3382
3323 GCGCGGCGCACACAGAGCGCGCAGCGCTGAGAGTGTGAGGCTGAGTGTGCTGCTGCTG 3382
3541 GCGCGGCGCACACAGAGCGCGCAGCGCTGAGAGTGTGAGGCTGAGTGTGCTGCTGCTG 3600
3541 GCGCGGCGCACACAGAGCGCGCAGCGCTGAGAGTGTGAGGCTGAGTGTGCTGCTGCTG 3600
3383 AGGCTGATGTCCGCTGAGAGTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3442
3383 AGGCTGATGTCCGCTGAGAGTGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3442

QY	1868	GAAGCAAGAGTCAAGCAGCATCGGGAGCCAGGCCCGCCCTGCTACGTCAGACTCCG	1927
Db	1861	GGAGCAGAGGTCAAGCAGCATCGGGAGCCAGGCCCGCCCTGCTACGTCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTTCACGGGCTGCGGCCGATTGTGAACAATGAACTACGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTTCACGGGCTGCGGCCGATTGTGAACAATGAACTACGTCGTGGAGC	1980
QY	1988	CAGAACGTTCCGCAAGAAAAGAGGCCGAGCGTCTACCTCGAGGCTGAAGCACTGTT	2047
Db	1981	CAGAACGTTCCGCAAGAAAAGAGGCCGAGCGTCTACCTCGAGGCTGAAGCACTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGCGCCTCTGTGTGGG	2107
Db	2041	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGCGCCTCTGTGTGGG	2100
QY	2108	CCTGACGATATCCACAGGCGCTGCGCACCTTCGTCGTGCTGTGCGGCGCCAGAGACC	2167
Db	2101	CCTGACGATATCCACAGGCGCTGCGCACCTTCGTCGTGCTGTGCGGCGCCAGAGACC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCTACGACACCATCCCCCA	2220
QY	2192	GGAAGGCTCACGAGGTCTATCGCCACATCATCAAAACCCAGAACAGTAATCGGTGCG	2251
Db	2221	GGAAGGCTCACGAGGTCTATCGCCACATCATCAAAACCCAGAACAGTAATCGGTGCG	2280
QY	2252	TGCGTATGCCGTGTGTCAGAAAGGCCGCCCATGGGCACTGCCGCAAGGCTTCAAGGCCA	2311
Db	2281	TGCGTATGCCGTGTGTCAGAAAGGCCGCCCATGGGCACTGCCGCAAGGCTTCAAGGCCA	2340
QY	2312	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCAGATTCGTGGCTCACTGACAGA	2371
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCAGATTCGTGGCTCACTGACAGA	2400
QY	2372	GACCAAGCCGCTGAGGAGTCCGTCGTATCGACAGAGCTCCTCCCTGAATGAGGCCAG	2431
Db	2401	GACCAAGCCGCTGAGGAGTCCGTCGTATCGACAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2432	CAGTGGCCTTTGACAGCTCTTCTCTACGCTTCATGTGCCACCAAGCGGTGCCATCAGGGG	2491
Db	2461	CAGTGGCCTTTGACAGCTCTTCTCTACGCTTCATGTGCCACCAAGCGGTGCCATCAGGGG	2520
QY	2492	CAAGTCTACGTCCAGTGCACGAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCG	2551
Db	2521	CAAGTCTACGTCCAGTGCACGAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCG	2580
QY	2552	CAGCCTGTGCTACGCGCAGCATGAGAACAAAGCTGTTGCGGGGATTCCGGGGAGCGGCT	2611
Db	2581	CAGCCTGTGCTACGCGCAGCATGAGAACAAAGCTGTTGCGGGGATTCCGGGGAGCGGCT	2640
QY	2612	GCTCCTGCGTTTGGTGCATGATTTCTTGTGTGTGACACCTTCACCTCACCCACGCCAAAC	2671
Db	2641	GCTCCTGCGTTTGGTGCATGATTTCTTGTGTGTGACACCTTCACCTCACCCACGCCAAAC	2700
QY	2672	CTTCTCTAGGACCTGCTCCGAGGTGTCCTGAGTATGCTGCTGCTGTGAATTCGGGAA	2731
Db	2701	CTTCTCTAGGACCTGCTCCGAGGTGTCCTGAGTATGCTGCTGCTGTGAATTCGGGAA	2760
QY	2732	GACAGTGTGAATTCCTCTGTAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2791
Db	2761	GACAGTGTGAATTCCTCTGTGTAGAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
QY	2792	GCCGGCCCAAGGCTATTTCCCTGCTGCGGCTGCTGCTGATACCCGGAACCTTGAGGT	2851
Db	2821	GCCGGCCCAAGGCTATTTCCCTGCTGCGGCTGCTGCTGATACCCGGAACCTTGAGGT	2880
QY	2852	GCAGAGCGCACTACTCCAGCTATGCGCGACCTCCATCAGAGCCAGTCTCACTTCAACC	2911
Db	2881	GCAGAGCGCACTACTCCAGCTATGCGCGACCTCCATCAGAGCCAGTCTCACTTCAACC	2940
QY	2912	CGGCTCAAGGCTGGAGGAAATGCGTCCGAACTCTTTGGGGTCTTTCGGGCTGAAGTG	2971

Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCCGTCCGAACCTCTTTGGGGTCTTGCGGCTGAAGTG	3000
QY	2972	TCACAGCCTGTTTCTGGATTGTGCAAGGTGAACAGCCTCCAGACGGGTGTGCACCAATCTA	3031
Db	3001	TCACAGCCTGTTTCTGGATTGTGCAAGGTGAACAGCCTCCAGACGGGTGTGCACCAATCTA	3060
QY	3032	CAAGATCCTCCTGCTGCAGGCGGTACAGGTTTCAACGATGTGTGTGCAAGCTCCCATTTCA	3091
Db	3061	CAAGATCCTCCTGCTGCAGGCGGTACAGGTTTCAACGATGTGTGTGCAAGCTCCCATTTCA	3120
QY	3092	TCAGCAAGTTTGGAGAACCACCATTTTTCCTGCGGCTCATCTGACACGCGCTCCCT	3151
Db	3121	TCAGCAAGTTTGGAGAACCACCATTTTTCCTGCGGCTCATCTGACACGCGCTCCCT	3180
QY	3152	CTGCTACTCCATCTGAAAGCCCAAGAACGACAGGAGATGTGCTGGGGCCAAAGGCGCGC	3211
Db	3181	CTGCTACTCCATCTGAAAGCCCAAGAACGACAGGAGATGTGCTGGGGCCAAAGGCGCGC	3240
QY	3212	CGGCCCCCTGCCCCCTCCGAGGCCGTGCAGTGCGTGTGCCAACCAAGCATTCCTGCTCAAGCT	3271
Db	3241	CGGCCCCCTGCCCCCTCCGAGGCCGTGCAGTGCGTGTGCCAACCAAGCATTCCTGCTCAAGCT	3300
QY	3272	GACTCGACACCGTGTCACTTACGTGCCACTCCTGGGGTCACTCAGACAGCCCAAGCGCA	3331
Db	3301	GACTCGACACCGTGTCACTTACGTGCCACTCCTGGGGTCACTCAGACAGCCCAAGCGCA	3360
QY	3332	GCTGAGTCGAAAGCTCCCGGGGACGACGCTGACTGCCCTGGAAGCCGACGCCAACCCGGC	3391
Db	3361	GCTGAGTCGAAAGCTCCCGGGGACGACGCTGACTGCCCTGGAAGCCGACGCCAACCCGGC	3420
QY	3392	ACTGCCCTCAGACTTCAAGACCATCTGTGAAGTGTATGAGGCCACCCGCCACAGCCAGGCCGA	3451
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTGTGAAGTGTATGAGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3452	GAGCAGACACACGACGCTGTCAAGCCGCGGCTCTAGTCCCAAGGAGGAGGGCGGCC	3511
Db	3481	GAGCAGACACACGACGCTGTCAAGCCGCGGCTCTAGTCCCAAGGAGGAGGGCGGCC	3540
QY	3512	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAATGTTGGCCGAGGCTG	3571
Db	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAATGTTGGCCGAGGCTG	3600
QY	3572	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3631
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3632	GAGTGTCAAGACACCTGCGCTTCACTTCCCAAGGCTGGCGCTCGGCTCCACCCCA	3691
Db	3661	GAGTGTCAAGACACCTGCGCTTCACTTCCCAAGGCTGGCGCTGGCGCTCCACCCCA	3720
QY	3692	GGGCCAGCTTTTCTCAACAGAGAGCCGGCTTCCATCTCCCAATAGATGTCATCC	3751
Db	3721	GGGCCAGCTTTTCTCAACAGAGAGCCGGCTTCCATCTCCCAATAGATGTCATCC	3780
QY	3752	CCAGATTGCGCATTTTCAACCCCTGCGCTGCCCTCTTGGCTTCCACCCCAACCATCC	3811
Db	3781	CCAGATTGCGCATTTTCAACCCCTGCGCTGCCCTCTTGGCTTCCACCCCAACCATCC	3840
QY	3812	AGGTGAGAACCTGAGAGAACCCCTGGGAGCTCTGGGAATTTGAGTGACCAAGGTGTG	3871
Db	3841	AGGTGAGAACCTGAGAGAACCCCTGGGAGCTCTGGGAATTTGAGTGACCAAGGTGTG	3900
QY	3872	CCCTGTACACAGGCGAGGACCTTGACCTGATGGGGTCCCTGTGGGTCAAATTGGGGG	3931
Db	3901	CCCTGTACACAGGCGAGGACCTTGACCTGATGGGGTCCCTGTGGGTCAAATTGGGGG	3960
QY	3932	GAGTGTCTGGGAGTAATAATACTGAATATATAGTTTTTCAAGTTTGAAAAAA 3986	
Db	3961	GAGTGTCTGGGAGTAATAATACTGAATATATAGTTTTTCAAGTTTGAAAAAA 4015	

RESULT 11

RESULT 11

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 17:46:48 ; Search time 901.534 Seconds
(without alignments)
18019.401 Million cell updates/sec

Title: US-09-424-686f-10
Perfect score: 3824
Sequence: 1 gtttcagcgacgcgtgcgtc.....aaaaaaaaaaaaaaaaaaaa 3824

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002s:*
- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3767.8	98.5	3855	2	AAV22382 Human tel
2	3586	93.8	4042	2	AAV72117 Human cat
3	3571	93.4	4037	2	AAV22428 Human tel
4	3563.8	93.2	4023	2	AAV60320 Human tel
5	3559.4	93.1	4070	6	ABL53711 Human tel
6	3559	93.1	4015	2	AAZ00724 Human tel
7	3559	93.1	4015	2	AAZ00724 Human tel
8	3559	93.1	4015	2	AAZ30154 Human tel
9	3559	93.1	4015	4	AAH45901 Human hte
10	3559	93.1	4015	6	AAD46821 Human tel
11	3559	93.1	4015	6	ABA97534 Cancer ce
12	3559	93.1	4015	7	ACC58039 Human tel
13	3559	93.1	4015	7	ACC57552 Human tel
14	3559	93.1	4015	7	ABZ22474 Human tel
15	3559	93.1	4015	7	ACC44482 Human tel
16	3557.4	93.0	4015	2	AAZ08150 Human tel
17	3557.4	93.0	4015	7	ABZ18391 Human tel
18	3557	93.0	4027	2	AAH89424 Human EST
19	3557	93.0	4027	3	AAA29388 hEST2, a
20	3557	93.0	4027	9	ADC47060 Human TBR
21	3557	93.0	4027	9	ADE40481 Human tel
22	3536	92.5	3918	2	AAH18269 Telomeras
23	3536	92.5	3918	2	AAH18278 Telomeras

24	3504.8	91.7	3964	2	AAH18254 Aax18254 Human tel
25	3429	89.7	3955	2	AAV22379 Aav22379 Human tel
26	3328.6	87.0	3798	2	AAV27876 Aav27876 Human tel
27	2944	77.0	3453	7	ABZ76217 Human TER
28	2944	77.0	13766	6	AAD46790 pGRN145 p
29	2943	77.0	3399	6	ABV78144 Human tel
30	2943	77.0	3399	6	ABZ35720 Human e1o
31	2943	77.0	3399	6	ABX09963 Human tel
32	2943	77.0	3399	6	ABL91685 Human pol
33	2940	76.9	3396	4	AH48235 Heart mus
34	2940	76.9	3396	4	AAH49601 Human cod
35	2940	76.9	3396	4	AH44366 Human tel
36	2936.8	76.8	3396	2	AAX18266 Telomeras
37	2932	76.7	8742	6	AAD46793 PWGB5a p1
38	2851.8	74.6	3543	7	ABZ69628 Plasmid C
39	2822.8	73.8	3500	2	AAX18275 Telomeras
40	2785	72.8	3167	2	AAX18271 Altered C
41	2785	72.8	3167	2	AAX18280 Altered C
42	2747	71.8	3203	2	AAX18268 Altered C
43	2741.4	71.7	7688	2	AAX18351 Telomeras
44	2620.4	68.5	7615	2	AAX18349 Telomeras
45	2617	68.4	3323	2	AAX18277 Altered C

ALIGNMENTS

RESULT 1	AAV22382	standard; cDNA; 3855 BP.
ID	AAV22382	
XX	AAV22382;	
AC	13-AUG-1998	(first entry)
DT		
XX		
DE	Human telomerase reverse transcriptase Delta182 variant encoding cDNA.	
XX		
KW	Human; telomerase reverse transcriptase; hTRT; TRT; diagnosis; prognosis;	
KW	cell proliferation; cancer; ageing; ribonucleoprotein; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	56..2479
FT		/*tag= a
FT		/product= "telomerase reverse transcriptase variant"
XX		
PN	GB2317891-A.	
XX		
PD	08-APR-1998.	
XX		
PF	01-OCT-1997;	97GB-00020890.
XX		
PR	01-OCT-1996;	96US-00724643.
PR	18-APR-1997;	97US-00844419.
PR	25-APR-1997;	97US-00846017.
PR	06-MAY-1997;	97US-00851843.
PR	09-MAY-1997;	97US-00854050.
PR	14-AUG-1997;	97US-00911312.
PR	14-AUG-1997;	97US-00912951.
PR	14-AUG-1997;	97US-00915503.
XX		
PA	(GERO-) GERON CORP.	
PA	(UYTE-) UNIV TECHNOLOGY CORP.	
XX		
PI	Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;	
PI	Andrews WH;	
XX		
DR	WPI; 1998-171633/16.	
DR	P-PSDB; AAW46997.	
XX		
PT	Pure and recombinant human Telomerase Reverse Transcriptase and its	

PT variants - are useful in the diagnosis, prognosis and treatment of cell
proliferation conditions especially cancer and ageing.

XX Disclosure; Fig 20; 387pp; English.

XX The present sequence encodes a human telomerase reverse transcriptase
CC (hTERT) variant from the present invention. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods

XX Sequence 3855 BP, 651 A, 1300 C, 1226 G, 678 T, 0 U, 0 Other;

Query Match 98.5%; Score 3767.8; DB 2; Length 3855;

Best Local Similarity 99.0%; Pred. No. 0;

Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

QY	8	GCAGCGCTGCGTCTCTGTCGCGCAGTGGGAGAGCCCTGCGCCCGCCAGCCCGCGATGCC	67
DB	1	GCAGCGCTGCGTCTCTGTCGCGCAGTGGGAGAGCCCTGCGCCCGCCAGCCCGCGATGCC	60
QY	68	GCGCGCTGCGTCTCTGTCGCGCAGTGGGAGAGCCCTGCGCCCGCCAGCCCGCGATGCC	127
DB	61	GCGCGCTGCGTCTCTGTCGCGCAGTGGGAGAGCCCTGCGCCCGCCAGCCCGCGATGCC	120
QY	128	GCGCGTGGCCAGTTCGTCGCGCAGTGGGAGAGCCCTGCGCCCGCCAGCCCGCGATGCC	187
DB	121	GCGCGTGGCCAGTTCGTCGCGCAGTGGGAGAGCCCTGCGCCCGCCAGCCCGCGATGCC	180
QY	188	GGACCCGCGCGCTTCCGCGCGCTGGTGGCCAGTGGTGTGCTGCGCTGGGAGCGC	247
DB	181	GGACCCGCGCGCTTCCGCGCGCTGGTGGCCAGTGGTGTGCTGCGCTGGGAGCGC	240
QY	248	ACGCGCGCGCGCTTCCGCGCGCTGGTGGCCAGTGGTGTGCTGCGCTGGGAGCGC	307
DB	241	ACGCGCGCGCGCTTCCGCGCGCTGGTGGCCAGTGGTGTGCTGCGCTGGGAGCGC	300
QY	308	CCGAGTGTGAGAGGCTGTGAGAGCGCGCGCGAGAGAGTGTGCTGCGCTGGGAGCGC	367
DB	301	CCGAGTGTGAGAGGCTGTGAGAGCGCGCGCGAGAGAGTGTGCTGCGCTGGGAGCGC	360
QY	368	GCTGCTGAGAGCG	427
DB	361	GCTGCTGAGAGCG	420
QY	428	CTGCGCCCAACACGCTGACCGACGCACTGCGCGCGAGAGCGCGCGCGCGCGCGCGCG	487
DB	421	CTGCGCCCAACACGCTGACCGACGCACTGCGCGCGAGAGCGCGCGCGCGCGCGCGCG	480
QY	488	CCGCGTGGGCGAGCAGCTGTGCTTCACTGTGCACTGCGCGCGCTTTTGTGCTGT	547
DB	481	CCGCGTGGGCGAGCAGCTGTGCTTCACTGTGCACTGCGCGCGCTTTTGTGCTGT	540
QY	548	GGCTCCCAAGTGGCTTACAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	607
DB	541	GGCTCCCAAGTGGCTTACAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	600
QY	608	TCAAGCG	667

DB	601	TCAAGCG	660
QY	668	CTGGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	727
DB	661	CTGGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	720
QY	728	GAGCG	787
DB	721	GAGCG	780
QY	788	TGCG	847
DB	781	TGCG	840
QY	848	GCGTGGACCGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	907
DB	841	GCGTGGACCGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	900
QY	908	CACCTCTTTTGAAGGTTGCGCTCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCG	967
DB	901	CACCTCTTTTGAAGGTTGCGCTCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCG	960
QY	968	GCACCAAGCG	1027
DB	961	GCACCAAGCG	1020
QY	1028	CCCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGCAAGAGAGCGAGCG	1087
DB	1021	CCCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGCAAGAGAGCGAGCG	1080
QY	1088	GCGCT	1147
DB	1081	GCGCT	1140
QY	1148	GACCATCTTTCTGTTTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1207
DB	1141	GACCATCTTTCTGTTTCAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1200
QY	1208	GCGCGAGCGCTACTGCGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1267
DB	1201	GCGCGAGCGCTACTGCGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1260
QY	1268	GTGCGCTTACGCGGTTCTCTCAAGAGCGCACTGCGCGCGCGCGCGCGCGCGCGCGCG	1327
DB	1261	GTGCGCTTACGCGGTTCTCTCAAGAGCGCACTGCGCGCGCGCGCGCGCGCGCGCGCG	1320
QY	1328	AGCGGTGTCTGTGCG	1387
DB	1321	AGCGGTGTCTGTGCG	1380
QY	1388	CACAGACCG	1447
DB	1381	CACAGACCG	1440
QY	1448	CGGCTTCTGCG	1507
DB	1441	CGGCTTCTGCG	1500
QY	1508	CAAGCAAGCGCGCTTCTCAAGAAACCAAGAACTCATCTCTCTGCGGAGAGCATGCCAA	1567
DB	1501	CAAGCAAGCGCGCTTCTCAAGAAACCAAGAACTCATCTCTCTGCGGAGAGCATGCCAA	1560
QY	1568	GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1627
DB	1561	GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA	1620
QY	1628	GAGCCAGAGGTTGCTGTGTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1687
DB	1621	GAGCCAGAGGTTGCTGTGTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	1680
QY	1688	CAAGTCTCTGACCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	1747
DB	1681	CAAGTCTCTGACCTGCTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	1740

QY 1748 TGTACGAGAGACCACTTTCAAAAGACAGGCTTTTCTACCGGAAGTGTCTGAG 1807
Db 1741 TGTACGAGAGACCACTTTCAAAAGACAGGCTTTTCTACCGGAAGTGTCTGAG 1800
QY 1808 CAAGTGCAGAGCATTTGAAATCAGACAGCACTTGAAGAGGTGAGCTGGGAGCTGTC 1867
Db 1801 CAAGTGCAGAGCATTTGAAATCAGACAGCACTTGAAGAGGTGAGCTGGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGCCCGCTGTGACTGACGTCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTGAGCAGCATCGGGAAGCCAGCCCGCTGTGACTGACGTCAGACTCCG 1920
QY 1928 CTTTCATCCCAAGCCTGAGCGGCTGCGGCGATTGTGAACATGACTACGTCGTGGAGC 1987
Db 1921 CTTTCATCCCAAGCCTGAGCGGCTGCGGCGATTGTGAACATGACTACGTCGTGGAGC 1980
QY 1988 CAGAACGTTCCGAGAGAAAGAGGGCCGAGCGCTCTCACTCGAGGGTGAAGCACTGTT 2047
Db 1981 CAGAACGTTCCGAGAGAAAGAGGGCCGAGCGCTCTCACTCGAGGGTGAAGCACTGTT 2040
QY 2048 CAGCGTGTCAACTACGAGCGGGCGCGCGCCCGCTCTGTGGCGCTCTGTGCTGG 2107
Db 2041 CAGCGTGTCAACTACGAGCGGGCGCGCGCCCGCTCTGTGGCGCTCTGTGCTGG 2100
QY 2108 CTTGAGCATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGTGGGGGCCAGAGCC 2167
Db 2101 CTTGAGCATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGTGGGGGCCAGAGCC 2160
QY 2168 GCGCGCTGAGCTGTA-----CATCCCCA 2191
Db 2161 GCGCGCTGAGCTGTA-----CATCCCCA 2220
QY 2192 GGAAGAGCTCACGAGGTTCATCGCCAGCATCATCAACCCAGAACACGTACTGCGTGC 2251
Db 2221 GGAAGAGCTCACGAGGTTCATCGCCAGCATCATCAACCCAGAACACGTACTGCGTGC 2280
QY 2252 TCGGTATGCCGTGTGTCAGAAAGGCCCGCCATGGGCACTCCGCAAGGCTTTCAAGAGCA 2311
Db 2281 TCGGTATGCCGTGTGTCAGAAAGGCCCGCCATGGGCACTCCGCAAGGCTTTCAAGAGCA 2340
QY 2312 AGTCTACGTCCAGTGCAGAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTCTGCA 2371
Db 2341 AGTCTACGTCCAGTGCAGAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGCTCTGCA 2400
QY 2372 GCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGGGGGATTCCGGCGGAGCGGCTGC 2431
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Db 2461 TCTGCGTTTGTGGATGATTTCTTGTGTGACACCTCACTCAACCCAGCAAAACCT 2520
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Db 2521 TCTCAGGAGCCCTGTGTCGAGGTGTCCTGAGTATGCTGCTGCTGTAAGTGGGAGA 2580
QY 2552 CAGTGTGTAACCTTCCCTGTAGAAGACGAGGCTTGGGTGGACAGGCTTTTGTTCAGATGC 2611
Db 2581 CAGTGTGTAACCTTCCCTGTAGAAGACGAGGCTTGGGTGGACAGGCTTTTGTTCAGATGC 2640
QY 2612 CGGCCCCAGGCTATTTCCCTGTGTCGAGGCTGCTGATACCCGAGCCCTGGAGGTGC 2671
Db 2641 CGGCCCCAGGCTATTTCCCTGTGTCGAGGCTGCTGATACCCGAGCCCTGGAGGTGC 2700
QY 2672 AGAGCACTACTCCAGCTATGCGGAGCCCTCCATCAGAGCCAGTCTCACTTCAACCGCG 2731
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Db 2761 GCTTCAAGGCTGGAGAAACATGCTGCAAACTCTTTGGGGTCTTGGCGCTGAAGTGC 2820

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Db 3001 GCTACTCCATCTGAAAGCCAGAACGAGGATGTGCTGGGGGCCAAGGGCGCGCCG 3060
QY 3032 GCCCTCTGCCCTCCGAGGCGGTGACGTGGCTGTGCAACCAAGCATCTCTGCTCAAGCTGA 3091
Db 3061 GCCCTCTGCCCTCCGAGGCGGTGACGTGGCTGTGCAACCAAGCATCTCTGCTCAAGCTGA 3120
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Db 3121 CTCGACACCGTGTACCTACGTGACCTCTGCGGTCTGAGAGACAGAGCCAGACGAC 3180
QY 3152 TGAAGTGGAAAGCTCCCGGGGACGACGCTGACCTGAGGCGCCAGCCAGCCGCGAC 3211
Db 3181 TGAAGTGGAAAGCTCCCGGGGACGACGCTGACCTGAGGCGCCAGCCAGCCGCGAC 3240
QY 3212 TGCCCTCAGACTTCAAGACCATCTGACTGATGAGCCACCCGCCACAGCCAGCCGAG 3271
Db 3241 TGCCCTCAGACTTCAAGACCATCTGACTGATGAGCCACCCGCCACAGCCAGCCGAG 3300
QY 3272 GCAAGACACGAGAGCCCTGTGACGCGGCTCTGACCTCCAGAGGAGGAGGCGGCCA 3331
Db 3301 GCAAGACACGAGAGCCCTGTGACGCGGCTCTGACCTCCAGAGGAGGAGGCGGCCA 3360
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Db 3361 CACCCAGGCGCGCACCGCTGGAGTCTGAGGCTGAGTGAAGTGTGCGCGAGCCTGCA 3420
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QY 3812 AAAAAAAAAA 3824
Db 3841 AAAAAAAAAA 3853

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Db 1321 CCCCAGACGCCGTGTGTGTCGGGGAGAGAGCCCCAGGGCTCTGTGGCGGCCCGAGG 1380
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Db 2308 ----- 2307
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Db 2521 TCAGGGCAAGTCTTACCTGAGTGGCAGGGATCCGCAAGGCTCCATCTCTCAAGC 2580
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QY 3803 AAAAAAAAAAAAAAAAAAAAAA 3824
DB 4021 AAAAAAAAAAAAAAAAAAAAAA 4042

RESULT 3
AAV22428
ID AAV22428 standard; cDNA; 4037 BP.
XX
AC AAV22428;
XX
DT 13-AUG-1998 (first entry)
XX
DE Human telomerase reverse transcriptase encoding cDNA refined sequence.
XX
KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis; prognosis;
XX cell proliferation; cancer; ageing; ribonucleoprotein; ss.
XX
OS Homo sapiens.
XX
FH Key 56..3454
FT CDS /tag= a
FT /product= "telomerase reverse transcriptase"
FT /note= "refined sequence"
XX
XX GB2317891-A.
XX PN
XX PD 08-APR-1998.
XX
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PF 01-OCT-1997; 97GB-00020890.
XX
PR 01-OCT-1996; 96US-00724643.
PR 18-APR-1997; 97US-00844419.
PR 25-APR-1997; 97US-00846017.
PR 06-MAY-1997; 97US-00851843.
PR 09-MAY-1997; 97US-00854050.
PR 14-AUG-1997; 97US-00911312.
PR 14-AUG-1997; 97US-00912951.
PR 14-AUG-1997; 97US-00915503.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Czech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;
PI Andrews WH;
XX
DR MPI; 1998-171633/16.
DR P-PSDB; AAW56113.
XX
XX Pure and recombinant human Telomerase Reverse Transcriptase and its
PT variants - are useful in the diagnosis, prognosis and treatment of cell
PT proliferation conditions especially cancer and ageing.
XX
XX Example 1; Fig 74; 387pp; English.
XX
CC The present sequence encodes human telomerase reverse transcriptase
CC (hTERT), which is a ribonucleoprotein. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods
XX
SQ Sequence 4037 BP; 682 A; 1362 C; 1275 G; 714 T; 0 U; 4 Other;

Query Match 93.4%; Score 3571; DB 2; Length 4037;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 3809; Conservative 4; Mismatches 4; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCTGCTGCTGCGACAGTGGAGAGCCCTGGCCCGGCCACCCCGGATGCC 67
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DB 61 GCGGCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGAGCCACTACCGGAGGTGCT 120
QY 128 GCCGTGGCCACGTTGCTGCGGCGCTGGGCGCCAGGGCTGGCGGCTGTGACGCGG 187
DB 121 GCCGTGGCCACGTTGCTGCGGCGCTGGGCGCCAGGGCTGGCGGCTGTGACGCGG 180
QY 188 GGAACCGGCGGCTTCCGCGCGCTGTGCGCAAGTGTGCTGTGCTGCGCGGAGCGC 247
DB 181 GGAACCGGCGGCTTCCGCGCGCTGTGCGCAAGTGTGCTGTGCTGCGCGGAGCGC 240
QY 248 ACGGCGGCGCGCGCGCGCGCGCTCTTCCGCGCAAGTGTGCTGTGCTGAGAGAGCTGTGCGC 307
DB 241 ACGGCGGCGCGCGCGCGCGCGCTCTTCCGCGCAAGTGTGCTGTGCTGAGAGAGCTGTGCGC 300
QY 308 CCGAGTGTGACAGAGCTGTGCGAGCGGCGCGCGGAGAAACGTTGCTGGCTTGGC 367
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Db 301 CCGAGTGTGACAGAGGCTGTGCGAGCGCGCGGAGAAAGCTGTGCTTCCGCTTCCG 360
QY 368 GCTGTGACGCGGCG 427
Db 361 GCTGTGACGCGGCG 420
QY 428 CCTGCCCAACACGCTGACCGGACGCTGCGGCGGAGCGGCGGCGGCGGCGGCGGCG 487
Db 421 CCTGCCCAACACGCTGACCGGACGCTGCGGCGGAGCGGCGGCGGCGGCGGCGG 480
QY 488 CCGCGTGGGCGACGAGCTGTGCTGTCACTGTGCGGACGCTGCGCGCTTGTGTGTGT 547
Db 481 CCGCGTGGGCGACGAGCTGTGCTGTCACTGTGCGGACGCTGCGCGCTTGTGTGTGT 540
QY 548 GCGTCCCAAGCTGCGGCTTACAGGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
Db 541 GCGTCCCAAGCTGCGGCTTACAGGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
QY 608 TCAGGCGG 667
Db 601 TCAGGCGG 660
QY 668 CTGGAACCATAGCGCTCAGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
Db 661 CTGGAACCATAGCGCTCAGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 728 GAGGCGCGGCGGCGAGTGCCAGCGGAGGTGCGGCGGCGGCGGCGGCGGCGGCGG 787
Db 721 GAGGCGCGGCGGCGAGTGCCAGCGGAGGTGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 788 TGCCCGCTGAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
Db 781 TGCCCGCTGAGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
QY 848 GCGTGAACCGAGTGAACGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 907
Db 841 GCGTGAACCGAGTGAACGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 900
QY 908 CACCTCTTTGAGGCTGCGCTCTCTGCGACGCGGCGGCGGCGGCGGCGGCGGCGG 967
Db 901 CACCTCTTTGAGGCTGCGCTCTCTGCGACGCGGCGGCGGCGGCGGCGGCGGCGG 960
QY 968 GCACCAAGCGGCG 1027
Db 961 GCACCAAGCGGCG 1020
QY 1028 CCGGCTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCAAGCGGCGGCGGCGG 1087
Db 1021 CCGGCTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCAAGCGGCGGCGGCGG 1080
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Db 1081 GCGCT 1140
QY 1148 GACCATCTTTCTGGGTTCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1207
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Db 1261 GTGCGGCGGCGGCTCTCTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1320
QY 1328 AGCGGCTGTCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1387
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Db 1381 CACAGACCGCGGCTGTGTGAGCTGTCTGCGGCGGCGGCGGCGGCGGCGGCGG 1440
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Db 1861 GGAAGCAGAGGTACAGGACGATCGGGAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1920
QY 1928 CTTATCCCGCAAGCTGACGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1987
Db 1921 CTTATCCCGCAAGCTGACGCGGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1980
QY 1988 CAGAACGTTCCGAGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2047
Db 1981 CAGAACGTTCCGAGAGAAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2040
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Db 2041 CAGCGTCTCAACTACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2100
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Db 2101 CTTGAGCATATCCACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2160
QY 2168 GCGGCGGCGGCTGTA-----CATCCCCCA 2191
Db 2161 GCGGCGGCGGCTGTA-----CATCCCCCA 2220
QY 2192 GGAAGGCTCAGGAGGTGATGCGGAGCATCAAAACCCAGAAACAGTACTGCGTGG 2251
Db 2221 GGAAGGCTCAGGAGGTGATGCGGAGCATCAAAACCCAGAAACAGTACTGCGTGG 2280
QY 2252 TCGGTATGCGGCTGTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2307
Db 2281 TCGGTATGCGGCTGTCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
QY 2308 ----- 2307
Db 2341 CGTCTTACCTTGACAGACCTCCAGCGGTAATGCGAGAGTTCTGCTCACTGACAG 2400
QY 2308 ----- 2307
Db 2401 GACCAAGCGGCTGAGGATGCGGCTGCTATCGAGCAGAGCTCTCTGTAATGAGGCC 2460
QY 2308 -----CG 2309
Db 2461 CAGTGGCTTTTGAAGCTTCTTCAAGCTTCAATGTGCCACCAAGCGGCTGCGCATCAGGG 2520

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QY 2310 CAAGTCTACGTCAGTGCAGGGGATCCCGAGGCTCCATCCTCTCCACGCTGCTG 2369
DB 2521 CAAGTCTACGTCAGTGCAGGGGATCCCGAGGCTCCATCCTCTCCACGCTGCTG 2580
QY 2370 CAGCTGTGTACGCGGACATGAGAAACAAGCTGTTTGGGGGATTCGGGGGACGGGCT 2429
DB 2581 CAGCTGTGTACGCGGACATGAGAAACAAGCTGTTTGGGGGATTCGGGGGACGGGCT 2640
QY 2430 GCTCTGCTGTGTGTGATGATTTCTGTGTGACACCTCACCTCACCCACGGGAAAC 2489
DB 2641 GCTCTGCTGTGTGTGATGATTTCTGTGTGACACCTCACCTCACCCACGGGAAAC 2700
QY 2490 CTTCTCAGGACCCCTGTCCGAGGTGTCCCTGAGTATGCTGCTGCTGTAACCTTGGGAA 2549
DB 2701 CTTCTCAGGACCCCTGTCCGAGGTGTCCCTGAGTATGCTGCTGCTGTAACCTTGGGAA 2760
QY 2550 GACAGTGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT 2609
DB 2761 GACAGTGTGAACTTCCCTGTAGAGACGAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT 2820
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DB 2821 GCCGGCCCAACGGCTATTTCCCTGTGTGCGGCTGTGCTGTGATACCCGAGCCCTGAGGT 2880
QY 2670 GCAGAGGCACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2729
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QY 2730 CGGCTTCAAGGCTGGGAGGAGAACATGCGTCCGAACTCTTTGGGGTCTTGGCGTGAAGTG 2789
DB 2941 CGGCTTCAAGGCTGGGAGGAGAACATGCGTCCGAACTCTTTGGGGTCTTGGCGTGAAGTG 3000
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DB 3001 TCACAGCTGTTTCTGATTTGAGGTGAACAGCCCTCCAGACGGTGTGACCAACATCTA 3060
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DB 3061 CAAGATCTCTCTGCTGAGGCGGTACAGGTTTCAACGATGTGTGCTGAGCTCCCATTTCA 3120
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DB 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACACGCGCTCCCT 3180
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QY 3030 CGGCTCTGCTGCTCCGAGGCGGTGAGTGTGCTGTGCAACCAAGCATTCCTGCTCAAGCT 3089
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DB 3301 GACTGACACCGTGTACCTACGTCGCTACTCTGCGGTCACTCAGGACAGCCAGAGCGCA 3360
QY 3150 GCTGAGTCGGAAGCTCCCGGGGACGAGCTGACTGCTGGAAGCCGACGCAACCCGGC 3209
DB 3361 GCTGAGTCGGAAGCTCCCGGGGACGAGCTGACTGCTGGAAGCCGACGCAACCCGGC 3420
QY 3210 ACTGCCCTCAGACTTCAAGACCATCTCTGAGTGTGAGCCACCCGACAGCCAGGGCGGA 3269
DB 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGAGTGTGAGCCACCCGACAGCCAGGGCGGA 3480
QY 3270 GAGCAGACACGAGAGCCCTGTGTACGCGGGCTCTACGTCCAGGAGGAGGGGGCGGC 3329
DB 3481 GAGCAGACACGAGAGCCCTGTGTACGCGGGCTCTACGTCCAGGAGGAGGGGGCGGC 3540
QY 3330 CACACCCAGGCGCGGACCGCTGGAGATCTGAGGCGCTGAGTGTGTTGGCGGAGGCGCTG 3389
DB 3541 CACACCCAGGCGCGGACCGCTGGAGATCTGAGGCGCTGAGTGTGTTGGCGGAGGCGCTG 3600
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QY 3390 CATGTCGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGCT 3449
DB 3601 CATGTCGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGCT 3660
QY 3450 GAGTGTCCAGACACACCTGCGCTTCTCACTTCCCAACAGGCTGCGCTCCACCCCA 3509
DB 3661 GAGTGTCCAGACACACCTGCGCTTCTCACTTCCCAACAGGCTGCGCTCCACCCCA 3720
QY 3510 GGGCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCAATCC 3569
DB 3721 GGGCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCAATCC 3780
QY 3570 CCAAGTTCGCAATTTGTTACCCCTGCGCTGCGCTGCTTGTGCTTCCACCCCAACATCC 3629
DB 3781 CCAAGTTCGCAATTTGTTACCCCTGCGCTGCGCTGCTTGTGCTTCCACCCCAACATCC 3840
QY 3630 AGGTGAGACCCCTGAGAGAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGTGTG 3689
DB 3841 AGGTGAGACCCCTGAGAGAGACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGTGTG 3900
QY 3690 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCTGTGCTCAAAATGGGGG 3749
DB 3901 CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCTGTGCTCAAAATGGGGG 3960
QY 3750 GAGTGTCTGTGGAGTAATAATGATATATAGTATTTTCACTTTGAAAAAATAAATAA 3809
DB 3961 GAGTGTCTGTGGAGTAATAATGATATATAGTATTTTCACTTTGAAAAAATAAATAA 4020
QY 3810 AAAAAAAAAAAAAA 3824
DB 4021 AAAAAAAAAAAAAA 4035
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RESULT 4
AAV60320
ID AAV60320 standard, cDNA; 4023 BP.
XX
AC AAV60320;
XX
DT 04-DEC-1998 (first entry)
XX
DE Human telomerase gene referred to as hEST2.
XX
KW Catalytic subunit; human; telomerase; telomere maintenance; diagnosis;
KW treatment; cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 59..3458
FT /tag= a
XX
PN WO9837181-A2.
XX
PD 27-AUG-1998.
XX
PF 20-FEB-1998; 98WO-US003404.
XX
PR 20-FEB-1997; 97US-0038750P.
PR 20-MAY-1997; 97US-0047151P.
PR 01-AUG-1997; 97US-0054549P.
PR 14-AUG-1997; 97US-0055762P.
PR 30-OCT-1997; 97US-0064322P.
XX
PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Counter CM, Meyerson M, Weinberg RA;
XX
DR MPI; 1998-495367/42.
XX
DR P-PSDB; AAW71376.
XX
PT New isolated human telomerase catalytic sub-unit gene - used to develop
PT products for increasing or reducing the life span of cells such as cancer
```


PT cells or transformed cells.

XX Claim 5; Fig 5A-B; 96bp; English.

XX The present sequence encodes the catalytic subunit of a human telomerase
PS holoenzyme. Disruption of the telomerase gene alters telomere
CC maintenance. The DNA is essential for telomerase activity, and the
CC protein is physically associated with telomerase and a constituent of
CC active telomerase complex. The products can be used for increasing or
CC reducing the lifespan of cells such as cancer cells or transformed cells.
CC They can also be used in the diagnosis and treatment of malignancies. In
CC addition, cells with a longer lifespan can be transplanted into or
CC grafted onto an individual (e.g. as skin grafts, as systems for delivery
CC of therapeutic proteins, such as hormones and enzymes), to whom they
CC provide therapeutic benefit

XX Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 U; 0 Other;

Query Match 93.2%; Score 3563.8; DB 2; Length 4023;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 3803; Conservative 0; Mismatches 2; Indels 218; Gaps 2;

QY 5 CAGGACGCGCTGCGTCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 64
DB 1 CAGGACGCGCTGCGTCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 60
QY 65 GCCCGCGCTGCGTCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 124
DB 61 GCCCGCGCTGCGTCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 120
QY 125*GCTGCGCTGCGTCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 184
DB 121 GCTGCGCTGCGTCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 180
QY 185 CGGAGACCCCGCGCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 244
DB 181 CGGAGACCCCGCGCTGTCGCGACAGTGGAGAGCCCTGGCCCGCCACCCCGCGAT 240
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DB 361 GCGCGTGTGTCGAGAGTGTGCGAGCGCGCGAGAGAGAGTGTGCTGCGCTT 420
QY 425 CTACCTGCGCGACAGTGTGTCGAGCGCGCGAGAGAGAGTGTGCTGCGCTT 484
DB 421 CTACCTGCGCGACAGTGTGTCGAGCGCGCGAGAGAGAGTGTGCTGCGCTT 480
QY 485 GCGCGTGTGTCGAGAGTGTGTCGAGCGCGCGAGAGAGAGTGTGCTGCGCTT 544
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QY 545 GGTGGCTCCAGTGTGCGCTTACAGTGTGCGAGCGCGCGAGAGAGTGTGCTGCGCTT 604
DB 541 GGTGGCTCCAGTGTGCGCTTACAGTGTGCGAGCGCGCGAGAGAGTGTGCTGCGCTT 600
QY 605 CACTCAGGCG 664
DB 601 CACTCAGGCG 660
QY 665 GGCCTGGAACATAGCGTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 724
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QY 725 GAGGAGGCG 784
DB 721 GAGGAGGCG 780

QY 785 CGTGGCTCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 844
DB 781 CGTGGCTCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 845 GACGCGTGAACGAGTGAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 904
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QY 905 AGCCACTCTTTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 964
DB 901 AGCCACTCTTTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 965 CCAGCACACG 1024
DB 961 CCAGCACACG 1020
QY 1025 TCCCGCGTGTAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1084
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QY 1085 GCGGCGCT 1144
DB 1081 GCGGCGCT 1140
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DB 1741 TTATGTACGAGACCAAGTTTCAAAAGACAGAGCTCTTTTCTACCGAAGAGTGTG 1800
QY 1805 GAGCAAGTGTCAAGCATTTGAATCAGACAGCACTTGAAGAGGCGAGCTGCGGAGCT 1864
DB 1801 GAGCAAGTGTCAAGCATTTGAATCAGACAGCACTTGAAGAGGCGAGCTGCGGAGCT 1860

QY	1865	GTCCGAAGCAGAGGTCAGGACGATCGGGAAAGCCAGGCCCTCTGTCGACGTCCAGACT	1924
Db	1861	GTCCGAAGCAGAGGTCAGGACGATCGGGAAAGCCAGGCCCTCTGTCGACGTCCAGACT	1920
QY	1925	CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGG	1984
Db	1921	CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGG	1980
QY	1985	AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACT	2044
Db	1981	AGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACT	2040
QY	2045	GTTACGCGTCTCAACTACAGAGCGGGCGCGCCCGCCCTCTGGGCGCTCTGTGCT	2104
Db	2041	GTTACGCGTCTCAACTACAGAGCGGGCGCGCCCGCCCTCTGGGCGCTCTGTGCT	2100
QY	2105	GGGCGCTGACGATATCCAGAGGCTGCGCACCTTCGTCTGCTGTGCGGCGCCAGAA	2164
Db	2101	GGGCGCTGACGATATCCAGAGGCTGCGCACCTTCGTCTGCTGTGCGGCGCCAGAA	2160
QY	2165	CCCGCGCCTGAGCTGTA-----CATCCC	2188
Db	2161	CCCGCGCCTGAGCTGTA-----CATCCC	2220
QY	2189	CCAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAAAAGGAGAACAGTACTGCGT	2248
Db	2221	CCAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAAAAGGAGAACAGTACTGCGT	2280
QY	2249	GCGTCGGTATGCCGTGGTCCAGAGAAGCGCGCCCATGGGCAAGTCCGCAAGGCTTCAAG-	2307
Db	2281	GCGTCGGTATGCCGTGGTCCAGAGAAGCGCGCCCATGGGCAAGTCCGCAAGGCTTCAAG-	2340
QY	2308	-----	2307
Db	2341	CCACGTCTTACTTGACAGACCTCCAGCCGTACATGCCAGAGTTCGTGGCTCACCTGCA	2400
QY	2308	-----	2307
Db	2401	GGAGACCAAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGC	2460
QY	2308	-----	2307
Db	2461	CAGCAGTGGCCTCTTCAGCCTCTTCTACGCTTCATGTGCCAACAGCCGTGCGCATCAG	2520
QY	2308	-----	2307
Db	2521	GGGCAAGTCCCTACGTCAGTCCAGGCCAGGGGATCCCGCAGGGCTCATCCTCTCCACGCTGCT	2580
QY	2367	CTGCAGCCTGTGCTACGCGGCAATGAGAAACAAGCTGTTGCGGGATTGCGCGGGAAGG	2426
Db	2581	CTGCAGCCTGTGCTACGCGGCAATGAGAAACAAGCTGTTGCGGGATTGCGCGGGAAGG	2640
QY	2427	GCTGCTCCTGCGTTTGTGAGATATTCTTGTGTGACACTCACTCAACCCACGCGAA	2486
Db	2641	GCTGCTCCTGCGTTTGTGAGATATTCTTGTGTGACACTCACTCAACCCACGCGAA	2700
QY	2487	AACCTTCCTCAGGACCTCGTCCGAGGTGTCCTCTGAGTATGGCTGCGTGAACCTTGG	2546
Db	2701	AACCTTCCTCAGGACCTCGTCCGAGGTGTCCTCTGAGTATGGCTGCGTGAACCTTGG	2760
QY	2547	GAAGACAGTGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGCGTTTGTCA	2606
Db	2761	GAAGACAGTGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGCGTTTGTCA	2820
QY	2607	GATGCCGGCCCAAGGCTATTTCCCTGCTGTGCGGCGCTGCTGCTGATACCCGAGCCCTGGA	2666
Db	2821	GATGCCGGCCCAAGGCTATTTCCCTGCTGTGCGGCGCTGCTGCTGATACCCGAGCCCTGGA	2880
QY	2667	GGTGCAGAGCGCACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAA	2726
Db	2881	GGTGCAGAGCGCACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAA	2940
QY	2727	CCCGCGCTTCAAGGCTGGAGGAAACATGCGTCGCAAACTTTTGGGCTCTTGGCGCTGAA	2786

Db	2941	CCGGGCTTCAAGGCTGGGAGGAACATGCGTGGAACTCTTGGGGTCTTGGGGCTGAA	3000
QY	2787	GTGTACAGCCTGTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGACCAACAT	2846
Db	3001	GTGTACAGCCTGTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGACCAACAT	3060
QY	2847	CTACAAGATCCTCTGCTGCAGGCGTACAGTTTCAACGATGTGTGCTGCAGTCCCAT	2906
Db	3061	CTACAAGATCCTCTGCTGCAGGCGTACAGTTTCAACGATGTGTGCTGCAGTCCCAT	3120
QY	2907	TCATCAGCAAGTTTGAAGAACCACATTTTCTCTGCGCTCATCTCTGACAACGGCTC	2966
Db	3121	TCATCAGCAAGTTTGAAGAACCACATTTTCTCTGCGCTCATCTCTGACAACGGCTC	3180
QY	2967	CCTCTGCTACTCCATCTCTGAAAAGCCAGAAGGATGTGCTGGGGGCCAAGGGCGC	3026
Db	3181	CCTCTGCTACTCCATCTCTGAAAAGCCAGAAGGATGTGCTGGGGGCCAAGGGCGC	3240
QY	3027	CGCCGGCCCTCTGCGCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCA	3086
Db	3241	CGCCGGCCCTCTGCGCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCA	3300
QY	3087	GCTGACTCGACACCCGTGTCACTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGAC	3146
Db	3301	GCTGACTCGACACCCGTGTCACTACGTGCCACTCTCTGGGGTCACTCAGGACAGCCAGAC	3360
QY	3147	GCAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGAGGCGCGACGCCAACCC	3206
Db	3361	GCAGCTGAGTCGGAAGCTCCCGGGACGACGCTGACTGCCCTGAGGCGCGACGCCAACCC	3420
QY	3207	GGCACTGCCCTCAAGCTTCAAGACCATCTGGACTGATGGCCACCCGCCACAGCCAGGC	3266
Db	3421	GGCACTGCCCTCAAGCTTCAAGACCATCTGGACTGATGGCCACCCGCCACAGCCAGGC	3480
QY	3267	CGAGAGCAGACACCAAGCAGCCCTGTCAAGCCGGCTCTACGTCCAGGAGGAGGGGCG	3326
Db	3481	CGAGAGCAGACACCAAGCAGCCCTGTCAAGCCGGCTCTACGTCCAGGAGGAGGGGCG	3540
QY	3327	GCCCCACACCCAGGCCGCAACCGCTGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGC	3386
Db	3541	GCCCCACACCCAGGCCGCAACCGCTGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGC	3600
QY	3387	CTGCATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCTTGAGCGAGTGTCCAGCCAAAG	3446
Db	3601	CTGCATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCTTGAGCGAGTGTCCAGCCAAAG	3660
QY	3447	GCTGAGTGTCCAGCACACCTGCGCTTCTCACTTCCCCACAGGCTGGCGCTCGGCTCCACC	3506
Db	3661	GCTGAGTGTCCAGCACACCTGCGCTTCTCACTTCCCCACAGGCTGGCGCTCGGCTCCACC	3720
QY	3507	CCAGGGCCAGCTTTCCTCACCAGGAGGCCGGCTTCCACTCCCCACATAGGAATAGTCCA	3566
Db	3721	CCAGGGCCAGCTTTCCTCACCAGGAGGCCGGCTTCCACTCCCCACATAGGAATAGTCCA	3780
QY	3567	TCCCCAGATTGCGCCATTGTTCACCCCTCGCCCTGCCCCCTCTTGTGCTTCCACCCCCACA	3626
Db	3781	TCCCCAGATTGCGCCATTGTTCACCCCTCGCCCTGCCCCCTCTTGTGCTTCCACCCCCACA	3840
QY	3627	TCCAGGTGAGAGCCCTGAGAAAGAACCTTGGGAGCTCTGGGAATTTGAGTGAACCAAGGT	3686
Db	3841	TCCAGGTGAGAGCCCTGAGAAAGAACCTTGGGAGCTCTGGGAATTTGAGTGAACCAAGGT	3900
QY	3687	GTGCCCTGTACACAGCGGAGGAGCCCTGACACCTGGATGGGGGTCCCTGTGGGTCAAAATTGG	3746
Db	3901	GTGCCCTGTACACAGCGGAGGAGCCCTGACACCTGGATGGGGGTCCCTGTGGGTCAAAATTGG	3960
QY	3747	GGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAIAAAAAAAA	3806
Db	3961	GGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAIAAAAAAAA	4020
QY	3807	AAA 3809	

D	b		1279	CAGTGCCTTAACGGGGTGCTCCTCAAGACGCACTGCCCCGTGGAGCTGCGGTCAACCCA	1338
O	y		1326	GCAGCCGGTGTCTGTGCCCGGAGAAGCCCAGGGCTCTGTGGCGCCCCCGAGAGAG	1385
D	b		1339	GCAGCCGGTGTCTGTGCCCGGAGAAGCCCAGGGCTCTGTGGCGCCCCCGAGAGAG	1398
O	y		1386	GACAAGAACCCCCGTGCTGTGTCAGCTGTCCGCGAAGACAGACCCTTGCAAGTg	1445
D	b		1399	GACAAGAACCCCCGTGCTGTGTCAGCTGTCCGCGAAGACAGACCCTTGCAAGTg	1458
O	y		1446	TACGGCTTGTGCGGGCTGCTGCGCCGGCTGTGCCCCAGGCTCTGGGCTCCAGG	1505
D	b		1459	TACGGCTTGTGCGGGCTGCTGCGCCGGCTGTGCCCCAGGCTCTGGGCTCCAGG	1518
O	y		1506	CACAACGAACGCCGCTTCTCTAGAAACACCAAGATTCACTCCCTGGGGAAGCATGCC	1565
D	b		1519	CACAACGAACGCCGCTTCTCTAGAAACACCAAGATTCACTCCCTGGGGAAGCATGCC	1578
O	y		1566	AAGCTCTCGCTGACAGAGCTGACGTGAAGATGAGCGTGGGGAAGCTGCGCTTGCTGCC	1625
D	b		1579	AAGCTCTCGCTGACAGAGCTGACGTGAAGATGAGCGTGGGGAAGCTGCGCTTGCTGCC	1638
O	y		1626	AGAGCCCCAGGGGTGTGCTGTCTCCGCGCGAGAGCACCGTCTGCGTAGAGATCTTG	1685
D	b		1639	AGAGCCCCAGGGGTGTGCTGTCTCCGCGCGAGAGCACCGTCTGCGTAGAGATCTTG	1698
O	y		1686	GCCAAGTTCTGCACTGGCTGATGATGTGTACTGCTGTGAGCTGCTCAGGCTTTCTTT	1745
D	b		1699	GCCAAGTTCTGCACTGGCTGATGATGTGTACTGCTGTGAGCTGCTCAGGCTTTCTTT	1758
O	y		1746	TATGTACCGAGAGACCAAGTTTCAAAGAACAAGGCTTTTTCTAACCGAAGAGTGTCTGG	1805
D	b		1759	TATGTACCGAGAGACCAAGTTTCAAAGAACAAGGCTTTTTCTAACCGAAGAGTGTCTGG	1818
O	y		1806	AGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGGAGCTG	1865
D	b		1819	AGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGGAGCTG	1878
O	y		1866	TCGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCTGCTGACGTCCAGACTC	1925
D	b		1879	TCGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCTGCTGACGTCCAGACTC	1938
O	y		1926	CGCTTCATCCCCAAGCCTGACGGGCTGCGCCGATTGTGAACATGACTACGTGTGGGA	1985
D	b		1939	CGCTTCATCCCCAAGCCTGACGGGCTGCGCCGATTGTGAACATGACTACGTGTGGGA	1998
O	y		1986	GCCAGAAGCTTCCGCAAGAAAAGAGGGCCGAGCGTCTCACTCGAGGTGAAGCACTG	2045
D	b		1999	GCCAGAAGCTTCCGCAAGAAAAGAGGGCCGAGCGTCTCACTCGAGGTGAAGCACTG	2058
O	y		2046	TTACAGCTGCTCAACTACGAGCGGGCGCGCCCGGCTCTTGAGCGCTGTGTCTG	2105
D	b		2059	TTACAGCTGCTCAACTACGAGCGGGCGCGCCCGGCTCTTGAGCGCTGTGTCTG	2118
O	y		2106	GGCTTGACGATATCAAGAGGGCTTGCGCACTTGTGTGCTGTGCGGCCAGAGAC	2165
D	b		2119	GGCTTGACGATATCAAGAGGGCTTGCGCACTTGTGTGCTGTGCGGCCAGAGAC	2178
O	y		2166	CCGCGCGCTGAGCTGA-----CATCCCC	2189
D	b		2179	CCGCGCGCTGAGCTGA-----CATCCCC	2238
O	y		2190	CAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAACCCAGAACACGTACTGCGTG	2249
D	b		2239	CAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAACCCAGAACACGTACTGCGTG	2298
O	y		2250	CGTGGTATGCGGTGTCCAGAAAGCGCCCATGGGCAAGTCCGCAAGGCTTCAAGA--	2307
D	b		2299	CGTGGTATGCGGTGTCCAGAAAGCGCCCATGGGCAAGTCCGCAAGGCTTCAAGAAGC	2358
O	y		2308	-----	2307
D	b		2359	CACGCTCTACTTGACAGACCTCCAGCCGTACTGCGACAGTTCGTGGCTCACTCGACG	2418

QY	2308	-----	2307
Db	2419	GAGACCAGCCCGCTGAGGATGCCGTGTCATCGAGAGACTCTCCCTGAATGAGCC	2478
QY	2308	-----	2307
Db	2479	AGCAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCACGCCGTGCCATCAGG	2538
QY	2308	-----	2307
Db	2308	GGCAAGTCTTACGTCCAGTGGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTC	2367
Db	2539	GGCAAGTCTTACGTCCAGTGGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTC	2598
QY	2368	TGCAGCCTGTGCTACGGCGACATGAGAACAAAGCTTTGCGGGGATTGCGCGGACGGG	2427
Db	2599	TGCAGCCTGTGCTACGGCGACATGAGAACAAAGCTTTGCGGGGATTGCGCGGACGGG	2658
QY	2428	CTGCTCCTGCGTTTGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGGCAAA	2487
Db	2659	CTGCTCCTGCGTTTGTGGATGATTTCTTGTGTGACACCTCACCTCACCCACGGCAAA	2718
QY	2488	ACCTTCTCAGAGACCCTGTGTCGAGGTGTCCTGAGTATGCGTGCCTGTAACCTTTCGG	2547
Db	2719	ACCTTCTCAGAGACCCTGTGTCGAGGTGTCCTGAGTATGCGTGCCTGTAACCTTTCGG	2778
QY	2548	AAGACAGTGTGAACCTCCCTGTAGAGACGAGGCCCTGGGTGGACAGCTTTTGTTCAG	2607
Db	2779	AAGACAGTGTGAACCTCCCTGTAGAGACGAGGCCCTGGGTGGACAGCTTTTGTTCAG	2838
QY	2608	ATGCCGCCCCACGGCCTATTCCCTGTGTGCGGCTGTGCTGTGATACCCGAGCCCTGGAG	2667
Db	2839	ATGCCGCCCCACGGCCTATTCCCTGTGTGCGGCTGTGCTGTGATACCCGAGCCCTGGAG	2898
QY	2668	GTGAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAAC	2727
Db	2899	GTGAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAAC	2958
QY	2728	CGCGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTTGGGCTTTGCGGCTGAAG	2787
Db	2959	CGCGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTTGGGCTTTGCGGCTGAAG	3018
QY	2788	TGTACAGCCTGTTTCTGATTTGCAGGTGAACAGCCTCCAGACGGTGTGACCAACATC	2847
Db	3019	TGTACAGCCTGTTTCTGATTTGCAGGTGAACAGCCTCCAGACGGTGTGACCAACATC	3078
QY	2848	TACAAGATCCTCCTGCTGTCAGGCGTACAGTTTCAACGCATGTGTGCTGCACTCCATT	2907
Db	3079	TACAAGATCCTCCTGCTGTCAGGCGTACAGTTTCAACGCATGTGTGCTGCACTCCATT	3138
QY	2908	CATCAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGCGTCACTCTGAACAGGCTCC	2967
Db	3139	CATCAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGCGTCACTCTGAACAGGCTCC	3198
QY	2968	CTCTGCTACTTCATCTCTGAAGCCCAAGAACGCAAGGGATGTGCTGGGGGCCAAGGGCGCC	3027
Db	3199	CTCTGCTACTTCATCTCTGAAGCCCAAGAACGCAAGGGATGTGCTGGGGGCCAAGGGCGCC	3258
QY	3028	GCCGCGCCTCTGCCCCCTCCGAGGCCGTGCAATGGCTGTGCCACCAAGCAATTCCTGCTCAAG	3087
Db	3259	GCCGCGCCTCTGCCCCCTCCGAGGCCGTGCAATGGCTGTGCCACCAAGCAATTCCTGCTCAAG	3318
QY	3088	CTGACTCGAACCCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAAGACG	3147
Db	3319	CTGACTCGAACCCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAAGACG	3378
QY	3148	CAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGAGGCCGCAAGCCACCCG	3207
Db	3379	CAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGAGGCCGCAAGCCACCCG	3438
QY	3208	GCACTGCCCTCAGACTTCAAGACCAATCCTGGACTGATGGCCACCCGCGCCACAGCCAGGCC	3267
Db	3439	GCACTGCCCTCAGACTTCAAGACCAATCCTGGACTGATGGCCACCCGCGCCACAGCCAGGCC	3498

QY 3268 GAGAGCAGACACACAGACCCCTGTACAGCCCGGCTCTACGTCCAGGAGGAGGGGCGG 3327
Db 3499 GAGAGCAGACACACAGACCCCTGTACAGCCCGGCTCTACGTCCAGGAGGAGGGGCGG 3558
QY 3328 CCCACACACACAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCC 3387
Db 3559 CCCACACACAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCC 3618
QY 3388 TGCATGTCCGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGTGTCCAGCCAGGG 3447
Db 3619 TGCATGTCCGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGTGTCCAGCCAGGG 3678
QY 3448 CTGAGTGTCCAGACACCTGCGCTTCTCACTTCCACAGGCTGGGCTGCGCTCCACCC 3507
Db 3679 CTGAGTGTCCAGACACCTGCGCTTCTCACTTCCACAGGCTGGGCTGCGCTCCACCC 3738
QY 3508 CAGGGCCAGCTTTCTCTCAACAGAGAGCCGCTTCCACTCCCAATAGGATAGTCCAT 3567
Db 3739 CAGGGCCAGCTTTCTCTCAACAGAGAGCCGCTTCCACTCCCAATAGGATAGTCCAT 3798
QY 3568 CCCAGATTGCGCAATTGTTCACCCCTGCGCTTCCCTTGTGCTTCCACCCCAACCAT 3627
Db 3799 CCCAGATTGCGCAATTGTTCACCCCTGCGCTTCCCTTGTGCTTCCACCCCAACCAT 3858
QY 3628 CCAGGTGAGACCCCTGAGAGGAGCCCTGGAGCTCTGGAAATTTGAGTGAACCAAGGTG 3687
Db 3859 CCAGGTGAGACCCCTGAGAGGAGCCCTGGAGCTCTGGAAATTTGAGTGAACCAAGGTG 3918
QY 3688 TGCCCTGTACACAGGCGAGGAGCCCTGCACCTGGATGGGGTCCCTGTGGGTCAATTGGG 3747
Db 3919 TGCCCTGTACACAGGCGAGGAGCCCTGCACCTGGATGGGGTCCCTGTGGGTCAATTGGG 3978
QY 3748 GGGAGGTGCTGTGGAGTAATACTGATATATGAGTTTTCAGTTTGAAGAAAA 3804
Db 3979 GGGAGGTGCTGTGGAGTAATACTGATATATGAGTTTTCAGTTTGAAGAAAA 4035

RESULT 6
AAZ00724
ID AAZ00724 standard; DNA; 4015 BP.

XX AAZ00724;

DT 06-OCT-1999 (first entry)

XX Human telomerase catalytic domain DNA.

XX Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
XX body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
XX acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
XX breast cancer; ss.

OS Homo sapiens.

PN DE19804372-A1.

XX 05-AUG-1999.

PF 04-FEB-1998; 98DE-01004372.

XX 04-FEB-1998; 98DE-01004372.

XX (DAHM/) DAHM M W.

XX DAHM MW;

DR WPI; 1999-431408/37.

PT Quantifying tumor cells by amplifying mRNA encoding the catalytic subunit
PT of telomerase.

XX Example; Fig 1A-B; 26pp; German.

CC This invention describes a novel method for the quantitation of tumour
CC cells in a body fluid which comprises (1) enrichment or isolation of
CC tumour cells in the sample, (2) amplification of mRNA from these cells
CC that encodes the catalytic subunit of telomerase and (3) quantifying the
CC amount of amplified mRNA. The method is applied to tumour cells derived
CC from (micro)metastases, e.g. associated with a wide range of tumours such
CC as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia,
CC melanoma, pulmonary carcinoma, cancer of colon or breast etc. This
CC sequence encodes a human telomerase protein catalytic domain
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 93.1%; Score 3559; DB 2; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCGTCTGCTGCGACAGTGGGAAGCCCTGGCCCCGGCCACCCCGGATGCC 67
Db 1 GCAGCGCTGCGTCTGCTGCGACAGTGGGAAGCCCTGGCCCCGGCCACCCCGGATGCC 60
QY 68 GCGCGCTCCCGCTGCGGAGCCGTGCGTCTGCTGCGACAGCCACTACCGGAGGTGCT 127
Db 61 GCGCGCTCCCGCTGCGGAGCCGTGCGTCTGCTGCGACAGCCACTACCGGAGGTGCT 120
QY 128 GCGCGTGGCCACGTTCTGTCGCGCGCTGGGGCCCCCAAGGCTGGCGCTGCTGCAAGCGCG 187
Db 121 GCGCGTGGCCACGTTCTGTCGCGCGCTGGGGCCCCCAAGGCTGGCGCTGCTGCAAGCGCG 180
QY 188 GGAACCCGCGGCTTTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 181 GGAACCCGCGGCTTTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 248 ACGGCG 307
Db 241 ACGGCG 300
QY 308 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 301 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 368 GCTGCTGAGCGGCG 427
Db 361 GCTGCTGAGCGGCG 420
QY 428 CCGCGCCCAACAGCTGACCGGACGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGCG 487
Db 421 CCGCGCCCAACAGCTGACCGGACGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGCG 480
QY 488 CCGCGTGGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Db 481 CCGCGTGGCGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCCCAAGCTGCGCTTACCAAGTGTGCGGGCGCGCGCGCTGCTGCTGCTGCTGCTGCT 607
Db 541 GCGTCCCAAGCTGCGCTTACCAAGTGTGCGGGCGCGCGCGCTGCTGCTGCTGCTGCTGCT 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGAACCAATAGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db 661 CTGAACCAATAGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGGCGCGGCGCGAGTGCCAGCGGAGTCTGCGCTTGCACAGAGGCCAGGCGTGGCGG 787
Db 721 GAGGCGCGGCGCGAGTGCCAGCGGAGTCTGCGCTTGCACAGAGGCCAGGCGTGGCGG 780
QY 788 TGCCCTGAGCGCGGAGCGGAGCGCGCTTGGGCAAGGCGGCTGCTGCGGCGCGGAGGAG 847
Db 781 TGCCCTGAGCGCGGAGCGGAGCGCGCTTGGGCAAGGCGGCTGCTGCGGCGCGGAGGAG 840
QY 848 GCGTGAACGAGTGAACCGTGTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907

Db	841	GCGTGACCGAGTAGCCGTTGTTCTGTGTGTGTCACTGCGACAGCCCGGAAGAGC	900
QY	908	CACCTCTTTGAGGGTGCCTCTCTGGCAGCGCCACTCCACCATCCGTGGCGGCCA	967
Db	901	CACCTCTTTGAGGGTGCCTCTGTGGCAGCGCCACTCCACCATCCGTGGCGGCCA	960
QY	968	GCACCAACGCGGGCCCCCAATCCACATCGCGGCCACCAAGTCCCTGGGACACGCTTGTCC	1027
Db	961	GCACCAACGCGGGCCCCCAATCCACATCGCGGCCACCAAGTCCCTGGGACACGCTTGTCC	1020
QY	1028	CCCGGTGTACGCCGAGACCAAGCACTTCCCTCTACTCTCTAGGGGACAAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCCCTCTACTCTCTAGGGGACAAGAGCAGCTGCG	1080
QY	1088	GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGA	1140
QY	1148	GACCATCTTTCTGGGTCCAGGCCCTGAGATGCCAGGACTCCCGCAGGTTGCCCGCCT	1207
Db	1141	GACCATCTTTCTGGGTCCAGGCCCTGAGATGCCAGGACTCCCGCAGGTTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACCAACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACCAACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCACCCCAAC	1327
Db	1261	GTGCCCCCTACGGGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCACCCCAAC	1320
QY	1328	AGCCGCTGTCTGTGCCCCGGGAGAAAGCCCAAGGCTCTGTGCGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCCGCTGTCTGTGCCCCGGGAGAAAGCCCAAGGCTCTGTGCGGCCCCCGAGAGAGAGA	1380
QY	1388	CACAGACCCCCCGTGCCTGTGTCAGCTGTCCGACAGACAGACAGCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCCGTGCCTGTGTCAGCTGTCCGACAGACAGACAGCCCCCTGGCAGGTGA	1440
QY	1448	CGGCTTCGTGCGGACCTGCTGCGCGCGGCTGTTGCCCCAGGCTCTGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGACCTGCTGCGCGCGGCTGTTGCCCCAGGCTCTGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCTTCCCTCAGGAACACCAAGAATTCACTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCTTCCCTCAGGAACACCAAGAATTCACTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGACGAGAGCTGACCTGGAAAGATGAGCGTGCGGGACTGCGCTTGCGCAG	1627
Db	1561	GCTCTCGCTGACGAGAGCTGACCTGGAAAGATGAGCGTGCGGGACTGCGCTTGCGCAG	1620
QY	1628	GAGCCCCAGGGGTGGCTGTGTTCCGCCCGCAGAGACACCGTCTGCGTGAAGAGATCCTGGC	1687
Db	1621	GAGCCCCAGGGGTGGCTGTGTTCCGCCCGCAGAGACACCGTCTGCGTGAAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACCTGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGGAAGAGTGTCTGAG	1807
Db	1741	TGTCACGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGGAAGAGTGTCTGAG	1800
QY	1808	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCAGACATCGGGAAGCCAGGCCCGCTGCTGACGTCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCAGACATCGGGAAGCCAGGCCCGCTGCTGACGTCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGAGC	1987

D	b	1921	CTTCATCCCCAAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCTGTGGGAGC	1980
Q	Y	1988	CAGAACGTTCCGAGAGAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2047
D	b	1981	CAGAACGTTCCGAGAGAAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT	2040
Q	Y	2048	CAGCGTCTCAACTACGAGCGGGCGCGGCCCTCCTCGTGGCGCCTCTGTCTGGG	2107
D	b	2041	CAGCGTCTCAACTACGAGCGGGCGCGGCCCTCCTCGTGGCGCCTCTGTCTGGG	2100
Q	Y	2108	CCTGAGCAGATATCCACAGGGCCTGCGCACCTTCGTGCTGCGTGTGCGGGCCAGAACCC	2167
D	b	2101	CCTGAGCAGATATCCACAGGGCCTGCGCACCTTCGTGCTGCGTGTGCGGGCCAGAACCC	2160
Q	Y	2168	GCCGCGTGAAGTGA-----CATCCCCCA	2191
D	b	2161	GCCGCGTGAAGTGA-----CATCCCCCA	2220
Q	Y	2192	GGAAGAGCTCACGAGAGTTCATCGCCAGCATCATCAACCCAGAACACGTACTGCGTGG	2251
D	b	2221	GGACAGGCTCACGAGAGTTCATCGCCAGCATCATCAACCCAGAACACGTACTGCGTGG	2280
Q	Y	2252	TCCGTATGCCGTGTGTCAGAGAGCCGCCCATGGGCACTCCGCAAGGCTTCAAGA----	2307
D	b	2281	TCCGTATGCCGTGTGTCAGAGAGCCGCCCATGGGCACTCCGCAAGGCTTCAAGACCA	2340
Q	Y	2308	-----	2307
D	b	2341	CGTCTACTACTGACAGAACCTCCAGCCGTACATGCCACAGTTCGTGGCTCACCTGCAGGA	2400
Q	Y	2308	-----	2307
D	b	2401	GACCAGCCCGCTGAGGGAGTCCCGTCTCATGAGACAGAGCTCCTCCCTGAATGAGGCCAG	2460
Q	Y	2308	-----GG	2309
D	b	2461	CAGTGGCTCTTGACAGCTCTTCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGG	2520
Q	Y	2310	CAAGTCTTACGTCAGAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTG	2369
D	b	2521	CAAGTCTTACGTCAGAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTG	2580
Q	Y	2370	CAGCCTGTGCTACGCGGACATGAGAACAAAGCTGTTGCGGGATTCCGCGGACCGGCT	2429
D	b	2581	CAGCCTGTGCTACGCGGACATGAGAACAAAGCTGTTGCGGGATTCCGCGGACCGGCT	2640
Q	Y	2430	GCTCCTGCGTTGTGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAAAC	2489
D	b	2641	GCTCCTGCGTTGTGTGATGATTTCTGTGTGTGACACCTCACCTCACCCACGCGAAAAAC	2700
Q	Y	2490	CTTCCTCAGGACCTGTGTCGAGGTGTCCTGATATGCGTGCCTGTGTGAACCTGCGGAA	2549
D	b	2701	CTTCCTCAGGACCTGTGTCGAGGTGTCCTGATATGCGTGCCTGTGTGAACCTGCGGAA	2760
Q	Y	2550	GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGCACGGCTTTGTTCAGAT	2609
D	b	2761	GACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGCACGGCTTTGTTCAGAT	2820
Q	Y	2610	GCCGCCCCACGGCCTATTTCCCTGTGCGGCTGTGCTGATACCCGGAACCTGGAGGT	2669
D	b	2821	GCCGCCCCACGGCCTATTTCCCTGTGCGGCTGTGCTGATACCCGGAACCTGGAGGT	2880
Q	Y	2670	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2729
D	b	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940
Q	Y	2730	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	2789
D	b	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
Q	Y	2790	TACACGCTGTTTCTGGATTTCAGAGGTGAACAGCTCCAGACGGTGTGACCAACATCTTA	2849
D	b	3001	TACACGCTGTTTCTGGATTTCAGAGGTGAACAGCTCCAGACGGTGTGACCAACATCTTA	3060

QY	308	CCGAGTGTCTCAGAGAGGCTGTGCCAGCGCGGGCGCGGAAGA	CGTGCTGGCCTTCGCGCTTCGC	367
Db	301	CCGAGTGTCTCAGAGAGGCTGTGCCAGCGCGGGCGCGGAAGA	CGTGCTGGCCTTCGCGCTTCGC	360
QY	368	GCTGCTGGACCGGGCCCCCGGGGGGGCCCCCCCCGAGGCGCTT	CACCACCAAGCGTGCAGACTA	427
Db	361	GCTGCTGGACCGGGCCCCCGGGGGGGCCCCCCCCGAGGCGCTT	CACCACCAAGCGTGCAGACTA	420
QY	428	CCTGCCCAACACGCTGACCGACCGCACTGCGGGGGAGCGGGG	CGGTGGGCGTGTGCGGTGCTGCG	487
Db	421	CCTGCCCAACACGCTGACCGACCGCACTGCGGGGGAGCGGGG	CGGTGGGCGTGTGCGGTGCTGCG	480
QY	488	CCGCGTGGGCGACGACGCTGTGTTCACTGTCTGGCACGCTCG	CGCGCTCTTTGTGTGTGT	547
Db	481	CCGCGTGGGCGACGACGCTGTGTTCACTGTCTGGCACGCTCG	CGCGCTCTTTGTGTGTGT	540
QY	548	GGCTCCCAGCTGCGCCTAACAGGTGTGCGGGCGCGCGCTTAA	CAGACTCGGCGCTGCCAC	607
Db	541	GGCTCCCAGCTGCGCCTAACAGGTGTGCGGGCGCGCGCTTAA	CAGACTCGGCGCTGCCAC	600
QY	608	TCAAGCCCCGCCCCCGCCAACGCTAGTGGACCCCCGAAGCG	CTGGATGCCAACGGGCG	667
Db	601	TCAAGCCCCGCCCCCGCCAACGCTAGTGGACCCCCGAAGCG	CTGGATGCCAACGGGCG	660
QY	668	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCT	TGCCAGCCCCGGGTGCCAG	727
Db	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCT	TGCCAGCCCCGGGTGCCAG	720
QY	728	GAGGCGCGGGGGCAGTGTGCCAGCCGAAGTCTGCCGTTGCCA	AAGAGGCCCAAGCGGTGGCG	787
Db	721	GAGGCGCGGGGGCAGTGTGCCAGCCGAAGTCTGCCGTTGCCA	AAGAGGCCCAAGCGGTGGCG	780
QY	788	TGCCCCCTGAGCCCGAGCGGACGCCCGTTGGGCAAGGGTCT	TGGGCCCAACCCGGGCAAGAC	847
Db	781	TGCCCCCTGAGCCCGAGCGGACGCCCGTTGGGCAAGGGTCT	TGGGCCCAACCCGGGCAAGAC	840
QY	848	GCGTGGACCGAGTGACCGGTGTTCTGTGTGTGTCACTTGCA	GAGACCCGCGGAAGAAGC	907
Db	841	GCGTGGACCGAGTGACCGGTGTTCTGTGTGTGTCACTTGCA	GAGACCCGCGGAAGAAGC	900
QY	908	CACCTCTTTGAGGGGTGGCTCTCTGGCAGCGGCCACTTCCAC	CCCATCCGTGGGCGCGCA	967
Db	901	CACCTCTTTGAGGGGTGGCTCTCTGGCAGCGGCCACTTCCAC	CCCATCCGTGGGCGCGCA	960
QY	968	GCAACCAAGCGGGCCCCCCCCATTCCACATCGCGGCCACACG	TCCCTGGGACAAGCCTTGTCC	1027
Db	961	GCAACCAAGCGGGCCCCCCCCATTCCACATCGCGGCCACACG	TCCCTGGGACAAGCCTTGTCC	1020
QY	1028	CCCGGTGTACCGCCGAGACCAAGCACTTCTCTACTCTCTCA	GCGGACAAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACCGCCGAGACCAAGCACTTCTCTACTCTCTCA	GCGGACAAGAGCAGCTGCG	1080
QY	1088	GCCCTCCTTCTACTCAAGCTCTCTGAGGCCAGCGCTGACTGG	CGCTCGGAAGCTCGTGA	1147
Db	1081	GCCCTCCTTCTACTCAAGCTCTCTGAGGCCAGCGCTGACTGG	CGCTCGGAAGCTCGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACATCCC	CGAGTTGCCCGCGCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACATCCC	CGAGTTGCCCGCGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAATGCGGCCCTGTTCCTGGAAGT	GCTTTGGGAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAATGCGGCCCTGTTCCTGGAAGT	GCTTTGGGAACCAAGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTG	CGAGCTGCCGTACCCCAAGC	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTG	CGAGCTGCCGTACCCCAAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCCGGAGAGAAGCCCCAGGGCTCTGT	GCGGGCCCCCGGAGGAGAAGA	1387
Db	1321	AGCCGGTGTCTGTGCCCCGGAGAGAAGCCCCAGGGCTCTGT	GCGGGCCCCCGGAGGAGAAGA	1380

QY	1388	CACAGACCCCCCGCTGCTGTGTGACGCTGCTCCGCACAGACAGCAGCCCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCCCGCTGCTGTGTGACGCTGCTCCGCACAGACAGCAGCCCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCGTGCGGCGCTGCTGCTGCGCGCGGCTGTGCTCCGCCAGAGGCTCTGGGCGTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGCGCTGCTGCTGCGCGCGGCTGTGCTCCGCCAGAGGCTCTGGGCGTCCAGGCA	1500
QY	1508	CAACGAACGCCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAACATGCCAA	1567
Db	1501	CAACGAACGCCGCTTCTCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAACATGCCAA	1560
QY	1568	GCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGGTGCGGGACTGCCCTTGGCTGCCAG	1627
Db	1561	GCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGGTGCGGGACTGCCCTTGGCTGCCAG	1620
QY	1628	GAGCCACAGGGGTTGGCTGTGTTCGGGCGCAGAGCAACCGTCTGCGTGAAGATCTCTGGC	1687
Db	1621	GAGCCACAGGGGTTGGCTGTGTTCGGGCGCAGAGCAACCGTCTGCGTGAAGATCTCTGGC	1680
QY	1688	CAAGTTCCTGCACCTGCGCTGATGATGTGTGACGTGCTGAGCTGCTCAGGCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGCGCTGATGATGTGTGACGTGCTGAGCTGCTCAGGCTTTCTTTTA	1740
QY	1748	TGTACCGAGACACGTTTCAAAAAGAACAGGCTTTTCTACCCGAAGATGTCTGGAG	1807
Db	1741	TGTACCGAGACACGTTTCAAAAAGAACAGGCTTTTCTACCCGAAGATGTCTGGAG	1800
QY	1808	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGACGTCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGCTGACGTCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCAAGCCCGGCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCAAGCCCGGCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCTGGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCTGGGAGC	1980
QY	1988	CAGAACGTTCCCGCAGAGAAAGAGGGGCCGACGCTCTCACTCGAAGGTGAAGCACTGTT	2047
Db	1981	CAGAACGTTCCCGCAGAGAAAGAGGGGCCGACGCTCTCACTCGAAGGTGAAGCACTGTT	2040
QY	2048	CAGCGTGTCAACTACGAGCGGGCGCGGCCGCCCTCCTGCGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGGCCGCCCTCCTGCGGCGCTCTGTGCTGGG	2100
QY	2108	CCTGGAACGATATCCACAGGGGCTGCGGCACTTCTGTGCTGCTGCTGCGGGGCCAGGACCC	2167
Db	2101	CCTGGAACGATATCCACAGGGGCTGCGGCACTTCTGTGCTGCTGCTGCGGGGCCAGGACCC	2160
QY	2168	GCCGCGCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCGCTGAGCTGTACTTGTCAAGGTGATGTGACGGGCGGCTACGACACCATCCCCCA	2220
QY	2192	GGACAGGCTCAGGAGGTGTCATGCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2251
Db	2221	GGACAGGCTCAGGAGGTGTCATGCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2280
QY	2252	TGCGTATGCCGTGCTCAGAAAGCGGCCCATGGGCAAGTCCGCAAGGCTTCAAGA----	2307
Db	2281	TGCGTATGCCGTGCTCAGAAAGCGGCCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2308	-----	2307
Db	2341	CGTCTACTACTTGACAGACCTCCAGCGCTACATGCGACAGTTCGTGCTCACTGCAGGA	2400
QY	2308	-----	2307
Db	2401	GACCAGCCCGCTGAGGGATGCCGTGCTCATGAGCAGAGCTCCTCCTGAATGAGGCCAG	2460
QY	2308	-----GG	2309

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Db 2461 CAGTGGCCTCTTGAAGTCTTCTCAGCTTCAATGTGCCACCACGCGGTGCGCATCAGGGG 2520
QY 2310 CAAGTCTACGTCCAGTGCAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTGTG 2369
Db 2521 CAAGTCTACGTCCAGTGCAGGGGATCCCGAGGGCTCCATCCTCTCCACGCTGCTGTG 2580
QY 2370 CAGCTGTGTACGGGACATGAGAACAAAGTGTGCGGGGATGCGGGGAGCGGGCT 2429
Db 2581 CAGCTGTGTACGGGACATGAGAACAAAGTGTGCGGGGATGCGGGGAGCGGGCT 2640
QY 2430 GCTCCTGCGTTGTGATGATTTCTTGTGTGACACCTCACTCACTCACTCACTCACTCACT 2489
Db 2641 GCTCCTGCGTTGTGATGATTTCTTGTGTGACACCTCACTCACTCACTCACTCACTCACT 2700
QY 2490 CTTCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGCTGCGGTGTAAGTGTGCGGAA 2549
Db 2701 CTTCTCAGGACCTGTGTCGAGGTGTCCCTGAGTATGCTGCGGTGTAAGTGTGCGGAA 2760
QY 2550 GACAGTGTGAATTCCTGTAGAGACGAGGCTGCGGTGCGACGCGCTTTTGTTCAGAT 2609
Db 2761 GACAGTGTGAATTCCTGTAGAGACGAGGCTGCGGTGCGACGCGCTTTTGTTCAGAT 2820
QY 2610 GCGGCGCCACGCGCTATTCCTGTGTGTCGCGGTGCTGTGATACCCGGAACCTGAGGT 2669
Db 2821 GCGGCGCCACGCGCTATTCCTGTGTGTCGCGGTGCTGTGATACCCGGAACCTGAGGT 2880
QY 2670 GCAGAGCGACTACTCCAGCTATGCCCCGAGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2729
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCCGAGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
QY 2730 CGGCTTCAAGGCTGGGAGGAAACATGCGTCCGAAACTCTTTGGGGTCTTGGCGGCTGAAGTG 2789
Db 2941 CGGCTTCAAGGCTGGGAGGAAACATGCGTCCGAAACTCTTTGGGGTCTTGGCGGCTGAAGTG 3000
QY 2790 TCACAGCCTGTTTCTGGAATTTGCAAGGTGAACAGCCTCCAGAGCGGTGTGCAACCAATCTA 2849
Db 3001 TCACAGCCTGTTTCTGGAATTTGCAAGGTGAACAGCCTCCAGAGCGGTGTGCAACCAATCTA 3060
QY 2850 CAAGATCCTCCTGCTGAGAGGCGGTACAGGTTTACAGCATGTGTGCTGAGCTCCCATTTCA 2909
Db 3061 CAAGATCCTCCTGCTGAGAGGCGGTACAGGTTTACAGCATGTGTGCTGAGCTCCCATTTCA 3120
QY 2910 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACACGCGCTCCCT 2969
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACACGCGCTCCCT 3180
QY 2970 CTGCTACTCCATCTGAAAGCCCAAGAACGAGGATGTGCTGCGGCGCAAGGCGCGC 3029
Db 3181 CTGCTACTCCATCTGAAAGCCCAAGAACGAGGATGTGCTGCGGCGCAAGGCGCGC 3240
QY 3030 CGGCGCTCTGCGCTCCGAGGCGGTGAGTGTGTCACCAAGCATTCCTGCTCAAGCT 3089
Db 3241 CGGCGCTCTGCGCTCCGAGGCGGTGAGTGTGTCACCAAGCATTCCTGCTCAAGCT 3300
QY 3090 GACTGACACCGGTGACCTTACGTCGACCTGCGGTCACTCAAGGACAGCCAGAGCGCA 3149
Db 3301 GACTGACACCGGTGACCTTACGTCGACCTGCGGTCACTCAAGGACAGCCAGAGCGCA 3360
QY 3150 GCTGAGTGGAGGCTCCCGGGGAGCAGAGCTGACTGCCCTGAGAGCGCGCAACCCGCG 3209
Db 3361 GCTGAGTGGAGGCTCCCGGGGAGCAGAGCTGACTGCCCTGAGAGCGCGCAACCCGCG 3420
QY 3210 ACTGCCCTCAGACTTCAAGACCATCTGAGTATGAGCCACCCGCGCAAGCCAGAGCGCA 3269
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGTATGAGCCACCCGCGCAAGCCAGAGCGCA 3480
QY 3270 GAGCAGACACGAGCGCTGTACGCGCGGCTCTACGTCGCCAGGAGGAGGAGGCGCGC 3329
Db 3481 GAGCAGACACGAGCGCTGTACGCGCGGCTCTACGTCGCCAGGAGGAGGAGGCGCGC 3540
QY 3330 CACACCCAGGCGCGGCTGAGGAGTGTGAGGCTGAGTGTGTTGGCCGAGGCGCTG 3389
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Db 3541 CACACCCAGGCGCGGACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGGCGCTG 3600
QY 3390 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGGCGCT 3449
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGGCGCT 3660
QY 3450 GAGTGTCCAGACACCTGCGCTTCTCACTTCCCAACAGGCTGCGGCTGCGCTCCACCCCA 3509
Db 3661 GAGTGTCCAGACACCTGCGCTTCTCACTTCCCAACAGGCTGCGGCTGCGCTCCACCCCA 3720
QY 3510 GGGCCAGCTTTTCTCTCAACGAGAGCGCGGCTTCCACTCCCAATAGATAGTCCATCC 3569
Db 3721 GGGCCAGCTTTTCTCTCAACGAGAGCGCGGCTTCCACTCCCAATAGATAGTCCATCC 3780
QY 3570 CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTGCGCTCTTGTGCTTCCACCCCAACATCC 3629
Db 3781 CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTGCGCTCTTGTGCTTCCACCCCAACATCC 3840
QY 3630 AGGTGAGACCCCTGAGAAAGAACCCCTGGAGGCTGTGGAATTTGAGTGAACCAAGGTGTG 3689
Db 3841 AGGTGAGACCCCTGAGAAAGAACCCCTGGAGGCTGTGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3690 CCTGTACACAGCGCGAGGACCCCTGACCTGATGAGGCGGTCCCTGTGGGTCAAAATTGGGGG 3749
Db 3901 CCTGTACACAGCGCGAGGACCCCTGACCTGATGAGGCGGTCCCTGTGGGTCAAAATTGGGGG 3960
QY 3750 GAGGTGCTGTGGAGTAAATACTGAATATATGATTTTTCAGTTTGAATAAAAAA 3804
Db 3961 GAGGTGCTGTGGAGTAAATACTGAATATATGATTTTTCAGTTTGAATAAAAAA 4015

RESULT 8
AAZ30154
ID AAZ30154 standard; cDNA; 4015 BP.
XX
AC AAZ30154;
XX
DT 26-JAN-2000 (first entry)
XX
DE cDNA encoding a human telomerase reverse transcriptase (TRT).
XX
KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "telomerase reverse transcriptase"
XX
PN WO950392-A1.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US006898.
XX
PR 31-MAR-1998; 98US-0112006P.
XX
PA (GERO-) GERON CORP.
XX
PI Gaeta FCA;
XX
DR WPI; 1999-610845/52.
DR P-PSDB; AAY43621.
XX
PT Eliciting an in vivo immune response for prevention and treatment of
PT cancers.
XX
PS Disclosure; Fig 2; 26pp; English.
XX
CC The present sequence encodes a human telomerase reverse transcriptase
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CC (TRT) polypeptide. The protein is used in the method of the invention.
CC The specification describes a method for activating a T lymphocyte,
CC comprising contacting the T lymphocyte with a dendritic cell that
CC expresses a TRT peptide in the context of a MHC class I or MHC class II
CC molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TRT gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TRT or to TRT-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used for
CC eliciting an in vivo immune response to telomerase by activating a T
CC lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 93.1%; Score 3559; DB 2; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCTCTCTGCGCAGCTGGAGAGCCCTGAGCCACCCCGCGATGCC 67
Db 1 GCAGCGCTGCTCTCTGCGCAGCTGGAGAGCCCTGAGCCACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGCAGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGT 127
Db 61 GCGCGCTCCCGCTGCGCAGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGT 120
QY 128 GCGCGCTGCGCAGCTGCTGCGCGCGCTGCGCGCCCGCGCGCTGCGCGCGCG 187
Db 121 GCGCGCTGCGCAGCTGCTGCGCGCGCTGCGCGCCCGCGCGCTGCGCGCGCG 180
QY 188 GGAAGCGCGCGCTTCCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCG 247
Db 181 GGAAGCGCGCGCTTCCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
QY 248 ACG 307
Db 241 ACG 300
QY 308 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 301 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 368 GCTGCTGACAGCG 427
Db 361 GCTGCTGACAGCG 420
QY 428 CTTGCCCAACAGCTGACCGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db 421 CTTGCCCAACAGCTGACCGACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 488 CCGCGTGGCGCAGAGCTGTGCTTCACTGCTGCGACGCTGCGCGCTTTGTGCTGT 547
Db 481 CCGCGTGGCGCAGAGCTGTGCTTCACTGCTGCGACGCTGCGCGCTTTGTGCTGT 540
QY 548 GGTCTCCAGCTGCGCTACAGAGTGTGCGCGCGCGCGCTGTACAGCTGCGCGCTGCCAC 607
Db 541 GGTCTCCAGCTGCGCTACAGAGTGTGCGCGCGCGCGCTGTACAGCTGCGCGCTGCCAC 600
QY 608 TCAAGCG 667
Db 601 TCAAGCG 660
QY 668 CTGAACCATAGCTCAGAGAGCGCGCGCTCCCTGCGCGCTGCGAGCCCGCGGTGCGAG 727
Db 661 CTGAACCATAGCTCAGAGAGCGCGCGCTCCCTGCGCGCTGCGAGCCCGCGGTGCGAG 720
QY 728 GAGCG 787
Db 721 GAGCG 780
QY 788 TGCCCTGAGCGCGAGCGAGCGCGCGCTTGTGCGAGGGTCTGTGCGCGCGCGCGCGAGAC 847

Db 781 TGCCCTGAGCGCGAGCGAGCGCGCGCTTGTGCGAGGGTCTGTGCGCGCGCGCGAGAC 840
QY 848 GCGTGAACCGAGTACCGGTGTTTCTGTGTGTGTCACTGCGAGACCCCGCGAAGAGC 907
Db 841 GCGTGAACCGAGTACCGGTGTTTCTGTGTGTGTCACTGCGAGACCCCGCGAAGAGC 900
QY 908 CACTCTTTGAGGGTGGCTCTCTGCGACCGCGCACTCCACCCATCCGTGGCGCGCA 967
Db 901 CACTCTTTGAGGGTGGCTCTCTGCGACCGCGCACTCCACCCATCCGTGGCGCGCA 960
QY 968 GCAACACG 1027
Db 961 GCAACACG 1020
QY 1028 CCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTAGCGCGACAGAGAGAGCTGCG 1087
Db 1021 CCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTAGCGCGACAGAGAGAGCTGCG 1080
QY 1088 GCGCTCTCTCTACTCTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1147
Db 1081 GCGCTCTCTCTACTCTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
QY 1148 GACCATTTTCTGGTTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1207
Db 1141 GACCATTTTCTGGTTCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1208 GCGCGAGCGCTACTGGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Db 1201 GCGCGAGCGCTACTGGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGCGCTTACGCGGGTGTCTCTCAAGACGACGCGCGCGCGCGCGCGCGCGCGCGCG 1327
Db 1261 GTGCGCTTACGCGGGTGTCTCTCAAGACGACGCGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1328 AGCGGTGTCTGTGCG 1387
Db 1321 AGCGGTGTCTGTGCG 1380
QY 1388 CACAGACCCCGCTGCTGTGAGCTGCTCCGCGACACAGACGCGCGCGCGCGCGCGCG 1447
Db 1381 CACAGACCCCGCTGCTGTGAGCTGCTCCGCGACACAGACGCGCGCGCGCGCGCGCG 1440
QY 1448 CCGCTTCTGTGCG 1507
Db 1441 CCGCTTCTGTGCG 1500
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QY 1688 CAAGTTCTTGCACTGGCTGATGAGTGTATCGTGTGAGCTGCTCAGGTCTTTCTTTTA 1747
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QY 1748 TGTTCACGAGACCACTTTTCAAAAGACAGGCTTTTCTACCGGAAGAGTCTTGAG 1807
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QY 1808 CAAGTTGCAAGCATTTGAAATCAGACGACCTTGAAGAGGGTGAAGCTGCGGAGCTGTC 1867
Db 1801 CAAGTTGCAAGCATTTGAAATCAGACGACCTTGAAGAGGGTGAAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAAGGACATCGGGAAGCGAGCGCGCGCTGTGACGTTCAGACTCCG 1927

Db	1861	GGAGCAGAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCTGGAGC	1980
QY	1988	CAGACGTTCCGCAGAGAAAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCAGAGAAAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGCGCGGCCCGCCGCTCTGGGCGCCTCTGTCTGGG	2107
Db	2041	CAGCGTCTCAACTACGAGCGGCGCGGCCCGCCGCTCTGGGCGCCTCTGTCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCTGCGGCACCTTCGTGCTGCGTGTGCGGCCAGAACCC	2167
Db	2101	CCTGACGATATCCACAGGGCTGCGGCACCTTCGTGCTGCGTGTGCGGCCAGAACCC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACCATCCCCA	2220
QY	2192	GGAAGAGCTCACGGAGTCAATGCCACGATCATCAAAACCCAGAAACAGTACTGCGTGC	2251
Db	2221	GGAAGAGCTCACGGAGTCAATGCCACGATCATCAAAACCCAGAAACAGTACTGCGTGC	2280
QY	2252	TCCGTAATGCCGTGTGCCAAGAGGCCGCCATGGGCACGTTCGCAAGGCTTCAAG--	2307
Db	2281	TCCGTAATGCCGTGTGCCAAGAGGCCGCCATGGGCACGTTCGCAAGGCTTCAAGCCA	2340
QY	2308	-----	2307
Db	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTCACTGCAAGA	2400
QY	2308	-----	2307
Db	2401	GACCAAGCCCGCTGAGGGATGCGCTGTCATCGAGCAGACTCCTCCCTGAATGAGGCCAG	2460
QY	2308	-----	2309
Db	2461	CAGTGGCCTCTTGACGCTTCTCTACGCTTCATGTCGCCACAGCCGTGCGCATCAGGGG	2520
QY	2310	CAAGTCTTACGTCAGTCCAGTCCAGGGATCCCGCAGGCTCCATCCTCCACGCTCTCTG	2369
Db	2521	CAAGTCTTACGTCAGTCCAGTCCAGGGATCCCGCAGGCTCCATCCTCCACGCTCTCTG	2580
QY	2370	CAGCCTGTGCTACGGCGCATGAGAACAAAGCTGTTGCGGGGATTGCGCGGACGGGCT	2429
Db	2581	CAGCCTGTGCTACGGCGCATGAGAACAAAGCTGTTGCGGGGATTGCGCGGACGGGCT	2640
QY	2430	GCTCCTGCGTTTGTGTGATGATTTCTTGTGTGACACTCACCTCACCCAGCGAAAC	2489
Db	2641	GCTCCTGCGTTTGTGTGATGATTTCTTGTGTGACACTCACCTCACCCAGCGAAAC	2700
QY	2490	CTTCCTCAGGACCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGTGAATTGCGGAA	2549
Db	2701	CTTCCTCAGGACCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGTGAATTGCGGAA	2760
QY	2550	GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGCACGGCTTTTGTCAGAT	2609
Db	2761	GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGCACGGCTTTTGTCAGAT	2820
QY	2610	GCCGCCCCACGCGCTATTCCCTCTGTGTCGCGCTGTCTGTGATACCCGACCTGGAAGT	2669
Db	2821	GCCGCCCCACGCGCTATTCCCTCTGTGTCGCGCTGTCTGTGATACCCGACCTGGAAGT	2880
QY	2670	GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAATCTCACTTCAACCG	2729
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAATCTCACTTCAACCG	2940
QY	2730	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGGGGCTGAAGTG	2789
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGGGGCTGAAGTG	3000

QY	2790	TCACAGCCTGTTTCTGGAATTTGCAAGGTGAACAGCCTCCAGACCGGTGTGCAACCAATCTA	2843
Db	3001	TCACAGCCTGTTTCTGGAATTTGCAAGGTGAACAGCCTCCAGACCGGTGTGCAACCAATCTA	3060
QY	2850	CAAGATCCTCCTGCTGACAGGCGTACAGGTTTCAAGCATGTGTGCTGCAGCTCCCATTTCA	2909
Db	3061	CAAGATCCTCCTGCTGACAGGCGTACAGGTTTCAAGCATGTGTGCTGCAGCTCCCATTTCA	3120
QY	2910	TCAGCAAGTTTGGAGAAGACCCCAATTTTCTCGGCGTCATCTCTGACA CGGCTTCCT	2969
Db	3121	TCAGCAAGTTTGGAGAAGACCCCAATTTTCTCGGCGTCATCTCTGACA CGGCTTCCT	3180
QY	2970	CTGCTACTCCATCCTGGAAGAACCAAGAACGACGGATGTGCTGGGGGCCAAGGGCGCGC	3029
Db	3181	CTGCTACTCCATCCTGGAAGAACCAAGAACGACGGATGTGCTGGGGGCCAAGGGCGCGC	3240
QY	3030	CGGCCCTCTGCCCCCTCCGAGGCGCGTGACAGTGGCTGTGCCAACGACATTCTGCTCAAGCT	3089
Db	3241	CGGCCCTCTGCCCCCTCCGAGGCGCGTGACAGTGGCTGTGCCAACGACATTCTGCTCAAGCT	3300
QY	3090	GACTGCACACCGTGTCACTTACGTGCCACTCTGGGGTCACTCAGACAGCCAGACGCA	3149
Db	3301	GACTGCACACCGTGTCACTTACGTGCCACTCTGGGGTCACTCAGACAGCCAGACGCA	3360
QY	3150	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCAACCCGGC	3209
Db	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCAACCCGGC	3420
QY	3210	ACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCGCCACAGCCAGGCCGA	3269
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACCCGCGCCACAGCCAGGCCGA	3480
QY	3270	GAGCAGACACCAAGCAGCCCTGTCAAGCCGCGGCTTACGTCCAGAGGAGGGCGGCC	3329
Db	3481	GAGCAGACACCAAGCAGCCCTGTCAAGCCGCGGCTTACGTCCAGAGGAGGGCGGCC	3540
QY	3330	CACACCCAGGCGCCGCAACCGCTGGAGTCTGAGGCTGAGTGAATTTGGCCGAGGCCCTG	3389
Db	3541	CACACCCAGGCGCCGCAACCGCTGGAGTCTGAGGCTGAGTGAATTTGGCCGAGGCCCTG	3600
QY	3390	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3449
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3450	GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGTCCGCTCCACCCCA	3509
Db	3661	GAGTGTCCAGCACACCTGCGCTCTTCACTTCCCCACAGGCTGGCGTCCGCTCCACCCCA	3720
QY	3510	GGGCCAGCTTTTCTCTCACCAAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3569
Db	3721	GGGCCAGCTTTTCTCTCACCAAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3780
QY	3570	CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTGCCCTCCTTGTGCTTCCACCCCAACCATCC	3629
Db	3781	CCAGATTGCGCATTTGTTCAACCCCTGCGCCCTGCCCTCCTTGTGCTTCCACCCCAACCATCC	3840
QY	3630	AGGTGGAGACCTTGAGAAAGAACCTTGGGAGCTCTGGGAATTTGGAGTGAACCAAGGTGTG	3689
Db	3841	AGGTGGAGACCTTGAGAAAGAACCTTGGGAGCTCTGGGAATTTGGAGTGAACCAAGGTGTG	3900
QY	3690	CCCTGTACACAGCCGAGGACCCCTGCACTTGATGGGGTCCCTGTGGGTCAAAATTGGGGG	3749
Db	3901	CCCTGTACACAGCCGAGGACCCCTGCACTTGATGGGGTCCCTGTGGGTCAAAATTGGGGG	3960
QY	3750	GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAAAAA 3804	
Db	3961	GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAAAAA 4015	

RESULT	9
AAH45901	
ID	AAH45901 standard; DNA; 4015 BP.

Accession	Organism	Gene	Feature	Location/Qualifiers
AAH45901;				
XX AC	06-SEP-2001	(first entry)		
XX DT				
XX XX	Human hTERT gene.			
XX DE				
XX XX	Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;			
KM KM	detection; Delta-region; diagnosis; cancer; ds.			
XX XX				
OS	Homo sapiens.			
XX XX				
FH	Key			
FT	exon			Location/Qualifiers
FT				1..274
FT				/*tag= a
FT				/number= 1
FT	exon			275..1628
FT				/*tag= b
FT				/number= 2
FT	exon			1629..1824
FT				/*tag= c
FT				/number= 3
FT	exon			1825..2005
FT				/*tag= d
FT				/number= 4
FT	exon			2006..2185
FT				/*tag= e
FT				/number= 5
FT	exon			2186..2341
FT				/*tag= f
FT				/number= 6
FT	primer_bind			complement(2309..2325)
FT				/*tag= g
FT				/note= "primer SYC1076 (AAH45902) binding site"
FT	primer_bind			complement(2311..2325)
FT				/*tag= h
FT				/note= "primer SYC1118 (AAH45905) binding site"
FT	exon			2342..2437
FT				/*tag= i
FT				/number= 7
FT	misc_binding			complement(2345..2374)
FT				/*tag= j
FT				/bound_moiety= "hybridisation probe CS3"
FT				/note= "AAH45908"
FT	misc_binding			complement(2427..2456)
FT				/*tag= k
FT				/bound_moiety= "hybridisation probe CS12"
FT				/note= "AAH45906"
FT	exon			2438..2523
FT				/*tag= l
FT				/number= 8
FT	misc_binding			complement(2458..2487)
FT				/*tag= m
FT				/bound_moiety= "hybridisation probe CS1"
FT				/note= "AAH45907"
FT	primer_bind			2489..2506
FT				/*tag= n
FT				/note= "primer SYC1097 (AAH45904) binding site"
FT	exon			2524..2637
FT				/*tag= o
FT				/number= 9
FT	primer_bind			2615..2631
FT				/*tag= p
FT				/note= "primer SYC1078 (AAH45903) binding site"
FT	exon			2638..2709
FT				/*tag= q
FT				/number= 10
FT	exon			2710..2898
FT				/*tag= r
FT				/number= 11
FT	exon			2899..3025
FT				/*tag= s
FT				/number= 12

FT	exon	3026. .3087	/tag= t
FT		/number= 13	
FT	exon	3088. .3212	/tag= u
FT		/number= 14	
FT	exon	3213. .3350	/tag= v
FT		/number= 15	
FT	exon	3351. .4015	/tag= w
FT		/number= 16	
XX			
PN	EP1108789-A2.		
XX			
PD	20-JUN-2001.		
XX			
XX	15-DEC-2000; 2000EP-00127228.		
PF	16-DEC-1999; 99US-00465491.		
XX			
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.		
XX			
PI	Chang SP, Santini CD;		
XX			
DR	WPI; 2001-376930/40.		
XX			
PT	Quantitating expression of mRNA encoding hTERT, the catalytic subunit of		
PT	telomerase, as an indicator of cancer, by amplifying RNA using primers		
PT	complementary to hTERT gene sequence and quantitating amplified products.		
PS	Claim 1; Page 5-7; 29pp; English.		
XX			
CC	The present sequence is that of the hTERT gene encoding the catalytic		
CC	subunit of the human telomerase, comprising 16 exons, which is useful in		
CC	a method for quantitating hTERT mRNA. The method is useful for detecting		
CC	the presence of beta-region (a 182 nucleotide region consisting of exons		
CC	7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis		
CC	of cancer. The method provides an accurate measure of telomerase activity		
CC	by selectively measuring mRNA that encodes an active hTERT protein		
XX			
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;		
	Query Match	93.1%; Score 3559; DB 4; Length 4015;	
	Best Local Similarity	94.6%; Pred. No. 0;	
	Matches 3797; Conservative	0; Mismatches 0; Indels 218; Gaps 2;	
QY	8 GCAGCGCTGCCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCCCCCGCATGCC	67	
DB	1 GCAGCGCTGCCTCTGCTGCGCAGCTGGGAAGCCCTGGCCCCCGGCACCCCCCGCATGCC	60	
QY	68 GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGTCT	127	
DB	61 GCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGTCT	120	
QY	128 GCCGCTGGCCAGTTCGTGCGGCGCTGGGGCCCCCAGGGCTGGCGCTGTGCAGCGCGG	187	
DB	121 GCCGCTGGCCAGTTCGTGCGGCGCTGGGGCCCCCAGGGCTGGCGCTGTGCAGCGCGG	180	
QY	188 GGACCCGGCGCTTCCGCGCGCTGTGTGGCCCACTGCTGTGTGCTGCCCTGGGACGC	247	
DB	181 GGACCCGGCGCTTCCGCGCGCTGTGTGGCCCACTGCTGTGTGCTGCCCTGGGACGC	240	
QY	248 ACGCGCGCCCCCGCGCCCCCTCTTCCGCCAGGTGTCTGCTGTAAGAGAGCTGTGGC	307	
DB	241 ACGCGCGCCCCCGCGCCCCCTCTTCCGCCAGGTGTCTGCTGTAAGAGAGCTGTGGC	300	
QY	308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGGAAGAAGTGTGCTGGCTTGGCTTGGC	367	
DB	301 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGGAAGAAGTGTGCTGGCTTGGCTTGGC	360	
QY	368 GCTGCTGAAGGGGGCCCGCGGGGGCCCCCGAGGCTTACCACCAAGAGTGGCAGCTA	427	

D	b	361	GCTGCTGGA	CGGGGCCCCCGGGGGCCCCCCCCGAGG	CCCTTCA	CCACCA	CGCTGCGCAGCTA	420
Q	y	428	CCTGCCCA	CACCGGTGACCGACGCACTGCGGGGGA	AGCGGGGCGTGGGGGCTGCTGTCG			487
D	b	421	CCTGCCCA	CACCGGTGACCGACGCACTGCGGGGGA	AGCGGGGCGTGGGGGCTGCTGTCG			480
Q	y	488	CCGCGTGG	CGACGCTGCTGTTCACTGCTGACAGCTGCG	CGCTCTTTGTGCTGT			547
D	b	481	CCGCGTGG	CGACGCTGCTGTTCACTGCTGACAGCTGCG	CGCTCTTTGTGCTGT			540
Q	y	548	GGCTCCAG	CTGCGCTTACCAGGTGTGCGGGCCGCGCTGT	ACCACTGCGCTGCCCTGCCAC			607
D	b	541	GGCTCCAG	CTGCGCTTACCAGGTGTGCGGGCCGCGCTGT	ACCACTGCGCTGCCCTGCCAC			600
Q	y	608	TCAAGCCCC	CCCCCGCCACACGCTAGTGA	CCCCGGAAGCGCTTGGATGCGAACGGG			667
D	b	601	TCAAGCCCC	CCCCCGCCACACGCTAGTGA	CCCCGGAAGCGCTTGGATGCGAACGGG			660
Q	y	668	CTGGAACCA	TAGCGCTCAGGGAGGCGCGG	GTCCCCCTGGGCGCTGCCAGCCCCGGGTGCAG			727
D	b	661	CTGGAACCA	TAGCGCTCAGGGAGGCGCGG	GTCCCCCTGGGCGCTGCCAGCCCCGGGTGCAG			720
Q	y	728	GAGCGCGG	GGGCGAGTGCCAGCCGAAGTCTGCCGT	TGCCCAAGAGGCCCAAGCGGTGGCG			787
D	b	721	GAGCGCGG	GGGCGAGTGCCAGCCGAAGTCTGCCGT	TGCCCAAGAGGCCCAAGCGGTGGCG			780
Q	y	788	TGCCCTGAG	CCCGGAGCGCGCGCTTGGG	CGAGGGGTCTTGCGGCCCA	CCCCGGGCGAC		847
D	b	781	TGCCCTGAG	CCCGGAGCGCGCGCTTGGG	CGAGGGGTCTTGCGGCCCA	CCCCGGGCGAC		840
Q	y	848	GCGTGGAC	CCGAGTGACCGGTGTTCTGTGTGT	TCACCTGCCAGACCCCGCGAAGAGC			907
D	b	841	GCGTGGAC	CCGAGTGACCGGTGTTCTGTGTGT	TCACCTGCCAGACCCCGCGAAGAGC			900
Q	y	908	CACCTCTT	TGAGGGGTGCGCTCTTGGACA	CGCGCACTCCACCCATCCGTGGGCGCGCA			967
D	b	901	CACCTCTT	TGAGGGGTGCGCTCTTGGACA	CGCGCACTCCACCCATCCGTGGGCGCGCA			960
Q	y	968	GCAACCA	CGCGGGCCCCCATCA	TCGCGGCCAACCA	CGTCTGGGACACGCTTGTCC		1027
D	b	961	GCAACCA	CGCGGGCCCCCATCA	TCGCGGCCAACCA	CGTCTGGGACACGCTTGTCC		1020
Q	y	1028	CCCGGTGT	ACGCCGAGACCAAGCA	TTCTCTACTCTCAGCGCA	CAAGGAGCAGTGC		1087
D	b	1021	CCCGGTGT	ACGCCGAGACCAAGCA	TTCTCTACTCTCAGCGCA	CAAGGAGCAGTGC		1080
Q	y	1088	GCCCTCCT	TCTACTAGCTCTGAGGCC	AGCCTGACTGCGCTCGAGGCTGTGA			1147
D	b	1081	GCCCTCCT	TCTACTAGCTCTGAGGCC	AGCCTGACTGCGCTCGAGGCTGTGA			1140
Q	y	1148	GACCATCT	TTCTGGGTTCCAGGCCCTG	GATGCCAGGACTCCCCGAGGTTGCCCGCT			1207
D	b	1141	GACCATCT	TTCTGGGTTCCAGGCCCTG	GATGCCAGGACTCCCCGAGGTTGCCCGCT			1200
Q	y	1208	GCCCCAGC	GCCTACTGCAAAATGCGGCC	CTGTTCTGAGCTGTGGGA	ACCA	CGCGCA	1267
D	b	1201	GCCCCAGC	GCCTACTGCAAAATGCGGCC	CTGTTCTGAGCTGTGGGA	ACCA	CGCGCA	1260
Q	y	1268	GTGCCCC	TACGGGTTGCTCTCAAGAC	GCAC	TGCCCCGTGCGGTCA	CCCCCG	1327
D	b	1261	GTGCCCC	TACGGGTTGCTCTCAAGAC	GCAC	TGCCCCGTGCGGTCA	CCCCCG	1320
Q	y	1328	AGCCGGT	GTCTGTGCCCCGGGAGAG	CCCCCAGGCTCTGTGGCGGGCCCCCGAGGAGAGGA			1387
D	b	1321	AGCCGGT	GTCTGTGCCCCGGGAGAG	CCCCCAGGCTCTGTGGCGGGCCCCCGAGGAGAGGA			1380
Q	y	1388	CACAGAC	CCCCCGTGGCTGTGTGAC	AGTGTCTCCGCGACACAGACAGCCCCCTGGCAGGTGA			1447
D	b	1381	CACAGAC	CCCCCGTGGCTGTGTGAC	AGTGTCTCCGCGACACAGACAGCCCCCTGGCAGGTGA			1440
Q	y	1448	CGGCTT	CGTGGGCGCTGCTGCGCG	CGGTGTGCCCCCAGGCTCTGGGCGTCCAGGCA			1507
D	b	1441	CGGCTT	CGTGGGCGCTGCTGCGCG	CGGTGTGCCCCCAGGCTCTGGGCGTCCAGGCA			1500

QY	1508	CAACGAACGCCGCTTCTCTCAGGAACACCAAGAGTTCA	TCTCCCTGGGGAAAGCATGCCAA	1567	
Db	1501	CAACGAACGCCGCTTCTCTCAGGAACACCAAGAGTTCA	TCTCCCTGGGGAAAGCATGCCAA	1560	
QY	1568	GCTCTCCGTCAGGAGCTGACGCTGGAAAGATGAGCGT	CGGGAACTGCGCTTGCGCGAG	1627	
Db	1561	GCTCTCCGTCAGGAGCTGACGCTGGAAAGATGAGCGT	CGGGAACTGCGCGACTGCGCTTGCGCGAG	1620	
QY	1628	GAGCCCCAGGGGTTGGCTGTGTTC	CGGGCCGAGAGCA	CCGTCTGCGTAGAGATCTCTGGC	1687
Db	1621	GAGCCCCAGGGGTTGGCTGTGTTC	CGGGCCGAGAGCA	CCGTCTGCGTAGAGATCTCTGGC	1680
QY	1688	CAAGTTCCTGCAC	TGCGCTGATGAGTGTGTAC	TGCTGTCGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCAC	TGCGCTGATGAGTGTGTGTAC	TGCTGTCGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGGAGACCA	CGTTTCAAAAAGAACAGCGCTCTTTTCTAC	CCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGGAGACCA	CGTTTCAAAAAGAACAGGCTCTTTTCTAC	CCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAAAGCAT	TGGAATCAGACAGACACTTGAAGAGGGTG	CAGCTGCGGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCAT	TGGAATCAGACAGACACTTGAAGAGGGTG	CAGCTGCGGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCAGCAT	TCGGGAAGCCAGCCCGCCCTGCTGAC	GTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCAGCAT	TCGGGAAGCCAGCCCGCCCTGCTGAC	GTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGAC	CGGGCTGCGGCCGATTTGTGAACATG	ACTACGTGCTGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGAC	CGGGCTGCGGCCGATTTGTGAACATG	ACTACGTGCTGGAGC	1980
QY	1988	CAGAACGTTCCGCAGAGAAAGAGAGG	CCGAGCGTCTCACTCGAGGTTGAAGGCA	CTGTT	2047
Db	1981	CAGAACGTTCCGCAGAGAAAGAGAGG	CCGAGCGTCTCACTCGAGGTTGAAGGCA	CTGTT	2040
QY	2048	CAGCGTGTCAACTACGAGCGGGCGCGCGCCCGCCCT	CCTGCGGCGCTTGTGCTGGG	2107	
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGCGCCCGCCCT	CCTGCGGCGCTTGTGCTGGG	2100	
QY	2108	CCTGACGATATCCACAGGGCCTGCGGCA	CTTCTGCTGCGTGTGCGGGCCAGGACC	2167	
Db	2101	CCTGACGATATCCACAGGGCCTGCGGCA	CTTCTGCTGCGTGTGCGGGCCAGGACC	2160	
QY	2168	GCCGCTGAGCTGTA	-----CATCCCCCA	2191	
Db	2161	GCCGCTGAGCTGTA	CTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCAT	CCCCCA	2220
QY	2192	GGACAGGCTCAGCGGAGGTCATGCGCAGCAT	CATCAAAACCCAGAAACAGTACTGCGTGCG	2251	
Db	2221	GGACAGGCTCAGCGGAGGTCATGCGCAGCAT	CATCAAAACCCAGAAACAGTACTGCGTGCG	2280	
QY	2252	TGCGTATGCCGTGGTCCAGAAAGCCGCCCAT	TGGGCAAGTCCGCAAGGCTTCAAGA	-----	2307
Db	2281	TGCGTATGCCGTGGTCCAGAAAGCCGCCCAT	TGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2340	
QY	2308	-----	-----	2307	
Db	2341	CGTCTCTACTTGA	CAGACCTCCAGCCGTACATGCGACA	GTTCGTGCTCACTGCAAGGA	2400
QY	2308	-----	-----	2307	
Db	2401	GACCAAGCCCGCTGAGGGATGCCGTGTCAT	CGAGCAGAGACTCCTCCCTGAATGAGGCCAG	2460	
QY	2308	-----	-----GG	2309	
Db	2461	CAGTGGCTCTTGCAGCGTCTTCTTACGCTTCAT	GTGTCACCAACGCGCGTGCGCATCAGGGG	2520	
QY	2310	CAAGTCTTACGTC	CAGTGCAGGGGATCCCGCAGAGGCTCCATCTCTTCCACGCTGCTGTG	2369	
Db	2521	CAAGTCTTACGTC	CAGTGCAGGGGATCCCGCAGAGGCTCCATCTCTTCCACGCTGCTGTG	2580	

QY 2370 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTCCGGGGATTCGGCGGAGCGGGCT 2429
DB 2581 CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTCCGGGGATTCGGCGGAGCGGGCT 2640
QY 2430 GCTCCTGCGTTTGGTGATGATTTCTTGTGTGACACCTCACCCTACCGCGGAAAC 2489
DB 2641 GCTCCTGCGTTTGGTGATGATTTCTTGTGTGACACCTCACCCTACCGCGGAAAC 2700
QY 2490 CTTCTTACGAGACCTTGTCGAGAGTGTCCTGAGTATGCTGCGTGTAAGTTCGGAA 2549
DB 2701 CTTCTTACGAGACCTTGTCGAGAGTGTCCTGAGTATGCTGCGTGTAAGTTCGGAA 2760
QY 2550 GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGACCGGCTTTGTTAGAT 2609
DB 2761 GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGACCGGCTTTGTTAGAT 2820
QY 2610 GCCGGCCCAAGGCTATTTCCCTGTGTCGAGGCTGCTGCTGATACCCGAGCCTGAGGT 2669
DB 2821 GCCGGCCCAAGGCTATTTCCCTGTGTCGAGGCTGCTGCTGATACCCGAGCCTGAGGT 2880
QY 2670 GCAGAGGAGTACTCTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCAGCTTCAACCG 2729
DB 2881 GCAGAGGAGTACTCTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCAGCTTCAACCG 2940
QY 2730 CGGCTTCAAGGCTGGAGAAACATGCGTCGAAACTCTTTGGGGCTTGGCGCTGAAGTG 2789
DB 2941 CGGCTTCAAGGCTGGAGAAACATGCGTCGAAACTCTTTGGGGCTTGGCGCTGAAGTG 3000
QY 2790 TCACAGCCTGTTTCTGATTTGACGTTGACAGCCTCCAGACGGTGTGACCAACATCTA 2849
DB 3001 TCACAGCCTGTTTCTGATTTGACGTTGACAGCCTCCAGACGGTGTGACCAACATCTA 3060
QY 2850 CAAGATCCTCTGCTGACAGGCGTACAGGTTTACGCAATGTGTGCTGACGCTCCATTTCA 2909
DB 3061 CAAGATCCTCTGCTGACAGGCGTACAGGTTTACGCAATGTGTGCTGACGCTCCATTTCA 3120
QY 2910 TCAGCAAGTTTGAAGAACCACCATTTTCTGCGCGTCACTCTGACAGCGGCTCCCT 2969
DB 3121 TCAGCAAGTTTGAAGAACCACCATTTTCTGCGCGTCACTCTGACAGCGGCTCCCT 3180
QY 2970 CTGCTACTCCATCCTGAAGACCAAGACGAGGATGTGCTGGGGCCAGGGCGCGC 3029
DB 3181 CTGCTACTCCATCCTGAAGACCAAGACGAGGATGTGCTGGGGCCAGGGCGCGC 3240
QY 3030 CGGCGCTCTGCGCTCGAGGCGGTGACAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3089
DB 3241 CGGCGCTCTGCGCTCGAGGCGGTGACAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
QY 3090 GACTCGACACCGTGTACCTACCTAAGTCCACTCTGCGGTCACTCAGAGACGCCAGACGCA 3149
DB 3301 GACTCGACACCGTGTACCTAAGTCCACTCTGCGGTCACTCAGAGACGCCAGACGCA 3360
QY 3150 GCTGAGTCCGAGAGTCCCGGGGAGACGAGTGTGCTGAGGCGCGACCAACCCGCGC 3209
DB 3361 GCTGAGTCCGAGAGTCCCGGGGAGACGAGTGTGCTGAGGCGCGACCAACCCGCGC 3420
QY 3210 ACTGCCCTCAGACTTCAAGACCATCTCTGAGTGTGAGCCACCCGCCACAGCCAGGCCGA 3269
DB 3421 ACTGCCCTCAGACTTCAAGACCATCTCTGAGTGTGAGCCACCCGCCACAGCCAGGCCGA 3480
QY 3270 GAGGAGACACGAGAGCCTGTCAAGCGCGGCTCTACGTTCCCAAGGAGGAGGGCGGCC 3329
DB 3481 GAGGAGACACGAGAGCCTGTCAAGCGCGGCTCTACGTTCCCAAGGAGGAGGGCGGCC 3540
QY 3330 CACACCCAGGCGCGGACCGCTGGAGTCTGAGGCGCTGAGTGTGAGCCGAGGCGCTG 3389
DB 3541 CACACCCAGGCGCGGACCGCTGGAGTCTGAGGCGCTGAGTGTGAGCCGAGGCGCTG 3600
QY 3390 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGGGGCT 3449
DB 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCCAGGGGCT 3660
QY 3450 GAGTGTCCAGACACCTGCGGCTTCTCACTTCCCAAGGCTGGCGCTCCAGCCCA 3509

DB 3661 GAGTGTCCAGACACCTGCGGCTTCTCACTTCCCAAGGCTGGCGCTCCAGCCCA 3720
QY 3510 GGGCCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCAATAGGATATGTCATCC 3569
DB 3721 GGGCCAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCAATAGGATATGTCATCC 3780
QY 3570 CCAAGTTCGCCATTTGTTCAACCCCTCGCCCTGCGCTTCTTGCCTTCCACCCCAACCATCC 3629
DB 3781 CCAAGTTCGCCATTTGTTCAACCCCTCGCCCTGCGCTTCTTGCCTTCCACCCCAACCATCC 3840
QY 3630 AGGTGAGAGCCCTGAGAGAGCCCTGGAGCTCTGGAAATTGGAGTGACCAAGGTGTG 3689
DB 3841 AGGTGAGAGCCCTGAGAGAGCCCTGGAGCTCTGGAAATTGGAGTGACCAAGGTGTG 3900
QY 3690 CCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGTCAAATTGGGGG 3749
DB 3901 CCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGTCAAATTGGGGG 3960
QY 3750 GAGTGTCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAGAAA 3804
DB 3961 GAGTGTCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAGAAA 4015

RESULT 10
AAD46821
ID AAD46821 standard; cDNA; 4015 BP.
XX AC AAD46821;
XX DT 27-JAN-2003 (first entry)
DE Human telomerase reverse transcriptase (TERT) cDNA.
XX
KW Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
KW transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KW telomerase reverse transcriptase; gene; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "Human telomerase reverse transcriptase"
PN WO200274948-A2.
XX PD 26-SEP-2002.
PF 21-MAR-2002; 2002WO-CA000378.
XX PR 21-MAR-2001; 2001US-0277811P.
PA (GERO-) GERON CORP.
PI Denning C, Clark AJ, Schiff JM;
XX WPI; 2002-759895/82.
DR P-PSDB; AAE29226.
XX
PT Mammalian cells, useful for producing animal tissues with carbohydrate
XX antigens that are compatible for transplantation into human patients.
PS Disclosure; Page 33-34; 71pp; English.
XX
CC The invention relates to animal tissues with carbohydrate antigens that
CC are compatible for transplantation into human patients. The mammalian
CC cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC with carbohydrate antigens that are compatible for transplantation into
CC human patients. The present sequence is human telomerase reverse
CC transcriptase (TERT) cDNA used in the invention

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
SQ
Query Match 93.1%; Score 3559; DB 6; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCGTCTGCTGCGCAGCTGGGAGAGCCCTGGCCCCCGGCAACCCCGGATGCC 67
DB 1 GCAGCGCTGCGTCTGCTGCGCAGCTGGGAGAGCCCTGGCCCCCGGCAACCCCGGATGCC 60
QY 68 GCGCGCTCCCCCGCTGCCAGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 127
DB 61 GCGCGCTCCCCCGCTGCCAGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
QY 128 GCGCGCTGCCACGTTCTGTCGGCGGCTGGGGCCCCCAAGGCTGGCGGCTGTGACGCGCG 187
DB 121 GCGCGCTGCCACGTTCTGTCGGCGGCTGGGGCCCCCAAGGCTGGCGGCTGTGACGCGCG 180
QY 188 GGACCCCGCGGCTTTCCCGCGCTGTGGGCCAGTGCCTGTGTGGGTGCCCTGGGACGC 247
DB 181 GGACCCCGCGGCTTTCCCGCGCTGTGGGCCAGTGCCTGTGTGGGTGCCCTGGGACGC 240
QY 248 ACGCGCGCCCCCGCGCGCGCTTCCGCGCAGGTGTCTGCTGGAAGAGTGTGGC 307
DB 241 ACGCGCGCCCCCGCGCGCGCTTCCGCGCAGGTGTCTGCTGGAAGAGTGTGGC 300
QY 308 CCGAGTGTCTGACAGAGGCTGTGCGAGCGCGCGCGGAGAAAGTGTGGCTTGGCTTGC 367
DB 301 CCGAGTGTCTGACAGAGGCTGTGCGAGCGCGCGCGGAGAAAGTGTGGCTTGGCTTGC 360
QY 368 GCTGCTGACGGGGCCCCCGGGGGCCCCCGAGGCTTACCAACAGCGTGCAGCTA 427
DB 361 GCTGCTGACGGGGCCCCCGGGGGCCCCCGAGGCTTACCAACAGCGTGCAGCTA 420
QY 428 CCTGCCCAACACGCTGACCGACGCTGCGGGGAGCGGGGCTGGGCTGTGCTGC 487
DB 421 CCTGCCCAACACGCTGACCGACGCTGCGGGGAGCGGGGCTGGGCTGTGCTGC 480
QY 488 CCGCGTGGGCGACGAGCTGTGTTCACTGTGCGACGCTGCGCGCTTTTGTGTGTGT 547
DB 481 CCGCGTGGGCGACGAGCTGTGTTCACTGTGCGACGCTGCGCGCTTTTGTGTGTGT 540
QY 548 GCGTCCCAAGTGCCTTACCAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGTGCAC 607
DB 541 GCGTCCCAAGTGCCTTACCAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGTGCAC 600
QY 608 TCAGGCGCGCGCGCGCGCACACGCTAGTGAACCCGGAAGCGCTTGGATGCAACGGGC 667
DB 601 TCAGGCGCGCGCGCGCGCACACGCTAGTGAACCCGGAAGCGCTTGGATGCAACGGGC 660
QY 668 CTGGAACCATAGCTCAGAGAGCGCGGGTCCCGCTGGGCTGCCAGCCCGGGTGCAG 727
DB 661 CTGGAACCATAGCTCAGAGAGCGCGGGTCCCGCTGGGCTGCCAGCCCGGGTGCAG 720
QY 728 GAGGCGCGGGGCGAGTGCAGCCGAAATCTGCCGTTGCCAAGAGGCCAGGCTGGCGC 787
DB 721 GAGGCGCGGGGCGAGTGCAGCCGAAATCTGCCGTTGCCAAGAGGCCAGGCTGGCGC 780
QY 788 TGCCCGCTGAGCGCGGAGCGCGCGCTTGGGCAAGGCTTGGGCCCAACCCGGGCAAGAC 847
DB 781 TGCCCGCTGAGCGCGGAGCGCGCGCTTGGGCAAGGCTTGGGCCCAACCCGGGCAAGAC 840
QY 848 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
DB 841 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGAGGTGCGCTCTTGGCAGCGCGCACTCCCAACCATCCGTGGGCGGCCA 967
DB 901 CACCTCTTTGAGAGGTGCGCTCTTGGCAGCGCGCACTCCCAACCATCCGTGGGCGGCCA 960
QY 968 GCACCAACCGCGCGCGCGCGCAATGCAGGCGCAACGATCCCTGGGACAGGCTTGTCC 1027

DB 961 GCACCAACGCGCGCGCGCGCGCAATGCAGGCGCAACGATCCCTGGGACACGCTTGTCC 1020
QY 1028 CCGGCTGTACGCGCGAGAACAGCACTTCCCTACTCCTCAGGCGCAACAGAGAGTGGC 1087
DB 1021 CCGGCTGTACGCGCGAGAACAGCACTTCCCTACTCCTCAGGCGCAACAGAGAGTGGC 1080
QY 1088 GCCCTCCTTCTACTAGCTCTGTAGGCGCAACCTGACTGAGGCTCGGAGCTCGTGA 1147
DB 1081 GCCCTCCTTCTACTAGCTCTGTAGGCGCAACCTGACTGAGGCTCGGAGCTCGTGA 1140
QY 1148 GACCATCTTTCTGGGTTCCAGGCGCGCTGATGCGAGGACTCCCGCGAGTTGCCCGCT 1207
DB 1141 GACCATCTTTCTGGGTTCCAGGCGCGCTGATGCGAGGACTCCCGCGAGTTGCCCGCT 1200
QY 1208 GCGCCAGCGCTACTGCGCAATGCGGCGCGCTGTTTCTGAGCTGCTTGGGAAACAGCGCA 1267
DB 1201 GCGCCAGCGCTACTGCGCAATGCGGCGCGCTGTTTCTGAGCTGCTTGGGAAACAGCGCA 1260
QY 1268 GTGCGCGCTACGCGGCTCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTCAACCCAGC 1327
DB 1261 GTGCGCGCTACGCGGCTCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTCAACCCAGC 1320
QY 1328 AGCGGTGTGTGTGCGCGCGGAGAAAGCGCGCGCTGTGTGGCGCGCGCGCGAGAGAGGA 1387
DB 1321 AGCGGTGTGTGTGCGCGCGGAGAAAGCGCGCGCTGTGTGGCGCGCGCGAGAGAGGA 1380
QY 1388 CACAGACCGCGCGCTGCTGTGTGAGCTGCTCGCGCAGCAGACAGCGCGCGCTGCGAGTGT 1447
DB 1381 CACAGACCGCGCGCTGCTGTGTGAGCTGCTCGCGCAGCAGACAGCGCGCGCTGCGAGTGT 1440
QY 1448 CGGCTTGTGCGGGGCTGCTGCTGCGCGCGCTGCTGCGCGCGCGCGCGCTGCGAGGCA 1507
DB 1441 CGGCTTGTGCGGGGCTGCTGCTGCGCGCGCTGCTGCGCGCGCGCGCGCTGCGAGGCA 1500
QY 1508 CAACGAACCGCGCTTCTCAGGAACAACAAGATTCTCTCTGGGAAAGCATGCCAA 1567
DB 1501 CAACGAACCGCGCTTCTCAGGAACAACAAGATTCTCTCTGGGAAAGCATGCCAA 1560
QY 1568 GCTCTGCTGAGAGAGCTGACGTGAAGATGAGCGTGCAGGCTGCGGCTTGGCTGCGCAG 1627
DB 1561 GCTCTGCTGAGAGAGCTGACGTGAAGATGAGCGTGCAGGCTGCGGCTTGGCTGCGCAG 1620
QY 1628 GAGCCCAAGGCTTGGCTGTGTTCGCGCGCGCAGAGCACCGTGTGAGAGATCTGCGC 1687
DB 1621 GAGCCCAAGGCTTGGCTGTGTTCGCGCGCGCAGAGCACCGTGTGAGAGATCTGCGC 1680
QY 1688 CAAGTCTGCACTGCTGATGATGTGTGACGTGCTGAGCTGCTCAGGCTTTCTTTTA 1747
DB 1681 CAAGTCTGCACTGCTGATGATGTGTGACGTGCTGAGCTGCTCAGGCTTTCTTTTA 1740
QY 1748 TGTACGAGAGACACGTTTCAAAAGAACAGGCTTTTCTTACCGGAAGATGTGAG 1807
DB 1741 TGTACGAGAGACACGTTTCAAAAGAACAGGCTTTTCTTACCGGAAGATGTGAG 1800
QY 1808 CAAGTTCAAAGCATTTGAATCAGACGACTTGAAGAGGCTGCACTGCGGAGCTGTC 1867
DB 1801 CAAGTTCAAAGCATTTGAATCAGACGACTTGAAGAGGCTGCACTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGTCAAGCAGCATCGGGAAGCAGGCGCGCGCTGCTGACGTCCAGACTCCG 1927
DB 1861 GGAAGCAGAGTCAAGCAGCATCGGGAAGCAGGCGCGCGCTGCTGACGTCCAGACTCCG 1920
QY 1928 CTTCAATCCCAAGCCTGACGCGGCTGCGCGCATTTGTGAACATGGACTACGTGAGGAGC 1987
DB 1921 CTTCAATCCCAAGCCTGACGCGGCTGCGCGCATTTGTGAACATGGACTACGTGAGGAGC 1980
QY 1988 CAGAAGCTTCCGAGAGAAAGAGGCGCGAGCTTCACTCGAGGCTGAAGGCACTGTT 2047
DB 1981 CAGAAGCTTCCGAGAGAAAGAGGCGCGAGCTTCACTCGAGGCTGAAGGCACTGTT 2040
QY 2048 CAGCGTCTCACTACGAGCGCGCGCGCGCGCGCTCTGGGCGCTCTGTGTGGG 2107
DB 2041 CAGCGTCTCACTACGAGCGCGCGCGCGCGCGCTCTGGGCGCTCTGTGTGGG 2100

QY 2108 CCTGAGCATATCCACAGGCGCTGGCGCACCTTCGTGCTGCTGCGGGGCCAGGACC 2167
Db 2101 CCTGAGCATATCCACAGGCGCTGGCGCACCTTCGTGCTGCTGCGGGGCCAGGACC 2160
QY 2168 GCGGCGCTGAGCTGTA-----CATCCCCCA 2191
Db 2161 GCGGCGCTGAGCTGTA-----CATCCCCCA 2191
QY 2192 GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTAAGCTGCG 2251
Db 2221 GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTAAGCTGCG 2280
QY 2252 TCGGTATGCGCTGCTCCAGAGGCGCCCATGGGACGTCGCGAAGGCTTCAAGA---- 2307
Db 2281 TCGGTATGCGCTGCTCCAGAGGCGCCCATGGGACGTCGCGAAGGCTTCAAGAAGCCA 2340
QY 2308 ----- 2307
Db 2341 CGTCTTAACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCACTGACAGA 2400
QY 2308 ----- 2307
Db 2401 GACCAAGCCGCTGAGGAGTCGCTGCTCATGAGCAGAGCTCCTCCGTAATGAGGCGCAG 2460
QY 2308 -----GG 2309
Db 2461 CAGTGGCTCTTCGACGCTTCTCTAAGCTTCAATGTCACCAAGCCGCTGCGCATCAGGGG 2520
QY 2310 CAACTCTTAAGTCCAGTGGCGAGGAGATCCCGCAGGCGCTCATCTCTCAAGCTGCTG 2369
Db 2521 CAACTCTTAAGTCCAGTGGCGAGGAGATCCCGCAGGCGCTCATCTCTCAAGCTGCTG 2580
QY 2370 CAGCTGTGCTACGCGCAGCATGAGAACAAAGCTGTTGCGGGGATTGCGGGGACGCGCT 2429
Db 2581 CAGCTGTGCTACGCGCAGCATGAGAACAAAGCTGTTGCGGGGATTGCGGGGACGCGCT 2640
QY 2430 GCTCTGCTGCTTGTGATGATTTCTGTTGCTGACACCTCACTCAAGCAAGCAAAAC 2489
Db 2641 GCTCTGCTGCTTGTGATGATTTCTGTTGCTGACACCTCACTCAAGCAAGCAAAAC 2700
QY 2490 CTTCTCTCAGGACCCCTGCTGCGAGGTCCTCCAGTATGCTGCTGCTGCTGCTGCTG 2549
Db 2701 CTTCTCTCAGGACCCCTGCTGCGAGGTCCTCCAGTATGCTGCTGCTGCTGCTGCTG 2760
QY 2550 GACAGTGTGATCTCTCTGTAGAAAGAGAGGCGCTGGGTGCAAGGCTTTTGTTCAGAT 2609
Db 2761 GACAGTGTGATCTCTCTGTAGAAAGAGAGGCGCTGGGTGCAAGGCTTTTGTTCAGAT 2820
QY 2610 GCGGCGCCACAGGCTATTCCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2669
Db 2821 GCGGCGCCACAGGCTATTCCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2880
QY 2670 GCAGAGCGACTACTCCAGTATGCGCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2729
Db 2881 GCAGAGCGACTACTCCAGTATGCGCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
QY 2730 CGGCTTCAAGGCTGGAGAGAACATGCGTCCGAAACTTTTGGGCTTGGCGCTGAAGTG 2789
Db 2941 CGGCTTCAAGGCTGGAGAGAACATGCGTCCGAAACTTTTGGGCTTGGCGCTGAAGTG 3000
QY 2790 TCACAGCCTGTTCTGATTTGACAGGTGACAGCCTCCAGACGCTGTGACCAACATCTA 2849
Db 3001 TCACAGCCTGTTCTGATTTGACAGGTGACAGCCTCCAGACGCTGTGACCAACATCTA 3060
QY 2850 CAAGATCTCTCTGCTGAGGCGCTACAGGTTTCAAGCATGTGTGCTGACGCTCCCATTTCA 2909
Db 3061 CAAGATCTCTCTGCTGAGGCGCTACAGGTTTCAAGCATGTGTGCTGACGCTCCCATTTCA 3120
QY 2910 TCAGCAAGTTTGAAGAACCCCAACATTTTCTGCGGCTCATCTCTGACAGGCGCTCCCT 2969
Db 3121 TCAGCAAGTTTGAAGAACCCCAACATTTTCTGCGGCTCATCTCTGACAGGCGCTCCCT 3180

QY 2970 CTGCTACTCCATCTCTGAAAGCCAGAACAGCAGGAGTGTGCTGGGGGCCAAGGGCGCCGC 3029
Db 3181 CTGCTACTCCATCTCTGAAAGCCAGAACAGCAGGAGTGTGCTGGGGGCCAAGGGCGCCGC 3240
QY 3030 CGGCGCTCTGCGCTCCGAGGCGCTGCAAGTGGCTGTGCTGCTGCTGCTGCTGCTG 3089
Db 3241 CGGCGCTCTGCGCTCCGAGGCGCTGCAAGTGGCTGTGCTGCTGCTGCTGCTGCTG 3300
QY 3090 GACTGACACCGCTGTCACTTACGTCCTCACTCTCTGGGCTCACTCAGAGACAGCCAGACGCA 3149
Db 3301 GACTGACACCGCTGTCACTTACGTCCTCACTCTCTGGGCTCACTCAGAGACAGCCAGACGCA 3360
QY 3150 GCTGATCGGAAAGCTCCCGGGGAGCAGCGCTGACTGCTGCTGAGAGCGCCAGACCCGCGC 3209
Db 3361 GCTGATCGGAAAGCTCCCGGGGAGCAGCGCTGACTGCTGCTGAGAGCGCCAGACCCGCGC 3420
QY 3210 ACTGCGCTCAGACTTCAAGACCATCTCTGAGTGTGCTGAGTGTGCTGCTGCTGCTG 3269
Db 3421 ACTGCGCTCAGACTTCAAGACCATCTCTGAGTGTGCTGAGTGTGCTGCTGCTGCTG 3480
QY 3270 GAGCAGACACCGACAGCGCTGTCAAGCGCGGCTCTACGTCCTCAGAGGAGGAGGCGCGC 3329
Db 3481 GAGCAGACACCGACAGCGCTGTCAAGCGCGGCTCTACGTCCTCAGAGGAGGAGGCGCGC 3540
QY 3330 CACACCCAGGCGCGCAGCGCTGGAGTCTGAGGCTGAGTGTGCTGCTGCTGCTGCTG 3389
Db 3541 CACACCCAGGCGCGCAGCGCTGGAGTCTGAGGCTGAGTGTGCTGCTGCTGCTGCTG 3600
QY 3390 CATGTCCGCTGAAAGCTGAGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 3449
Db 3601 CATGTCCGCTGAAAGCTGAGTGTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 3660
QY 3450 GAGTGTCCAGACACCTGCGCTCTTCACTTCCCAAGGCTGCGCTGCGCTGCGCTGCGCTG 3509
Db 3661 GAGTGTCCAGACACCTGCGCTCTTCACTTCCCAAGGCTGCGCTGCGCTGCGCTGCGCTG 3720
QY 3510 GGGCGAGCTTTCTCTCAAGAGAGGCGCGCTTCACTTCCCAAGGCTGCGCTGCGCTGCGCTG 3569
Db 3721 GGGCGAGCTTTCTCTCAAGAGAGGCGCGCTTCACTTCCCAAGGCTGCGCTGCGCTGCGCTG 3780
QY 3570 CCAGATTGCGCATTTGTCACCCCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 3629
Db 3781 CCAGATTGCGCATTTGTCACCCCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 3840
QY 3630 AGGTGAGACCTTGAGAGGACCCCTGAGGCTGTGGAATTTGAGTGAACAAAGGTGTG 3689
Db 3841 AGGTGAGACCTTGAGAGGACCCCTGAGGCTGTGGAATTTGAGTGAACAAAGGTGTG 3900
QY 3690 CCCTGTACACAGGCGAGGACCCCTGACCTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTG 3749
Db 3901 CCCTGTACACAGGCGAGGACCCCTGACCTGATGAGGCTGCTGCTGCTGCTGCTGCTGCTG 3960
QY 3750 GAGGTGCTGTGAGTAATACTGATATATGATTTTCAAGTTTGAAGAAAAA 3804
Db 3961 GAGGTGCTGTGAGTAATACTGATATATGATTTTCAAGTTTGAAGAAAAA 4015

RESULT 11
ABA97534
ID ABA97534 standard; DNA; 4015 BP.
XX ABA97534;
AC ABA97534;
DT 05-APR-2002 (first entry)
XX
DE Cancer cell discrimination method related human DNA.
XX
XX Human; telomerase; enzyme; cancer cell discrimination; gene;
KW reverse transcriptase; ds.
XX Homo sapiens.
OS
XX
PN JP2001309791-A.

Db 1681 CAAGTTCCTGCACTGGCTGATGATGTGTACGTCTGAGCTGCTCAGGTCTTTCTTTA 1740
Qy 1748 TGTACGAGAGACCAAGCTTTCAAAAGACAGGCTTTTCTAAGGAGTGTCTGAG 1807
Db 1741 TGTACGAGAGACCAAGCTTTCAAAAGACAGGCTTTTCTAAGGAGTGTCTGAG 1800
Qy 1808 CAAGTTCGAAAGCATTTGAATCAGACGACTTGAAGAGGTGAGCTGGGAGTCTC 1867
Db 1801 CAAGTTCGAAAGCATTTGAATCAGACGACTTGAAGAGGTGAGCTGGGAGTCTC 1860
Qy 1868 GGAAGCAGAGGTGAGCAGACATCGGGAAGCCAGCCCGCTGCTGACGTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTGAGCAGACATCGGGAAGCCAGCCCGCTGCTGACGTCCAGACTCCG 1920
Qy 1928 CTTGATCCCCAAGCCTGACGGGCTGCGGCGGATTTGAAATGACTAGCTGCTGGAGC 1987
Db 1921 CTTGATCCCCAAGCCTGACGGGCTGCGGCGGATTTGAAATGACTAGCTGCTGGAGC 1980
Qy 1988 CAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTCGAGGTTGAAGGCACTGTT 2047
Db 1981 CAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTCGAGGTTGAAGGCACTGTT 2040
Qy 2048 CAGCGTGTCTCACTACGAGCGGCGCGGCGGCGGCTCTGCGGCTCTGCTGGG 2107
Db 2041 CAGCGTGTCTCACTACGAGCGGCGCGGCGGCGGCTCTGCGGCTCTGCTGGG 2100
Qy 2108 CCTGACGATATCCACAGGGGCTGGCGGACCTTCTGCTGCTGCTGGGCGGAGACC 2167
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Qy 2168 GCGGCTGAGCTGTA-----CATCCCCA 2191
Db 2161 GCGGCTGAGCTGTA-----CATCCCCA 2220
Qy 2192 GGAAGAGGCTCAGGAGGTGATGCGGACATCATCAAAACCCAGAAACAGTACTGCTGCG 2251
Db 2221 GGAAGAGGCTCAGGAGGTGATGCGGACATCATCAAAACCCAGAAACAGTACTGCTGCG 2280
Qy 2252 TCGGTAATGCGGTGTCAGAAAGGCGGCGGATGGGCACTGCGCAAGGCTTTCAAGA---- 2307
Db 2281 TCGGTAATGCGGTGTCAGAAAGGCGGCGGATGGGCACTGCGCAAGGCTTTCAAGA----- 2340
Qy 2308 ----- 2307
Db 2341 CGTCTCTACTTGACAGACTCTCCAGCCGATCATGCGACAGTTGCTGCTCACTGACAGA 2400
Qy 2308 ----- 2307
Db 2401 GACCAAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCCTCTGAATGAGGCCAG 2460
Qy 2308 -----GG 2309
Db 2461 CAGTGGCTCTTGACGCTCTCTCTACGCTTCAATGTCACCAAGCCGCTGCGCATCAGGGG 2520
Qy 2310 CAAGTCTACGTCAGTGCAGGGGATCCCGCAGAGGCTCCATCTCTCAAGCTGCTCTG 2369
Db 2521 CAAGTCTACGTCAGTGCAGGGGATCCCGCAGAGGCTCCATCTCTCAAGCTGCTCTG 2580
Qy 2370 CAGCTGTGCTACGCGGACATGAGAAACAAGCTGTTGCGGGGATTCGCGGAGCAGGCT 2429
Db 2581 CAGCTGTGCTACGCGGACATGAGAAACAAGCTGTTGCGGGGATTCGCGGAGCAGGCT 2640
Qy 2430 GCTCTGCGTTTGTGATGATTTCTTGTGTTGACACCTCACTCAACCAAGGAAAC 2489
Db 2641 GCTCTGCGTTTGTGATGATTTCTTGTGTTGACACCTCACTCAACCAAGGAAAC 2700
Qy 2490 CTTCTCAGAGACCTGTCGAGGTGTCCTGAGTATGCTGCGTGAACCTTGCAGAA 2549
Db 2701 CTTCTCAGAGACCTGTCGAGGTGTCCTGAGTATGCTGCGTGAACCTTGCAGAA 2760
Qy 2550 GACAGTGTGAACCTTCTCTGTAAGACAGAGCCCTGGGTGACAGGCTTTTGTTCAGAT 2609

Db 2761 GACAGTGTGAACCTTCTCTGTAAGACAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT 2820
Qy 2610 GCGGAGCCACAGGCTATTTCCCTGCTGCTGGGCTGCTGATACCCGAGCCTGAGGT 2669
Db 2821 GCGGAGCCACAGGCTATTTCCCTGCTGCTGGGCTGCTGATACCCGAGCCTGAGGT 2880
Qy 2670 GCAAGGCACTACTCCAGTATGCCCCGAGCCTTCATCAGAGCCAGTCTCACTTCAACCG 2729
Db 2881 GCAAGGCACTACTCCAGTATGCCCCGAGCCTTCATCAGAGCCAGTCTCACTTCAACCG 2940
Qy 2730 CGGCTTCAAGGCTGGAGAAACATGCGTCCAACTTTTGGGCTTTGGGCTGAAGTG 2789
Db 2941 CGGCTTCAAGGCTGGAGAAACATGCGTCCAACTTTTGGGCTTTGGGCTGAAGTG 3000
Qy 2790 TCACAGCCTGTTTCTGATTTGAGGTGAACAGCCTTCAGACGCTGTCACCAATCTA 2849
Db 3001 TCACAGCCTGTTTCTGATTTGAGGTGAACAGCCTTCAGACGCTGTCACCAATCTA 3060
Qy 2850 CAAGATCCTCTGCTGACAGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTCA 2909
Db 3061 CAAGATCCTCTGCTGACAGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTCA 3120
Qy 2910 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACAGGCTCCCT 2969
Db 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACAGGCTCCCT 3180
Qy 2970 CTGCTACTCATCTGTAAGAACCAAGAACGAGGATGTGCTGAGGCGCAAGGCGCGC 3029
Db 3181 CTGCTACTCATCTGTAAGAACCAAGAACGAGGATGTGCTGAGGCGCAAGGCGCGC 3240
Qy 3030 CGGCTCTGCTGCTGAGGCGGCTGAGTGTGCAACCAAGCATTTCTGCTCAAGCT 3089
Db 3241 CGGCTCTGCTGCTGAGGCGGCTGAGTGTGCAACCAAGCATTTCTGCTCAAGCT 3300
Qy 3090 GACTGACACCGTGTGACCTACGTGCGGCTGCTGAGGCTCACTCAGAGCAGGCGGCA 3149
Db 3301 GACTGACACCGTGTGACCTACGTGCGGCTGCTGAGGCTCACTCAGAGCAGGCGGCA 3360
Qy 3150 GCTGAGTGGAGCTCCCGGGGAGCAGCGTGAAGCTGCTGAGGCGGCAAGCCGCGC 3209
Db 3361 GCTGAGTGGAGCTCCCGGGGAGCAGCGTGAAGCTGCTGAGGCGGCAAGCCGCGC 3420
Qy 3210 ACTGCCCTCAGACTTCAAGACCATCTGAGTATGAGCCAGCCGCGGCAAGGCGGCA 3269
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGAGTATGAGCCAGCCGCGGCAAGGCGGCA 3480
Qy 3270 GAGCAGACACGAGCGCTGTACGCGGCTCTACGTCCAGAGGAGGCGGCGC 3329
Db 3481 GAGCAGACACGAGCGCTGTACGCGGCTCTACGTCCAGAGGAGGCGGCGC 3540
Qy 3330 CACACCCAGGCGCGGACCGCTGGGAGTCTGAGGCTGAGTGTGTCGAGGCGCTG 3389
Db 3541 CACACCCAGGCGCGGACCGCTGGGAGTCTGAGGCTGAGTGTGTCGAGGCGCTG 3600
Qy 3390 CATGTCGGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTTCAGACCAAGGCT 3449
Db 3601 CATGTCGGCTGAAGGCTGAGTGTGCGGCTGAGGCTGAGGAGTGTTCAGACCAAGGCT 3660
Qy 3450 GAGTGTCCAGACACCTGCGGCTTCTCACTTCCCAACAGGCTGCGGCTCCACCCCA 3509
Db 3661 GAGTGTCCAGACACCTGCGGCTTCTCACTTCCCAACAGGCTGCGGCTCCACCCCA 3720
Qy 3510 GGGCCAAGCTTTCTCTACCAAGAGCCCGGCTTCCACTCCCAACATAGATTCATCC 3569
Db 3721 GGGCCAAGCTTTCTCTACCAAGAGCCCGGCTTCCACTCCCAACATAGATTCATCC 3780
Qy 3570 CCAAGTTCGCAATTTGTTCAACCCCTGCGGCTTCTCTTGTGCTTCCACCCCAACCATCC 3629
Db 3781 CCAAGTTCGCAATTTGTTCAACCCCTGCGGCTTCTCTTGTGCTTCCACCCCAACCATCC 3840
Qy 3630 AGGTGAGACCTTGAGAAAGAACCTTGAGAGCTTGGGAATTTGAGTGAACCAAGGTGTG 3689
Db 3841 AGGTGAGACCTTGAGAAAGAACCTTGAGAGCTTGGGAATTTGAGTGAACCAAGGTGTG 3900

QY 3690 CCCTGTACACAGGCGAGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAAAATTGGGGG 3749
Db 3901 CCTGTACACAGGCGAGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAAAATTGGGGG 3960
QY 3750 GAGGTGCTGTGGAGTAAATATCTGATATATGAGTTTTCAGTTTGAAGAAAAA 3804
Db 3961 GAGGTGCTGTGGAGTAAATATCTGATATATGAGTTTTCAGTTTGAAGAAAAA 4015
RESULT 12
ACC58039
ID ACC58039 standard; cDNA; 4015 BP.
XX ACC58039;
AC ACC58039;
XX 11-AUG-2003 (first entry)
XX Human telomerase reverse transcriptase cDNA.
XX
XX Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
XX short interfering RNA; siRNA; cancer; tumour; cytosolic; contraceptive;
XX immunosuppressive; antifertility; fungicide; antiparasitic;
XX antiinflammatory; human; gene therapy; gene; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS .56..3454
XX FT /*tag= a
XX FT /product= "TERT"
XX
XX WO2003035667-A2.
XX
XX 01-MAY-2003.
XX
XX 16-OCT-2002; 2002WO-US033065.
XX
XX 22-OCT-2001; 2001US-0345326P.
XX 20-FEB-2002; 2002US-0359196P.
XX 22-MAY-2002; 2002US-0363195P.
XX
XX (UNRP) UNIV ROCHESTER.
XX
XX Rowley PT;
XX
XX WPI; 2003-403336/38.
XX P-PSDB; ABR42384.
XX
XX
XX Novel double-stranded short interfering RNA having sense and antisense
XX nucleic acids which are complementary to each other and to target nucleic
XX acid e.g., telomerase RNA or mRNA encoding telomerase reverse
XX transcriptase.
XX
XX
XX Disclosure; Fig 3A-B; 37pp; English.
XX
XX The present sequence is that of human telomerase reverse transcriptase
XX (TERT) cDNA. The invention relates to the discovery that double-stranded
XX interfering RNAs, such as short interfering RNAs (siRNA), which target
XX telomerase RNA or TERT mRNA are capable of inhibiting telomerase
XX activity. Inhibition of telomerase in cancer cells leads to telomere
XX shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
XX telomerase activity can also be used for treatment of infertility, for
XX contraception or sterilisation, for immunosuppression, for treatment of
XX yeast, parasite and fungal infections, and in antiinflammatory therapies.
XX As telomerase is active in a limited number of cell types, e.g. tumour
XX cells, germ-line cells, certain stem cells of the haematopoietic system, T
XX and B cells, sun-damaged skin, and proliferative cervix, most normal
XX cells are not affected by telomerase RNA interference therapy
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 93.1%; Score 3559; DB 7; Length 4015;

Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;
QY 8 GCAGCGCTCGCTCTGTGCGCAGCAGTGGGAGAGCCCTGGCCCCGCCACCCCGCATGCC 67
Db 1 GCAGCGCTCGCTCTGTGCGCAGCAGTGGGAGAGCCCTGGCCCCGCCACCCCGCATGCC 60
QY 68 GCGCGCTCCCGCGTCCGAGACCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTCT 127
Db 61 GCGCGCTCCCGCGTCCGAGACCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTCT 120
QY 128 GCGCGTGGCCACGTTCTGTGCGGCGCTGGGGCCCCCAGGCGTGGCGGTGGTGCAGCGCG 187
Db 121 GCGCGTGGCCACGTTCTGTGCGGCGCTGGGGCCCCCAGGCGTGGCGGTGGTGCAGCGCG 180
QY 188 GGAACCCGCGGCTTTCCGCGCGCTGTGCGGCGCAGTGCCTGTGTGCTGCTGGAGCGC 247
Db 181 GGAACCCGCGGCTTTCCGCGCGCTGTGCGGCGCAGTGCCTGTGTGCTGCTGGAGCGC 240
QY 248 ACGGCG 307
Db 241 ACGGCG 300
QY 308 CCGAGTGTGCAAGGCTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 301 CCGAGTGTGCAAGGCTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 368 GCTGCTGACGCGGCG 427
Db 361 GCTGCTGACGCGGCG 420
QY 428 CCTGCCCAACGCGTGAACGCGCAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
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QY 488 CCGCGTGGCGGCGAGCGTGTGCTGCTGCTGCGCAGCGTGGCGCTTTGTGCTGT 547
Db 481 CCGCGTGGCGGCGAGCGTGTGCTGCTGCTGCGCAGCGTGGCGCTTTGTGCTGT 540
QY 548 GCGTCCAGTGTGCGCTTACCAAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db 541 GCGTCCAGTGTGCGCTTACCAAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGGAACCATAGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db 661 CTGGAACCATAGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGGCGCGGCGCGAGTGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
Db 721 GAGGCGCGGCGCGAGTGCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY 788 TGCCCTGAGCGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
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QY 968 GCACCAAGGCG 1027
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QY 3750 GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAGAAAA 3804
DB 3961 GAGGTGCTGTGGAGTAATAATCTGAATATATGAGTTTTCAGTTTGAAGAAAA 4015

RESULT 13
ACC57552
ID ACC57552 standard; cDNA; 4015 BP.
XX AC ACC57552;
XX DT 28-JUL-2003 (first entry)
XX DE Human telomerase reverse transcriptase cDNA.
XX KM Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
XX KM short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
XX KM immunosuppressive; antiinfectility; fungicide; antiparasitic;
XX KM antiinflammatory; human; gene therapy; gene; ss.
OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 56..3454
FT CDS /*tag= a
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PT /product= "TERT"
XX WO2003034985-A2.
PN 01-MAY-2003.
XX 16-OCT-2002; 2002WO-US033146.
XX 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX (UYRP ) UNIV ROCHESTER.
XX Rowley PT;
XX WPI; 2003-403289/38.
DR P-PSDB; ABR42063.
XX
PT Novel nucleic acid encoding or comprising interfering RNAs which target
PT telomerase RNA, useful for inhibiting telomerase activity for treating
PT cancer, infertility and disorders of the immune system.
XX
PS Disclosure; Fig 3; 52p; English.
XX
CC The present sequence is that of human telomerase reverse transcriptase
CC (TERT) cDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 93.1%; Score 3559; DB 7; Length 4015;
Best local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCGTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCAACCCCGGATGCC 67
DB 1 GCAGCGCTGCGTCTGCTGCGCAGCTGGAGAGCCCTGGCCCGGCAACCCCGGATGCC 60
QY 68 GCGCGCTCCCGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGGAGGTGCT 127
DB 61 GCGCGCTCCCGCTGCGGAGCCGCTGCTGCTGCGGAGCCACTACCGGAGGTGCT 120
QY 128 GCGCGCTGCGCAGTTCGTGCGGCGCTGGGGCCCCCAAGGCGCTGGTGCAGCGCG 187
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QY 368 GCTGCTGAGAGGCGCGCGCGCGCGCGCGCGCGCTTCAACCAAGCGTGCAGCTA 427
DB 361 GCTGCTGAGAGGCGCGCGCGCGCGCGCGCGCGCTTCAACCAAGCGTGCAGCTA 420
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DB 961 GCACCAAGCGGGGCG 1020
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QY 3090 GACTGACACCGTGTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3149
Db 3301 GACTGACACCGTGTACCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
QY 3150 GCTGAGTCGGAAGCTCCCGGGGACGAGCTGACTGCTGAGGCGCGCAGCCCAACCCGCGC 3209
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGAGCTGACTGCTGAGGCGCGCAGCCCAACCCGCGC 3420
QY 3210 ACTGCCCTCAGACTTCAAGACCATCTGACTGATGAGCCACCCGCCACAGCCAGGCCGA 3269
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGACTGATGAGCCACCCGCCACAGCCAGGCCGA 3480
QY 3270 GAGCAGACACCAAGCAGCCCTGTGACCGCGGCTTACCTCCAGAGGAGGAGGCGCGCC 3329
Db 3481 GAGCAGACACCAAGCAGCCCTGTGACCGCGGCTTACCTCCAGAGGAGGAGGCGCGCC 3540
QY 3330 CACACCCAGGCGCGGACCCGCTGGAGTCTGAGGCTGAGTGAAGTGTGTTGGCCGAGGCTG 3389
Db 3541 CACACCCAGGCGCGGACCCGCTGGAGTCTGAGGCTGAGTGAAGTGTGTTGGCCGAGGCTG 3600
QY 3390 CATGTCCCGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGCGAGTGTCCAGCCCAAGGCT 3449
Db 3601 CATGTCCCGCTGAAGGCTGAGTGTCCGCTGAGGCTGAGCGAGTGTCCAGCCCAAGGCT 3660
QY 3450 GAGTGTCCAGACACCTGCGGTCTTCACTTCCCAAGGCTGCGCTGCGCTCCACCCCA 3509
Db 3661 GAGTGTCCAGACACCTGCGGTCTTCACTTCCCAAGGCTGCGCTGCGCTCCACCCCA 3720
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QY 3510 GGGCCAGCTTTTCTCTCACCAGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCATCC 3569
Db 3721 GGGCCAGCTTTTCTCTCACCAGAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCATCC 3780
QY 3570 CCAGATTGGCATTGTTCAACCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3629
Db 3781 CCAGATTGGCATTGTTCAACCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3840
QY 3630 AGGTGAGACCTTGAGAGGAGACCTGGAGCTCTGGAATTTGAGTGAACCAAGGTGTG 3689
Db 3841 AGGTGAGACCTTGAGAGGAGACCTGGAGCTCTGGAATTTGAGTGAACCAAGGTGTG 3900
QY 3690 CCCTGTACACAGGCGAGACCTTGACCTGATGAGGCTCCCTGTGGTCAAAATTGGGGG 3749
Db 3901 CCCTGTACACAGGCGAGACCTTGACCTGATGAGGCTCCCTGTGGTCAAAATTGGGGG 3960
QY 3750 GAGTGTGTGGAGTAAATACTGAATATATAGATTTTCAAGTTTGAAGAAAAA 3804
Db 3961 GAGTGTGTGGAGTAAATACTGAATATATAGATTTTCAAGTTTGAAGAAAAA 4015
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RESULT 14

ABZ22474

ID ABZ22474 standard; cDNA; 4015 BP.

XX

AC ABZ22474;

XX

DT 25-MAR-2003 (first entry)

XX

DE Human telomerase reverse transcriptase encoding cDNA SEQ ID NO:1.

XX

KW Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;

KW vulnery; antilucer; epithelial cell migration promoter; wound;

KW epithelisation; skin wound; lesion; burn; surgical incision; ulcer;

KW epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 56..3454

FT /*tag= a

FT /product= "human telomerase reverse transcriptase"

PN

WO200291999-A2.

XX

PD 21-NOV-2002.

XX

PF 09-MAY-2002; 2002WO-US014867.

XX

PR 09-MAY-2001; 2001US-0289903P.

XX

PA (GERO-) GERON CORP.

XX

PI Jiang X, Chiu C, Harley CB;

XX

DR WPI; 2003-120591/11.

XX

DR P-PSDB; ABP56676.

XX

PT Composition for treating wounds and enhancing epithelization of a skin

PT surface, comprises vector encoding telomerase reverse transcriptase or

PT telomerized epithelial cells on a microparticle or a matrix.

XX

PS Disclosure; Page 31-32; 68pp; English.

XX

CC The present invention describes a pharmaceutical composition (I)

CC comprising a vector encoding telomerase reverse transcriptase (TERT) in

CC an excipient or device, or comprises telomerized epithelial cells on a

CC microparticle or a matrix suitable for topical administration or

CC administration to a wound site. (I) has vulnery and antilucer

CC activities and can be used to promote epithelial cell migration. (I) is

CC useful for treating a wound and enhancing epithelisation of a skin

CC surface. The wound is especially skin wound including acute lesion such

CC as traumatic lesion, burn, or surgical incision, chronic lesion such as
CC chronic venous ulcer, diabetic ulcer or compression ulcer and the wound
CC is further monitored for closure. The telomerase activity or TERT
CC expression is increased in epithelial cells at the site of treatment and
CC also in fibroblasts or endothelial cells at the site of treatment. The
CC epithelial cells are especially keratinocytes. A polynucleotide encoding
CC TERT is useful for the preparation of a medicament for treatment of a
CC wound or an epithelial surface in a human or animal. An epithelial cell
CC with increased telomerase activity or increased expression of TERT is
CC useful for preparation of a medicament for the treatment of a wound in a
CC human or animal. (1) is also useful for treating wounds of other
CC epidermal surfaces including mucosal surfaces such as bronchus, mouth,
CC nose, oesophagus, stomach, or intestine. The present sequence encodes
CC human TERT (hTERT), which is given in the exemplification of the present
CC invention. hTERT is located to chromosome 5

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match	93.1%;	Score 3559;	DB 7;	Length 4015;
Best Local Similarity	94.6%;	Pred. No. 0;		
Matches 3797;	Conservative	0;	Mismatches	0;
			Indels	218;
			Gaps	2;

QY	8	GCAGCGCTGCCTCCTGCTGCGCACAGTGGAGAAAGCCCTTGCCCCGGGCCAACCCCGCGATGCC	67
Db	1	GCAGCGCTGCCTCCTGCTGCGCACAGTGGAGAAAGCCCTTGCCCCGGGCCAACCCCGCGATGCC	60
QY	68	CGCGCTCCCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	127
Db	61	CGCGCTCCCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	120
QY	128	GCCGCTGGCCACGTTGTTGCGCGCGCCCTGGGGCCCCAGGGCTGCGCGCTGTGCAGCGCGG	187
Db	121	GCCGCTGGCCACGTTGTTGCGCGCGCCCTGGGGCCCCAGGGCTGCGCGCTGTGCAGCGCGG	180
QY	188	GGACCCCGCGGCTTCCGCGCGCTGTTGCGCCAGTGCTGTGTGCGTGCCCTGGGACGC	247
Db	181	GGACCCCGCGGCTTCCGCGCGCTGTTGCGCCAGTGCTGTGTGCGTGCCCTGGGACGC	240
QY	248	ACGCGCGCCCCCGCGCGCCCTCCTTCCGCCAGGTGTCTGCTTGAAGAGCTGTGTGC	307
Db	241	ACGCGCGCCCCCGCGCGCCCTCCTTCCGCCAGGTGTCTGCTTGAAGAGCTGTGTGC	300
QY	308	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGGAGAACGTGTGCGCTTCCGCTTCCG	367
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGGAGAACGTGTGCGCTTCCGCTTCCG	360
QY	368	GCTGCTGACCGGGCCCCCGCGGGGCCCCCCCGAGGCTTCAACCAAGCGTGCAGCTA	427
Db	361	GCTGCTGACCGGGCCCCCGCGGGGCCCCCCCGAGGCTTCAACCAAGCGTGCAGCTA	420
QY	428	CCTGCCCAACACGTTGACCGCACGCACTGCGGGGGAGCGGGCGTGGGGCTGCTGTCCG	487
Db	421	CCTGCCCAACACGTTGACCGCACGCACTGCGGGGGAGCGGGCGTGGGGCTGCTGTCCG	480
QY	488	CCGCGTGGGCGACGACGTGTGTTCACTGTGACACGCTGCGCGCTCTTTGTGTGCTGT	547
Db	481	CCGCGTGGGCGACGACGTGTGTTCACTGTGACACGCTGCGCGCTCTTTGTGTGCTGT	540
QY	548	GGCTCCCACTGCGCCTACCAAGTGTGCGGGCCGCGCTGTACCAAGTCCGCGCTGCCAC	607
Db	541	GGCTCCCACTGCGCCTACCAAGTGTGCGGGCCGCGCTGTACCAAGTCCGCGCTGCCAC	600
QY	608	TCAGGCCCCCGCCCCCGCACACGTTAGTGAACCCCGAAGGCGTCTGGATGCGAAGCGGC	667
Db	601	TCAGGCCCCCGCCCCCGCACACGTTAGTGAACCCCGAAGGCGTCTGGATGCGAAGCGGC	660
QY	668	CTGGAACCATAGCGTCAAGGAGCGCGGGTCCCCCTGGGCTTGCCAGCCCGGGTGCAG	727
Db	661	CTGGAACCATAGCGTCAAGGAGCGCGGGTCCCCCTGGGCTTGCCAGCCCGGGTGCAG	720
QY	728	GAGGCGCGGGGCAAGTGCAGCCGAAAGTCTGCGTTGCCAAGAGGCCAGCGGTGGCGC	787
Db	721	GAGGCGCGGGGCAAGTGCAGCCGAAAGTCTGCGTTGCCAAGAGGCCAGCGGTGGCGC	780

QY	788	TGCCCCCTGAGCCCGAGCCGAGACGCCCCGTTGGGCAGAGGGTCTTGGGCCCAACCCGCGCAGAGAC	847
Db	781	TGCCCCCTGAGCCCGAGCCGAGACGCCCGTTGGGCAGAGGGTCTTGGGCCCAACCCGCGCAGAGAC	840
QY	848	GCGTGGACCCGAGTGACCCGTGCTTCTGTGTGTGTACACTGCCAGACCCCGCGGAAGAC	907
Db	841	GCGTGGACCCGAGTGACCCGTGCTTCTGTGTGTGTACACTGCCAGACCCCGCGGAAGAC	900
QY	908	CACCTCTTTGGAGGGGTGCGCTCTCTGGCAGCGGCCACTCCCAACCATCCGTGGGCGGCCA	967
Db	901	CACCTCTTTGGAGGGGTGCGCTCTCTGGCAGCGGCCACTCCCAACCATCCGTGGGCGGCCA	960
QY	968	GCACCAACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCGCTGTCC	1027
Db	961	GCACCAACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACGCGCTGTCC	1020
QY	1028	CCCGGTGTACGCCCGAGACCAAGCACTTCTCTACTCTCTCAGGCCGACCAAGAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCCCGAGACCAAGCACTTCTCTACTCTCTCAGGCCGACCAAGAGAGCAGCTGCG	1080
QY	1088	GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGAGGCTGTGA	1147
Db	1081	GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCACGCTGACTGGCGCTCGAGGCTGTGA	1140
QY	1148	GACCATCTTTCTGGGTCCAGGCCCTGATGCCAGGAACTCCCCGAGGTTGCCCGCT	1207
Db	1141	GACCATCTTTCTGGGTTCAGGCCCTGATGCCAGGAACTCCCCGAGGTTGCCCGCT	1200
QY	1208	GCCCCAGCGCTACTGCGCAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACAGCGCGCA	1267
Db	1201	GCCCCAGCGCTACTGCGCAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACAGCGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCACCCCAGC	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCACCCCAGC	1320
QY	1328	AGCCGCTGTCTGTGCCCGCGGAGAGAGCCCCAGGGCTCTGTGGCGGCCCCCGAGAGAGGA	1387
Db	1321	AGCCGCTGTCTGTGCCCGCGGAGAGAGCCCCAGGGCTCTGTGGCGGCCCCCGAGAGAGGA	1380
QY	1388	CACAGACCCCCCTGCGCTGTGTGACGTGCTCCGCCAGCACAGCAAGCCCTTGCGCAGGTGA	1447
Db	1381	CACAGACCCCCCTGCGCTGTGTGACGTGCTCCGCCAGCACAGCAAGCCCTTGCGCAGGTGA	1440
QY	1448	CGGCTTCGTGCGGGCTTGCCCTGCGCCGCTGTGTGCCCCCAAGGCTCTTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGGCTTGCCCTGCGCCGCTGTGTGCCCCCAAGGCTCTTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGGCTTCTCTAGGAACACCAAGAGTTCAATCTCCCTGCGGAAAGCATGCCAA	1567
Db	1501	CAACGAACGCGGCTTCTCTAGGAACACCAAGAGTTCAATCTCCCTGCGGAAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGAGAGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTCGCTGAGAGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAAGAGATCCTGGC	1687
Db	1621	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1740
QY	1748	TGTACGAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAGAGTGTCTGAG	1807
Db	1741	TGTACGAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAGAGTGTCTGAG	1800
QY	1808	CAAGTTCGAAAGCATTTGAATCAGACGCACTTGAAGAGGCTGAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTCGAAAGCATTTGAATCAGACGCACTTGAAGAGGCTGAGCTGCGGAGCTGTC	1860

QY	1868	GGAAGCAGAGGTCAGGCGACATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCGACATCGGGAAGCCAGGCCCGCCCTGCTGACGTCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTCGGGCCGATTGTGAACATGGACTACGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTCGGGCCGATTGTGAACATGGACTACGTCGTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGGCGGGCGCCCCCGGCTCTGCGGCGCTGTGCTGGG	2107
Db	2041	CAGCGTCTCAACTACGAGCGGGCGGGCGCCCCCGGCTCTGCGGCGCTGTGCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAGAGACC	2167
Db	2101	CCTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAGAGACC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTACTTTCGAAGTGATGTGACGGGGCGGTACGACACCATCCCCCA	2220
QY	2192	GGAACAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACAGTACTGCGTGG	2251
Db	2221	GGACAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACAGTACTGCGTGG	2280
QY	2252	TCCGTATGCCGTGTCCAAAGAGCCCGCCCATGGGCAACGTCGCCAAGGCTTCAAGA----	2307
Db	2281	TCCGTATGCCGTGTCCAAAGAGCCCGCCCATGGGCAACGTCGCCAAGGCTTCAAGACCA	2340
QY	2308	-----	2307
Db	2341	CGTCTTACCTTGACAGACCTCCAGCCCGTACATGCGACAGTTCTGTGCTCACCTGCAGAA	2400
QY	2308	-----	2307
Db	2401	GACCAGCCCGCTGAGGAGTCCGCTGCTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2308	-----GG	2309
Db	2461	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCACCAAGCCGTGCCATCAGGGG	2520
QY	2310	CAAGTCTTACGTCAGTCCAGTCCAGGGATCCCGCAGGGCTCCATCCTCTCCAGCGTCTGTG	2369
Db	2521	CAAGTCTTACGTCAGTCCAGTCCAGGGATCCCGCAGGGCTCCATCCTCTCCAGCGTCTGTG	2580
QY	2370	CAGCCTGTGCTACGCGCGACATGAGAACAAAGCTGTTGGGGGATTTCGGCGGACGGGCT	2429
Db	2581	CAGCCTGTGCTACGCGCGACATGAGAACAAAGCTGTTGGGGGATTTCGGCGGACGGGCT	2640
QY	2430	GCTCCTGCGTTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCACCCACGCGAAAAAC	2489
Db	2641	GCTCCTGCGTTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCACCCACGCGAAAAAC	2700
QY	2490	CTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGCTGCGTGTGAACCTTGCAGAA	2549
Db	2701	CTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGCTGCGTGTGAACCTTGCAGAA	2760
QY	2550	GACAGTGTGAACCTTCCCTGTGAGAAAGACGAGGCCCTGGGTGGCAACGGCTTTGTTCAGAT	2609
Db	2761	GACAGTGTGAACCTTCCCTGTGAGAAAGACGAGGCCCTGGGTGGCAACGGCTTTGTTCAGAT	2820
QY	2610	GCCGCCCCACGGCCTATTTCCCTGTGTGCGGCGCTGCTGTGATACCCGAGACCCTGAGGT	2669
Db	2821	GCCGCCCCACGGCCTATTTCCCTGTGTGCGGCGCTGCTGTGATACCCGAGACCCTGAGGT	2880
QY	2670	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAAGCCAGTCTCACTTCAACCG	2729
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAAGCCAGTCTCACTTCAACCG	2940
QY	2730	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAACCTTTTGGGGTCTTGCGGCTGAAGTG	2789

Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGCTCGCAAACCTCTTGGGGTCTTGCGGCTGAAGTG	3000
QY	2790	TCACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	2849
Db	3001	TCACAGCCTGTTTCTGGATTTCAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	3060
QY	2850	CAAGATCCTCCTGCTGCAGGCGGTACAGTTTCAACGATGTGTGCTGCAGCTCCCATTTCA	2909
Db	3061	CAAGATCCTCCTGCTGCAGGCGGTACAGTTTCAACGATGTGTGCTGCAGCTCCCATTTCA	3120
QY	2910	TCAGCAAGTTTGGAGAACCACCATTTTCTCTGCGGCTCATCTCTGACACGGCTCCCT	2969
Db	3121	TCAGCAAGTTTGGAGAACCACCATTTTCTCTGCGGCTCATCTCTGACACGGCTCCCT	3180
QY	2970	CTGCTACTCCATCCTTGAAAAGCCAAAGAACGCAAGGATGTGCTGGGGGCCAAGGCGCCGC	3029
Db	3181	CTGCTACTCCATCCTTGAAAAGCCAAAGAACGCAAGGATGTGCTGGGGGCCAAGGCGCCGC	3240
QY	3030	CGGCCCTCTGCGCTCCGAGGCGGTGCAGTGGCTGTGCCAACCAAGCATTCCTGCTCAAGCT	3089
Db	3241	CGGCCCTCTGCGCTCCGAGGCGGTGCAGTGGCTGTGCCAACCAAGCATTCCTGCTCAAGCT	3300
QY	3090	GACTGCACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCA	3149
Db	3301	GACTGCACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGCA	3360
QY	3150	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACCCAACCCGGC	3209
Db	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACCCAACCCGGC	3420
QY	3210	ACTGCCCTCAGACTTCAAGAACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3269
Db	3421	ACTGCCCTCAGACTTCAAGAACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3270	GAGCAGACACCAAGCAGCCCTGTCAACGCCGGGCTCTACGTCCCAAGAGGAGGGGCGGCC	3329
Db	3481	GAGCAGACACCAAGCAGCCCTGTCAACGCCGGGCTCTACGTCCCAAGAGGAGGGGCGGCC	3540
QY	3330	CACACCCAGGCCCGCAACCGCTGGAGTCTGAAGCCTGAGTGAAGTTTGGCCGAGGCTG	3389
Db	3541	CACACCCAGGCCCGCAACCGCTGGAGTCTGAAGCCTGAGTGAAGTTTGGCCGAGGCTG	3600
QY	3390	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAAGCCTGAGCGAGTGTCCAGCCAAAGGCT	3449
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAAGCCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3450	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCAACAGGCTGGCGCTCGGCTCCACCCCA	3509
Db	3661	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCAACAGGCTGGCGCTCGGCTCCACCCCA	3720
QY	3510	GGGCCAAGCTTTCCTCAACCAAGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCCATCC	3569
Db	3721	GGGCCAAGCTTTCCTCAACCAAGAGCCCGGCTTCCACTCCCAACATAGGAATAGTCCATCC	3780
QY	3570	CCAGATTCCGCATTTGTCAACCCCTGCGCCTGCCCCCTTTGCTTCCACCCCAACCATCC	3629
Db	3781	CCAGATTCCGCATTTGTCAACCCCTGCGCCTGCCCCCTTTGCTTCCACCCCAACCATCC	3840
QY	3630	AGGTGAGACCTTGAGAGAAGGACCCCTGGAGCTCTGGGAATTTGAGTGACCAAAAGGTGTG	3689
Db	3841	AGGTGAGACCTTGAGAGAAGGACCCCTGGAGCTCTGGGAATTTGAGTGACCAAAAGGTGTG	3900
QY	3690	CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCTGTGGGTCAAAATTGGGGG	3749
Db	3901	CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCTGTGGGTCAAAATTGGGGG	3960
QY	3750	GAGGTGCTGTGGAGTAAATACTGAATATATGATTTTTCAGTTTGAAGAAAAA	3804
Db	3961	GAGGTGCTGTGGAGTAAATACTGAATATATGATTTTTCAGTTTGAAGAAAAA	4015

ACC44482
ID ACC44482 standard; DNA; 4015 BP.
XX AC ACC44482;
XX 29-AUG-2003 (first entry)
XX Human telomerase reverse transcriptase gene.
XX
XX Gene; ds; human; telomerase reverse transcriptase; adipogenic capacity;
XX primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
XX anorectic; adiponectin; insulin.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 56..3454
FT /*tag=a
FT /product="telomerase reverse transcriptase"
XX
XX WO2003031640-A2.
XX
XX 17-APR-2003.
XX
XX 07-OCT-2002; 2002WO-US031635.
XX
XX 06-OCT-2001; 2001US-0327650P.
XX 06-OCT-2001; 2001US-0327651P.
XX
XX (BOST-) BOSTON MEDICAL CENT CORP.
XX
XX Kirkland J, Tchkonja T;
XX
XX WPI; 2003-421278/39.
XX P-PSDB; ABR58045.
XX
XX New primary preadipocyte strain expressing telomerase reverse
XX transcriptase, useful in research applications, screening assays,
XX clinical applications, and in the administration of therapeutic agents,
XX particularly for obesity.
XX
XX Disclosure; Page 11-13; 53pp; English..
XX
XX The invention relates to the generation of primary preadipocyte cell
XX strains that express telomerase reverse transcriptase (TERT- the
XX catalytic subunit of telomerase), and maintain and/or enhance replicative
XX potential and maintain adipogenic capacity of the cell. This sequence
XX represents the gene encoding the TERT protein. The cell strain can be
XX used in research to study all aspect of adipogenesis, especially in
XX relation to researching treatments for e.g. obesity. The cell can also be
XX used to identify adipogenesis modulators for use as therapeutic agents
XX such as hormones, growth factors, cytokines, enzymes, cholesterol binding
XX proteins, cholesterol removing proteins or their combinations.
XX Alternatively, the therapeutic agent may be an adipocytokine, preferably
XX adiponectin, or insulin
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
XX
XX
XX Query Match 93.1%; Score 3559; DB 7; Length 4015;
XX Best Local Similarity 94.6%; Pred. No. 0;
XX Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 188 GGACCCGCGGCTTTCCGCGCTGTGTGGCCCAAGTGCCTGTGTGCTGCTGCTGGAGCG 247
DB 181 GGACCCGCGGCTTTCCGCGCTGTGTGGCCCAAGTGCCTGTGTGCTGCTGCTGGAGCG 240
QY 248 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 307
DB 241 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 308 CCGAGTGTGAGAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
DB 301 CCGAGTGTGAGAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 368 GCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
DB 361 GCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
QY 428 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 487
DB 421 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 488 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 547
DB 481 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
QY 548 GCGTCCGAGCTGCGCTACAGGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
DB 541 GCGTCCGAGCTGCGCTACAGGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
QY 608 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 667
DB 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 668 CTGGAACCATAGCGTCAAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
DB 661 CTGGAACCATAGCGTCAAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 728 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
DB 721 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 788 TGCCCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
DB 781 TGCCCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
QY 848 GCGTGAACGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
DB 841 GCGTGAACGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTGAAGGT 967
DB 901 CACCTCTTGAAGGT 960
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Search completed: February 29, 2004, 21:00:05
Job time : 966.534 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 19:44:23 ; Search time 9601.49 Seconds

(without alignments)
17262.293 Million cell updates/sec

Title: US-09-424-686F-10

Perfect score: 3824

Sequence: 1 gttcagcgagcgctgcgtc.....aaaaaaaaaaaaaaaa 3824

Scoring table: IDENTITY_NUC

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

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23: em_pat:*

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28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

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37: em_htg_vrt:*

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39: em_htgo_hum:*

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41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	3767.8	98.5	3855	6 AR390472	AR390472 Sequence
4	3767.8	98.5	3855	6 AR393086	AR393086 Sequence
5	3767.8	98.5	3855	6 AX810039	AX810039 Sequence
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9	3586	93.8	4042	6 BD136185	BD136185 Human tel
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ALIGNMENTS

RESULT 1

E36795

LOCUS E36795 3855 bp DNA linear PAT 18-JUN-2001

DEFINITION Human telomerase catalytic subunit promoter.

ACCESSION E36795

VERSION E36795.1 GI:13022758

KEYWORDS UP 1999253177-A/3.

SOURCE JP 1999253177-A/3.

ORGANISM unidentified

REFERENCE 1 (bases 1 to 3855)

AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M., Calvin,B.H. and William,H.A.

TITLE Human telomerase catalytic subunit promoter

JOURNAL Patent: JP 1999253177-A 3 21-SEP-1999;

Pred. No. is the number of results predicted by chance to have a

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RESULT 2

AR243330

LOCUS AR243330

DEFINITION Sequence 4 from patent US 6475789.

ACCESSION AR243330

VERSION AR243330.1 GI:27290541

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3855)

AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B., Harley,C.B. and Andrews,W.H.

TITLE Human telomerase catalytic subunit: diagnostic and therapeutic methods

JOURNAL Patent: US 6475789-A 4 05-NOV-2002;

FEATURES

Location/Qualifiers

source 1..3855

/organism="unknown"

/mol_type="mrna"

ORIGIN

Query Match 98.5%; Score 3767.8; DB 6; Length 3855;

Best Local Similarity 99.0%; Pred. No. 0;

Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

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Db 61 GCGCGCTCCCGCTGCGCGAGCGCGCTCCCTGCTGCGAGCCACTACCGCGAGTGTCT 120

QY 128 GCGCGTGGCCACGTTCGTGCGCGCGCTGGGGGCCCCAGGGCTGGGCTGTGACGCGCG 187

Db 121 GCGCGTGGCCACGTTCGTGCGCGCGCTGGGGGCCCCAGGGCTGGGCTGTGACGCGCG 180

QY 188 GGAACCCGCGGCTTTCCGCGCGCTGCTGGCCAGTGTGCTGTGCTGCTGCGAGCGC 247

Db 181 GGAACCCGCGGCTTTCCGCGCGCTGCTGGCCAGTGTGCTGTGCTGCTGCGAGCGC 240

QY 248 ACGGCG 307

Db 241 ACGGCG 300

QY 308 CCGAGTGTGACAGAGGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367

Db 301 CCGAGTGTGACAGAGGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

QY 368 GCTGCTGGACCGGGGCG 427

Db 361 GCTGCTGGACCGGGGCG 420

QY 428 CTTGCCCAACACGCTGACCGACCACTGCGGGGAGAGCGGGGCGGTGGGGGCTGTGCTCG 487

Db 421 CTTGCCCAACACGCTGACCGACCACTGCGGGGAGAGCGGGGCGGTGGGGGCTGTGCTCG 480

QY 488 CCGCGTGGGCGAGACGCTGTGCTTCACTGTGCGACGCTGCGCGCTCTTTGTGCTGT 547

Db 481 CCGCGTGGGCGAGACGCTGTGCTTCACTGTGCGACGCTGCGCGCTCTTTGTGCTGT 540

QY 548 GCGTCCCAAGCTGCGCTTACAGAGTGTGCGGGCGCGCGCTGTACAGCTCGGCGCTGCCAC 607

Db 541 GCGTCCCAAGCTGCGCTTACAGAGTGTGCGGGCGCGCGCTGTACAGCTCGGCGCTGCCAC 600

QY 608 TCAGGCG 667

Db 601 TCAGGCG 660

QY 668 CTGAACCATAGCGTCAAGGAGCGCGGGGTCCCGCTGGGCTGCGACGCCCGGGTGCAG 727

Db 661 CTGAACCATAGCGTCAAGGAGCGCGGGGTCCCGCTGGGCTGCGACGCCCGGGTGCAG 720

QY 728 GAGGCGCGGGGCAAGTGCAGACCGCAAGTCTGCGGTGGCCCAAGAGCGCGTGGCGC 787

Db 721 GAGGCGCGGGGCAAGTGCAGACCGCAAGTCTGCGGTGGCCCAAGAGCGCGTGGCGC 780

QY 788 TGCCCTGAGCGCGGAGCGGACCGCGTGGGCAAGGGTCTGGGCGCCACCGCGGACGAC 847

Db 781 TGCCCTGAGCGCGGAGCGGACCGCGTGGGCAAGGGTCTGGGCGCCACCGCGGACGAC 840

QY 848 GCGTGAACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907

Db 841 GCGTGAACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900

QY 908 CACCTCTTTGAGAGGTGCGCTCTGTGCAAGCGCGCACTCCACCATCCGTGGCGCGCA 967

Db 901 CACCTCTTTGAGAGGTGCGCTCTGTGCAAGCGCGCACTCCACCATCCGTGGCGCGCA 960

QY 968 GCAACACCG 1027

Db 961 GCAACACCG 1020

QY 1028 CCGGCTGACCGCGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 1087

Db 1021 CCGGCTGACCGCGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080

QY 1088 GCGCTCTTCT 1147

Db 1081 GCGCTCTTCT 1140

QY 1148 GACCATCTTCTGAGTTCAGCGCGCTGATGCAAGGAGTCCCGCAGATTGCGCGCGCT 1207

Db 1141 GACCATCTTCTGAGTTCAGCGCGCTGATGCAAGGAGTCCCGCAGATTGCGCGCGCT 1200

QY 1208 GCGCGAGCGCTACTGCAAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267

Db 1201 GCGCGAGCGCTACTGCAAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260

QY 1268 GTGCGCTTACCGGGTGTCTCTCAAGACGACTGCGCGCTGCGAGCTGCGTCAACCGCAGC 1327

Db 1261 GTGCGCTTACCGGGTGTCTCTCAAGACGACTGCGCGCTGCGAGCTGCGTCAACCGCAGC 1320

QY 1328 AGCGGTGTCTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387

Db 1321 AGCGGTGTCTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380

QY 1388 CACAGACCGCGCTGCGCTGTGACGCTGCTCGCGACACAGACGCCCTGGCAGGTGTA 1447

Db 1381 CACAGACCGCGCTGCGCTGTGACGCTGCTCGCGACACAGACGCCCTGGCAGGTGTA 1440

QY 1448 CCGCTTGTGCGCGCGCTGCG 1507

Db 1441 CCGCTTGTGCGCGCGCTGCG 1500

QY 1508 CACGAAACGCGCTTCTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA 1567

Db 1501 CACGAAACGCGCTTCTCTCAGGAACACCAAGAGTTCATCTCCCTGGGGAAGCATGCCAA 1560

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Db 1561 GCTCTCGCTGACAGAGTACGTGAAGATGAGCGTGGGGAAGTGGCGTGGCGAG 1620

QY 1628 GAGCCAGGGGTGGTGTGTTCGGCGCGAGAGACCGCTGTGCGTGAAGATCTCTGGC 1687

Db 1621 GAGCCAGGGGTGGTGTGTTCGGCGCGAGAGACCGCTGTGCGTGAAGATCTCTGGC 1680

QY 1688 CAAGTCTGACCTGCTGATGATGTGTACGTGTGAGAGTGTCTCTCTTTTA 1747

Db 1681 CAAGTCTGACCTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1740

QY	1748	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTCTGAG	1807
Db	1741	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAAGTGTCTGAG	1800
QY	1808	CAAGTTGCAAAAGCATTTGGAATCAGACGACTTGAAGAGGTGCACTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACGACTTGAAGAGGTGCACTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTACGGCAGCATCGGAAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTACGGCAGCATCGGAAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGAGC	1980
QY	1988	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACGTT	2047
Db	1981	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACGTT	2040
QY	2048	CAGCGTGTbACTACGAGCGGGCGCGGGCCCCCGGCTCTCTGGGGCTCTGTGTGGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGGGCCCCCGGCTCTCTGGGGCTCTGTGTGGG	2100
QY	2108	CCTGGAACGATATCCACAGGGCTGCGGCACTTCTGTCTGCTGTGCGGGCCAGGACCC	2167
Db	2101	CCTGGAACGATATCCACAGGGCTGCGGCACTTCTGTCTGCTGTGCGGGCCAGGACCC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGGTACGACACCATCCCCCA	2220
QY	2192	GGAACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAAACACGTACTGCGTCG	2251
Db	2221	GGAACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAAACACGTACTGCGTCG	2280
QY	2252	TGCGTATGCCGTGTTCAGAAAGCCGCCATGAGGACGTCGCAAGGCCCTTCAAGAGCA	2311
Db	2281	TGCGTATGCCGTGTTCAGAAAGCCGCCATGAGGACGTCGCAAGGCCCTTCAAGAGCA	2340
QY	2312	AGTCCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGCA	2371
Db	2341	AGTCCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGCA	2400
QY	2372	GCTGTGCTACGCGGCAATGAGAAACAAGCTGTTTGGGGGATTGGCGGAGCGGGCTGC	2431
Db	2401	GCTGTGCTACGCGGCAATGAGAAACAAGCTGTTTGGGGGATTGGCGGAGCGGGCTGC	2460
QY	2432	TCCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCACGCGAAAACCT	2491
Db	2461	TCCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCACGCGAAAACCT	2520
QY	2492	TCCTCAGGACCTGTGCCAGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTGGCGGAGA	2551
Db	2521	TCCTCAGGACCTGTGCCAGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTGGCGGAGA	2580
QY	2552	CAGTGTGTAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAACGGCTTTTGTTCAGATGC	2611
Db	2581	CAGTGTGTAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCAACGGCTTTTGTTCAGATGC	2640
QY	2612	CGGCCCAACGGCTATTTCCCTGTGTGCGGGCTGCTGTGGAATACCCGGAACCTTGGAGGTGC	2671
Db	2641	CGGCCCAACGGCTATTTCCCTGTGTGCGGGCTGCTGTGGAATACCCGGAACCTTGGAGGTGC	2700
QY	2672	AGAGCGACTACTCCAGCTATGCCCCGGACCTCCATCAGAGCCAAGTCTCACTTCAACCGCG	2731
Db	2701	AGAGCGACTACTCCAGCTATGCCCCGGACCTCCATCAGAGCCAAGTCTCACTTCAACCGCG	2760
QY	2732	GCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGCTTGGCGGCTGAAGTGTG	2791
Db	2761	GCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGCTTGGCGGCTGAAGTGTG	2820
QY	2792	ACAGCCTGTTTCTGGAATTGCAAGTGAACAGCCTCCAGACGGTGTGCAACCAACATCTACA	2851

Db	2821	ACAGCCTGTTTCTGGATTGTGACAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACA	2880
QY	2852	AGATCCTCCTGCTGCAGGCGGTACAGTTTCAACGATGTGTGCTGCAGCTCCATTTTCATC	2911
Db	2881	AGATCCTCCTGCTGCAGGCGGTACAGTTTCAACGATGTGTGCTGCAGCTCCATTTTCATC	2940
QY	2912	AGCAAGTTTGAAGAAACCCACATTTTCTCGCGCTCATCTCTGACACAGGCTCCCTCT	2971
Db	2941	AGCAAGTTTGAAGAAACCCACATTTTCTCGCGCTCATCTCTGACACAGGCTCCCTCT	3000
QY	2972	GCTACTCCATCCTGAAGAACCAAGAACGAGGATGTGCTGGGGGCCAAGGCGCCCG	3031
Db	3001	GCTACTCCATCCTGAAGAACCAAGAACGAGGATGTGCTGGGGGCCAAGGCGCCCG	3060
QY	3032	GCCCTCTGACCTCCGAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3091
Db	3061	GCCCTCTGACCTCCGAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3120
QY	3092	CTCGACACCGGTTCACCTACGTGCCACTCTTGGGGTCACTCAGSACAGCCAGACGACG	3151
Db	3121	CTCGACACCGGTTCACCTACGTGCCACTCTTGGGGTCACTCAGSACAGCCAGACGACG	3180
QY	3152	TGAGTCGGAAGCTCCCGGGGACGACGCTGTACTGCCCTTGAGAGCCGACGCCAACCCGGCAC	3211
Db	3181	TGAGTCGGAAGCTCCCGGGGACGACGCTGTACTGCCCTTGAGAGCCGACGCCAACCCGGCAC	3240
QY	3212	TGCCCTCAGACTTCAAGACCATCTTGACTGTATGGCCACCCGCCCAACGCCAGGCCGAGA	3271
Db	3241	TGCCCTCAGACTTCAAGACCATCTTGACTGTATGGCCACCCGCCCAACGCCAGGCCGAGA	3300
QY	3272	GCAGACACCAAGACCCCTGTACGCGCGGCTCTACGTCCACAGGAGGAGGGGCGGCCCA	3331
Db	3301	GCAGACACCAAGACCCCTGTACGCGCGGCTCTACGTCCACAGGAGGAGGGGCGGCCCA	3360
QY	3332	CACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGAAGTTTGCCGAGGCGCTGCA	3391
Db	3361	CACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGAAGTTTGCCGAGGCGCTGCA	3420
QY	3392	TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCTGA	3451
Db	3421	TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCTGA	3480
QY	3452	GTGTCCAGCACACCTGCGGCTTCACTTCCCAACAGGCTGAGCTCGGCTCCACCCACAG	3511
Db	3481	GTGTCCAGCACACCTGCGGCTTCACTTCCCAACAGGCTGAGCTCGGCTCCACCCACAG	3540
QY	3512	GCCAGCTTTCCTCACCAGAGCCCGGCTTCCACTCCCAACATAGATATGTCATCCCC	3571
Db	3541	GCCAGCTTTCCTCACCAGAGCCCGGCTTCCACTCCCAACATAGATATGTCATCCCC	3600
QY	3572	AGATTGCGCAATTGTTCAACCCCTCGCCCTGCCCTTGTGCTTCAACCCCAACCATCCAG	3631
Db	3601	AGATTGCGCAATTGTTCAACCCCTCGCCCTGCCCTTGTGCTTCAACCCCAACCATCCAG	3660
QY	3632	GTGAGAACCTTGAGAAAGAACCCCTGGAGCTCTGGGAATTTGAGATGACCAAAAGGTGTGCC	3691
Db	3661	GTGAGAACCTTGAGAAAGAACCCCTGGAGCTCTGGGAATTTGAGATGACCAAAAGGTGTGCC	3720
QY	3692	CTGTACACAGCGCAGGACCCCTGCACTGTGAATGGGGTCCCTGTGGGTCAAATTTGGGGGGA	3751
Db	3721	CTGTACACAGCGCAGGACCCCTGCACTGTGAATGGGGTCCCTGTGGGTCAAATTTGGGGGGA	3780
QY	3752	GGTGTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAAAAAAAAAAAAA	3811
Db	3781	GGTGTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAAAAAAAAAAAAA	3840
QY	3812	AAAAAAAAAAAAA 3824	
Db	3841	AAAAAAAAAAAAA 3853	

RESULT 3

AR390472	LOCUS	AR390472	3855 bp	mRNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 4 from patent US 6610839.					
ACCESSION	AR390472					
VERSION	AR390472.1	GI:40112396				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 3855)					
AUTHORS	Morin, G.B. and Andrews, W.H.					
TITLE	Promoter for telomerase reverse transcriptase					
JOURNAL	Patent: US 6610839-A 4 26-AUG-2003;					
FEATURES	Location/Qualifiers					
source	1..3855					
	/organism="unknown"					
	/mol_type="mRNA"					
ORIGIN						
Query Match	98.5%;	Score 3767.8;	DB 6;	Length 3855;		
Best Local Similarity	99.0%;	Pred. No. 0;				
Matches 3815;	Conservative	0;	Mismatches	2;	Indels	36; Gaps 1;
QY	8	GCAGCGCTGCCTCCTGCTGCGGCACTGGGAAGCCCTGGCCCCGGCCACCCCCCGGATGCC	67			
DB	1	GCAGCGCTGCCTCCTGCTGCGGCACTGGGAAGCCCTGGCCCCGGCCACCCCCCGGATGCC	60			
QY	68	GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGTCTGCGAGCCACTACCGCGAGGTGCT	127			
DB	61	GCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGTCTGCGAGCCACTACCGCGAGGTGCT	120			
QY	128	GCCGCTGGCCACGTTCTGTCGCGCGCCTGCGGCCCAAGCTGGCGCTGGTGTGCGTGCCTGGGACGC	187			
DB	121	GCCGCTGGCCACGTTCTGTCGCGCGCCTGCGGCCCAAGCTGGCGCTGGTGTGCGTGCCTGGGACGC	180			
QY	188	GGACCCCGCGGCTTTCCGCGCGCTGTGTGCGGCCCAAGTGTGTGTGCGTGCCTGGGACGC	247			
DB	181	GGACCCCGCGGCTTTCCGCGCGCTGTGTGCGGCCCAAGTGTGTGTGCGTGCCTGGGACGC	240			
QY	248	ACGCGCGCCCCCGCGCGCCCTCTCTCCGCCAAGTGTCTGCTGAAGAGCTGTGCC	307			
DB	241	ACGCGCGCCCCCGCGCGCCCTCTCTCCGCCAAGTGTCTGCTGAAGAGCTGTGCC	300			
QY	308	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGCAAGAACGTGCTGCGCTTCGGCTTCGC	367			
DB	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGCAAGAACGTGCTGCGCTTCGGCTTCGC	360			
QY	368	GCTGTGAGACGGGGCCCGCGGGGGGGCCCCCCCCCGAAGGCTTCAACCAACGCTGCGGAGCTA	427			
DB	361	GCTGTGAGACGGGGCCCGCGGGGGGGCCCCCCCCCGAAGGCTTCAACCAACGCTGCGGAGCTA	420			
QY	428	CCTGCCCAACACGGTGAACCGCACTGCGGGGGGAGCGGGCGCTGGGGGCTGCTGTGCC	487			
DB	421	CCTGCCCAACACGGTGAACCGCACTGCGGGGGGAGCGGGCGCTGGGGGCTGCTGTGCC	480			
QY	488	CCGCGTGGGGCGACGACGTGCTGGTTCACTGCTGTGGACGCTGCGCGCTCTTGTGTGCTGT	547			
DB	481	CCGCGTGGGGCGACGACGTGCTGGTTCACTGCTGTGGACGCTGCGCGCTCTTGTGTGCTGT	540			
QY	548	GGCTCCCAAGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACCAAGCTCGGCGGTGCCAC	607			
DB	541	GGCTCCCAAGCTGCGCTTACAGGTGTGCGGGCGCGCTGTACCAAGCTCGGCGGTGCCAC	600			
QY	608	TCAGGCCCCCGCCCCCGCAACAGCTAGTGAACCCGAAGGCGTCTGGATGCAACGGGC	667			
DB	601	TCAGGCCCCCGCCCCCGCAACAGCTAGTGAACCCGAAGGCGTCTGGATGCAACGGGC	660			
QY	668	CTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCTTGCGCTGACAGCCCGCGGTGCGAG	727			
DB	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCTTGCGCTGACAGCCCGCGGTGCGAG	720			
QY	728	GAGGCGCGGGGCGAGTGCAGCCGGAAGTCTGCGCTTGCACAGAGGCGCCAGGCGGTGGCGC	787			

Db	72.1	GAGGCGCGGGGGCAGTGCACCCGGAAGTCTGCCGTTGCCCCAAGAAGGCCCAAGGCGGTGCGC	780
QY	788	TGCCCCCTGAGCCGGAGCGGACGCCCGTTGGGCAGAGGGTCTGGGCCCAACCCGGGCAAGAC	847
Db	781	TGCCCTTGAGCCCGGAGCCGACGCCCGTTGGGCAGAGGGTCTTGGGCCCAACCCGGGCAAGAC	840
QY	848	GCGTGGACCGAGTGACCGTGTTTCTGTGTGTGTCACTGCGCAGACCCCGCGAAGAAGC	907
Db	841	GCGTGGACCGAGTGACCGTGTTTCTGTGTGTGTCACTGCGCAGACCCCGCGAAGAAGC	900
QY	908	CACCTCTTTGGAGGGGTGGCTCTCTGGCAGCGCGCACTCCCAACCATCCGTGGGCGCGCA	967
Db	901	CACCTCTTTGGAGGGGTGGCTCTCTGGCAGCGCGCACTCCCAACCATCCGTGGGCGCGCA	960
QY	968	GCACCAACGCGGGCCCCCATCCACATCGCGGCGCACACGTCCCTGGGACACGCGCTGTCC	1027
Db	961	GCACCAACGCGGGCCCCCATCCACATCGCGGCGCACACGTCCCTGGGACACGCGCTGTCC	1020
QY	1028	CCCCGTGTACGCCCGAGACCAAGCACTTCTCTACTCTCAAGCGACAAGAGCAGACTGCG	1087
Db	1021	CCCCGTGTACGCCCGAGACCAAGCACTTCTCTACTCTCAAGCGACAAGAGCAGACTGCG	1080
QY	1088	GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCGCTGACTGGCGCTCGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCGCTGACTGGCGCTCGAGGCTCGTGA	1140
QY	1148	GACCATCTTTCTGGGTTCCAGGCCCTGAGTGCACAGGACTCCCCGAGGTTGCCCGGCT	1207
Db	1141	GACCATCTTTCTGGGTTCCAGGCCCTGAGTGCACAGGACTCCCCGAGGTTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGCTGCTTGGAACCAACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGCTGCTTGGAACCAACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGCTCTCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTACCCACG	1327
Db	1261	GTGCCCCCTACGGGGTGCTCTCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTACCCACG	1320
QY	1328	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGA	1387
Db	1321	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGA	1380
QY	1388	CACAGACCCCCCGTCCCTGTGTGACGTGCTCCGCCAGCACAGCAGCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCCGTCCCTGTGTGACGTGCTCCGCCAGCACAGCAGCCCCCTGGCAGGTGA	1440
QY	1448	CGGCTTGTGCGGACCTGCTGCGCCCGGCTGTGCCCCCAGGCGCTCTGGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGCGGACCTGCTGCGCCCGGCTGTGCCCCCAGGCGCTCTGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCTTCTCAGGAACACCAAGATTCACTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCTTCTCAGGAACACCAAGATTCACTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGAGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTCGCTGAGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGAGAGCAACCGTCTGCGTGAAGATCCTGGC	1687
Db	1621	GAGCCCAAGGGTTGGCTGTGTTCCGGCCGAGAGCAACCGTCTGCGTGAAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTAAGTCTGTCAGCTGCTCAGGTCCTTTCTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTAAGTCTGTCAGCTGCTCAGGTCCTTTCTTTA	1740
QY	1748	TGTCAACGAGACCAAGTTTCAAAAGAACAGAGCTCTTTTCTAACCGAAGAGTCTGAG	1807
Db	1741	TGTCAACGAGACCAAGTTTCAAAAGAACAGAGCTCTTTTCTAACCGAAGAGTCTGAG	1800
QY	1808	CAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGAGCTGTC	1860

QY	1868	GGAAGCAGAGGTCAGGCAAGCATCCGGAAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCAAGCATCCGGAAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACCGGGCTGCGGCCGATTGTGAACATGCACTACGTGCTGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACCGGGCTGCGGCCGATTGTGAACATGCACTACGTGCTGGAGC	1980
QY	1988	CAGAACGTTCCGCAAGAAAGAGGGCCGAGCGTCTCACTCTGAGAGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCAAGAAAGAGGGCCGAGCGTCTCACTCTGAGAGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCAACTACGACGGGGCGCGGCCGCCCGGCTCTGTGGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCAACTACGACGGGGCGCGGCCGCCCGGCTCTGTGGGCGCTCTGTGCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCTTGCGGCACCTTCGTGCTGCGTGTGCGGGCCAGAGACC	2167
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QY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTA-----CATCCCCA	2220
QY	2192	GGAACAGGCTCAGCGAGGTATCGCCAGCATCATCAAAACCCAGAAACACGTAAGCTGCG	2251
Db	2221	GGAACAGGCTCAGCGAGGTATCGCCAGCATCATCAAAACCCAGAAACACGTAAGCTGCG	2280
QY	2252	TCGGTATGCCGTGTCCAGAAAGCCGCCATGGGCAAGCTCCGCAAGGCTTCAAGAGCA	2311
Db	2281	TCGGTATGCCGTGTCCAGAAAGCCGCCATGGGCAAGCTCCGCAAGGCTTCAAGAGCA	2340
QY	2312	AGTCCTACGTCCAGTCCAGGCGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGCA	2371
Db	2341	AGTCCTACGTCCAGTCCAGGCGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTGCA	2400
QY	2372	GCCTGTGCTACGCGCAATGGAACAAGCTGTTGCGGGGATTGCGCGGACGGGCTGC	2431
Db	2401	GCCTGTGCTACGCGCAATGGAACAAGCTGTTGCGGGGATTGCGCGGACGGGCTGC	2460
QY	2432	TCCTGCGTTGGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAACCT	2491
Db	2461	TCCTGCGTTGGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAACCT	2520
QY	2492	TCCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGTAAGTTCGCGAAGA	2551
Db	2521	TCCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCTGTAAGTTCGCGAAGA	2580
QY	2552	CAGTGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAAGGCTTTTGTTCAGATGC	2611
Db	2581	CAGTGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCAAGGCTTTTGTTCAGATGC	2640
QY	2612	CGGCCACAGGCTATTTCCCTGTGTGCGGCTGTGCTGATACCCCGGACCCCTGAGGTGC	2671
Db	2641	CGGCCACAGGCTATTTCCCTGTGTGCGGCTGTGCTGATACCCCGGACCCCTGAGGTGC	2700
QY	2672	AGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCG	2731
Db	2701	AGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCG	2760
QY	2732	GCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGCGGCTGAAGTGC	2791
Db	2761	GCTTCAAGGCTGGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGCGGCTGAAGTGC	2820
QY	2792	ACAGCCTGTTTCTGATTTGCAAGGTGAACAGCCTCCAGACGGGTGTGCAACCAACATCTACA	2851
Db	2821	ACAGCCTGTTTCTGATTTGCAAGGTGAACAGCCTCCAGACGGGTGTGCAACCAACATCTACA	2880
QY	2852	AGATCCTCCTGCTGCAAGCGTACAGTTTCAACGATGTGTCTGCAAGTCCCATTTTCATC	2911
Db	2881	AGATCCTCCTGCTGCAAGCGTACAGTTTCAACGATGTGTCTGCAAGTCCCATTTTCATC	2940

QY	2912	AGCAAGTTTGAAGAACCCCAACATTTTTCCTGCGGTCATCTCTGACACGGCCTCCCTCT	2971
Db	2941	AGCAAGTTTGAAGAACCCCAACATTTTTCCTGCGGTCATCTCTGACACGGCCTCCCTCT	3000
QY	2972	GCTACTCCATCCTGAAAAAGCCAAAGAACGCAGGGATGTCTGTGGGGGCCAAGGGCGCGCG	3031
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QY	3032	GCCCTCTGCCCCCGAGAGCCCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3091
Db	3061	GCCCTCTGCCCCCGAGAGCCCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3120
QY	3092	CTCGACACCCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAAGCGCAGC	3151
Db	3121	CTCGACACCCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAAGCGCAGC	3180
QY	3152	TGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTCCCTGAGAGCCGACGCCAACCCGGCAC	3211
Db	3181	TGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTCCCTGAGAGCCGACGCCAACCCGGCAC	3240
QY	3212	TGCCCTCAGACTTCAAGACCATCTGACTGTGGCCACCCGCCACAGCCAGCCGCGAGA	3271
Db	3241	TGCCCTCAGACTTCAAGACCATCTGACTGTGGCCACCCGCCACAGCCAGCCGCGAGA	3300
QY	3272	GCAGACACCAGACGCCCTGTCAAGCCGGGCTTACGTCCAGAGGAGGAGGGCGGCCCA	3331
Db	3301	GCAGACACCAGACGCCCTGTCAAGCCGGGCTTACGTCCAGAGGAGGAGGGCGGCCCA	3360
QY	3332	CACCCAGGCCCGCACCCGCTGGAGTCTGAGGCTGAGTGAAGTTTGGCCGAGGCTTGA	3391
Db	3361	CACCCAGGCCCGCACCCGCTGGAGTCTGAGGCTGAGTGAAGTTTGGCCGAGGCTTGA	3420
QY	3392	TGTCCGGCTGAGGCTGAGTGTCCGGCTGAGGCTTGAAGGCTTGAAGGAGTGTCCAGCCAGGCTGA	3451
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QY	3452	GTGTCCAGACACCTGCGGCTTTCACCTTCCCAACAGGCTGGCGTCCGCTCCACCCACAG	3511
Db	3481	GTGTCCAGACACCTGCGGCTTTCACCTTCCCAACAGGCTGGCGTCCGCTCCACCCACAG	3540
QY	3512	GCCAGCTTTTCTCACACGAGGCCGGCTTCCACTCCCCACATAGGAATAGTCATCCCC	3571
Db	3541	GCCAGCTTTTCTCACACGAGGCCGGCTTCCACTCCCCACATAGGAATAGTCATCCCC	3600
QY	3572	AGATTGCGCAATTGTTCAACCCCTCGCCCTGCCCCCTTTGCTTCCACCCCCACCATCCAG	3631
Db	3601	AGATTGCGCAATTGTTCAACCCCTCGCCCTGCCCCCTTTGCTTCCACCCCCACCATCCAG	3660
QY	3632	GTGAGACCCCTGAGAAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCC	3691
Db	3661	GTGAGACCCCTGAGAAAGGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTGCC	3720
QY	3692	CTGTACACAGCGGAGGACCCCTGCACCTGGAATGGGGGTCCCTGTGGGTCAAAATTGGGGGA	3751
Db	3721	CTGTACACAGCGGAGGACCCCTGCACCTGGAATGGGGGTCCCTGTGGGTCAAAATTGGGGGA	3780
QY	3752	GGTGTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAATAAAAAAAAAAAAAA	3811
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DEFINITION	Sequence 4 from patent US 6617110.
ACCESSION	AR393086
VERSION	AR393086.1 GI:40118361
KEYWORDS	.
SOURCE	Unknown.

ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 3855) Cech,T.R., Lipner,J., Nakamura,T., Chapman,K.B., Morth,G.B., Harley,C.B. and Andrews,W.H.
TITLE	Cells immortalized with telomerase reverse transcriptase for use in drug screening
JOURNAL	Patent: US 6617110-A 4 09-SEP-2003;
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QY	68	GCGCGCTCCCGCTGCGCGCAGCGCGTGCCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	127		
Db	61	GCGCGCTCCCGCTGCGCGCAGCGCGTGCCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT	120		
QY	128	GCCGCTGCGCAGCTTCGTGCGCGCCTTGGGGCCCAAGGCTGCGCGCTGTGCAAGCGCG	187		
Db	121	GCCGCTGCGCAGCTTCGTGCGCGCCTTGGGGCCCAAGGCTGCGCGCTGTGCAAGCGCG	180		
QY	188	GGACCCCGCGGCTTCCGCGCGCTGTGGCCCAAGTGCCTGGTGTGCGTCCCTGGAGCG	247		
Db	181	GGACCCCGCGGCTTCCGCGCGCTGTGGCCCAAGTGCCTGGTGTGCGTCCCTGGAGCG	240		
QY	248	ACGCGCGCGCGCGCGCGCGCGCTTCTTCCGCCAAGTGTCTGCTGTAAGAGCTGTGCG	307		
Db	241	ACGCGCGCGCGCGCGCGCGCGCTTCTTCCGCCAAGTGTCTGCTGTAAGAGCTGTGCG	300		
QY	308	CCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGAAGAACGTGTGCGCTTGGCTTGC	367		
Db	301	CCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGTGCGCTTGGCTTGC	360		
QY	368	GCTGCTGGACGGGGCG	427		
Db	361	GCTGCTGGACGGGGCG	420		
QY	428	CCTGCCCAACACGGTGACCGCAGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGTCG	487		
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QY	488	CCGCGTGGGGCGCAGCAGTGTGTTCACTGCTGGCAAGCTGCGCGCTTTGTGTGCTGT	547		
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QY	548	GAGTCCCAAGCTGCGCCTACAGGTGCGGGCGCGCGCTGTACCAAGTGGCGCTGCCAC	607		
Db	541	GAGTCCCAAGCTGCGCCTACAGGTGCGGGCGCGCGCTGTACCAAGTGGCGCTGCCAC	600		
QY	608	TCAGGCG	667		
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QY	668	CTGGAACCATAGCGTCAGGAGGCGCGGGGTCCCGCTGGGCTGCGCAGCGCGCGGTGCGAG	727		
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QY	788	TGCGCCCTGAGCCGGAGCGGAGCGCGCGTTGGGCAAGGGGTCTGTGGGCCACCCGGGCGAG	847		
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QY	848	GCCTGACCCGAGTGAACCGTGGTTTCTGTGTGTGTCAACCTGCCAGACCCGCCGAGAAGC	907
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QY	908	CACCTCTTTGGAGGGTGCCTCTCTGGCAACCGCCCACTCCCAACCATCCCGTGGGCCGCCA	967
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QY	968	GCACCAACGG	1027
Db	961	GCACCAACGG	1020
QY	1028	CCCGGTGTACCGCCGAGACCAAGCACTTCCCTCTACTCTCTCAGGCGACAAGAGCAAGCTGCC	1087
Db	1021	CCCGGTGTACCGCCGAGACCAAGCACTTCCCTCTACTCTCTCAGGCGACAAGAGCAAGCTGCC	1080
QY	1088	GCCCTCCTTCTACTCAAGCTCTCTGAGGGCCAGCCCTGACTGGCGCTCGAGGCTCTGTGA	1147
Db	1081	GCCCTCCTTCTACTCAAGCTCTCTGAGGGCCAGCCCTGACTGGCGCTCGAGGCTCTGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCGCCCTGGATGCGAGGGACTCCCGCAGGTTGCCCGCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCGCCCTGGATGCGAGGGACTCCCGCAGGTTGCCCGCT	1200
QY	1208	GCCCCAGCGCTACTGCAAAATGCGGGCCCTGTCTTCTGGAGCTGCTTGGAAACACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGCAAAATGCGGGCCCTGTCTTCTGGAGCTGCTTGGAAACACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCACG	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCACG	1320
QY	1328	AGCCGGTGTGTGCCCCGGAGAGAGCCCGAGGGCTGTGTGGCGGGCCCCCGAGAGAGAGGA	1387
Db	1321	AGCCGGTGTGTGCCCCGGAGAGAGCCCGAGGGCTGTGTGGCGGGCCCCCGAGAGAGAGGA	1380
QY	1388	CACAGACCCCGCTGCGCTGTGTGAGCTGCTCCGCCAGCACAGCAGCAGCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCGCTGCGCTGTGTGAGCTGCTCCGCCAGCACAGCAGCAGCCCTGGCAGGTGA	1440
QY	1448	CGGCTTGTGCGGGCTGCTGCGCCGCGCTGTGCCCCCAGGCTCTTGGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGCGGGCTGCTGCGCCGCGCTGTGCCCCCAGGCTCTTGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGTTGGCTGCAG	1627
Db	1561	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGTTGGCTGCAG	1620
QY	1628	GAGCCAGAGGGTTGGCTGTGTTCCGGCCGACAGACCCGTCTGCGTGAGAGAGATCTTGCC	1687
Db	1621	GAGCCAGAGGGTTGGCTGTGTTCCGGCCGACAGACCCGTCTGCGTGAGAGAGATCTTGCC	1680
QY	1688	CAAGTCTCTGCACTGGCTGATGAGTGTGTAAGTGTGAGCTGCTCAGGTCTTTCTTTTA	1747
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QY	1748	TGTCAACGAGACCAAGTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1807
Db	1741	TGTCAACGAGACCAAGTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1800
QY	1808	CAAGTTCGAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGGAGCTGTC	1867
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QY	1868	GGAAGCAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGTGACGTCCAGACTCCG	1920

QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACAATGAACTACGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACAATGAACTACGTCGTGGAGC	1980
QY	1988	CAGAACGTTCGCGAGAGAAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCGCGAGAGAAAAGAGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGGCGCGGCCGCCCGGCTCCTGGGGCCTCTGTGTGGG	2107
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QY	2108	CCTGACGATATCCACAGGGCCTGGCGCACTTCGTGTGTGTGTGGGGCCAGAACCC	2167
Db	2101	CCTGACGATATCCACAGGGCCTGGCGCACTTCGTGTGTGTGTGGGGCCAGAACCC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACCATCCCCA	2220
QY	2192	GGAACAGCTCAGGAGGTCAATGCCAGCATCATCAAAACCCAGAACACGTACTGGCGG	2251
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QY	2252	TCGGTATGCCGTGTGCCAGAAAGCCGCCCATGGGCACGTGCCAAGGCTTCAAGAGCA	2311
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QY	2312	AGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGGCTCCATCCTCTCCACGCTGCTGCA	2371
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Db	2401	GCCTGTGCTACGGCGACATGAGAACCAAGCTGTTTGGGGGATTCGGCGGAGCGGCTGC	2460
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QY	2552	CAGTGTGAACCTTCCCTGTAGAGAAGAGGCCCTGGGTGGCAAGGCTTTGTTCAGATGC	2611
Db	2581	CAGTGTGAACCTTCCCTGTAGAGAAGAGGCCCTGGGTGGCAAGGCTTTGTTCAGATGC	2640
QY	2612	CGGCCACGGCCTATTTCCCTGTGCGGCTGCTGCTGATACCCGGAACCTGAGGTGC	2671
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Db	3241	TGCCCTCAGACTTCAAGACCATCCTGCACTGATGGCCAACCCGCCACAGCCAGGCCGAGA	3300
QY	3272	GCAGACACCAGACGCCCTGTCAACGCCGGGCTTACGTCCCAAGGAGGAGGGCGGCCCA	3331
Db	3301	GCAGACACCAGACGCCCTGTCAACGCCGGGCTTACGTCCCAAGGAGGAGGGCGGCCCA	3360
QY	3332	CACCCAGGCCCGCACCCGCTGGGAGTCTGAGGCCCTGAGTGAAGTGTGGCCGAGCCTGCA	3391
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QY	3512	GCCAGCTTTTCTCAACAGGAGCCCGGCTTCCACTCCCAATAGGAATGTCATCCC	3571
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QY	3572	AGATTGSCCATGTGTCAACCCCTGCGCCTGCGCTTCTTGCTTCCACCCCAATCCAG	3631
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QY	3632	GTGAGACCTGAGAAGGAGCCCTGGAGCTCTGGAATTTGAGTGACCAAGGTGTGCC	3691
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QY	3692	CTGTACACAGGCGAGGAGCCCTGCACCTGATGGGGGTCCCTGTGGGTCAAAATTGGGGGA	3751
Db	3721	CTGTACACAGGCGAGGAGCCCTGCACCTGATGGGGGTCCCTGTGGGTCAAAATTGGGGGA	3780
QY	3752	GGTGTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGTGAAAAAATTTGGGGGA	3811
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ACCESSION	AX810039			
VERSION	AX810039.1	GI:38523862		
KEYWORDS				
SOURCE				
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,			

TITLE Harley, C.B. and Andrews, W.H.
Human telomerase catalytic subunit
JOURNAL Patent: EP 133094-A 4 06-AUG-2003;
Geron Corporation (US); University Technology Corporation (US)

FEATURES Location/Qualifiers

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ORIGIN

Query Match 98.5%; Score 3767.8; DB 6; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

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DB 1561 GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
QY 1628 GAGCCCAAGGCTTGGCTGTGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1687
DB 1621 GAGCCCAAGGCTTGGCTGTGTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1680

QY	1688	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCCTTCTTTTA	1740
QY	1748	TGTCACGGAGAACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAAGAGTGTCTGAG	1807
Db	1741	TGTCACGGAGAACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAAGAGTGTCTGAG	1800
QY	1808	CAAGTTGCAAAAGCATTGGAATCAGACGACTTGAAGAGGATGACCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTGGAATCAGACGACTTGAAGAGGATGACCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTGAGGACAGCATCGGGAAGCCAGGCCCCGCTGTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTGAGGACAGCATCGGGAAGCCAGGCCCCGCTGTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACCGGCTGCGGCCGATTTGTGAACATGGAATACTAGTCGTGGAGC	1987
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LOCUS BD011046 3855 bp DNA linear PAT 31-JAN-2002
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011046
VERSION BD011046.1 GI:18639419
KEYWORDS JP 2001081042-A/3.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 3855)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 3 27-MAR-2001;
GERON CORP, UNIVERSITY TECHNOLOGY CORP

COMMENT OS Unidentified
PN JP 2001081042-A/3
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
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14-AUG-1997 US 08/912951, 14-AUG-1997 US 08/915503 PI THOMAS
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MORIN,

PI CALVIN B HARLEY, WILLIAM H ANDREWS
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CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 56..2479.

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ORIGIN

Query Match 98.5%; Score 3767.8; DB 6; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

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QY 68 GCGCGCTCCCCCTGCGAGCGCTGCTCTGCTGCGCAGCCACTACCGCGAGGTGCT 127
Db 61 GCGCGCTCCCCCTGCGAGCGCTGCTCTGCTGCGCAGCCACTACCGCGAGGTGCT 120
QY 128 GCGCGTGGCAGCTTCTGCGCGCGCTGGGGCCCCCAGGGCTGGGCTGTGAGCGCG 187
Db 121 GCGCGTGGCAGCTTCTGCGCGCGCTGGGGCCCCCAGGGCTGGGCTGTGAGCGCG 180
QY 188 GGAACCGGCGGCTTCTGCGCGCGCTGGGGCCCCCAGGGCTGGGCTGTGAGCGCG 247
Db 181 GGAACCGGCGGCTTCTGCGCGCGCTGGGGCCCCCAGGGCTGGGCTGTGAGCGCG 240
QY 248 ACGGCG 307
Db 241 ACGGCG 300

QY 308 CCGAGTGTGAGAGAGGCTGTGCGCAGCGCGCGCGCGCGAGAGACGTGCTGCGCTTCCG 367
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Db	1441	CGGCTTCGTGCGGGCCTGCTGCGCGCGCTGGTGCCCCAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTATCTCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCCGCTTCTCAGGAACACCAAGAAGTTATCTCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAAGGAGCTGACGTGGGAATGAGCGTGCGGAGCTGCGCTTGCGCGAG	1627
Db	1561	GCTCTCGCTGCAAGGAGCTGACGTGGGAATGAGCGTGCGGAGCTGCGCTTGCGCGAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTGTTCCGCGCGCAGAGACACCGCTGCGGTGAGAGATCCTGGC	1687
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QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGAGCTCAGAGTCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGAGCTCAGAGTCTTTCTTTTA	1740
QY	1748	TGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAGAGTGTCTGGAG	1807
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Db	1861	GGAAGCAGAGGTCAGGCAAGCATGTGGGAAGCCAGGCCCGCCTGTGACGTCCAGACTCCG	1920
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Db	2161	GCCGCGTGAAGTGTAA-----CATCCCCCA	2220
QY	2192	GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTACTGCTGGC	2251
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KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4042)
AUTHORS Wick, M. and Hagen, G.
TITLE HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC AND
THERAPEUTIC USE
JOURNAL Patent: WO 9859040-A 1 30-DEC-1998;
WICK MARESA (DE); BAYER AG (DE)
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 93.8%; Score 3586; DB 6; Length 4042;
Best Local Similarity 94.6%; Pred. No. 0;
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KEYWORDS

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 Wick, M. and Hagen, G.

Regulatory dna sequences of the human catalytic telomerase sub-unit
gene, diagnostic and therapeutic use thereof

JOURNAL Patent: WO 9333998-A 2 08-JUL-1999;
WICK MARESA (DE); BAYER AG (DE)

FEATURES
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Location/Qualifiers

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ORIGIN

Query Match 93.8%; Score 3586; DB 6; Length 4042;
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Db 1861 AGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCGCGCTGCTGAGCTCA 1920
QY 1921 GACTCCGCTTCAATCCCAAGCCTGACGCGGCTGCGCGGATTTGAACATGACTACGTG 1980
Db 1921 GACTCCGCTTCAATCCCAAGCCTGACGCGGCTGCGCGGATTTGAACATGACTACGTG 1980

QY 1981 TGGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTGAGGGTGAAG 2040
Db 1981 TGGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTGAGGGTGAAG 2040
QY 2041 CACTGTTACAGGTGCTCAACTACAGCGGGCGCGCGCGCGCGCGCTCTGGCGCTCTG 2100
Db 2041 CACTGTTACAGGTGCTCAACTACAGCGGGCGCGCGCGCGCGCGCTCTGGCGCTCTG 2100
QY 2101 TGCTGGCTTGAACGATATCCAGAGGCGCTGGCGCACCTTCTGCTGCTGCTGCGGCG 2160
Db 2101 TGCTGGCTTGAACGATATCCAGAGGCGCTGGCGCACCTTCTGCTGCTGCTGCGGCG 2160
QY 2161 AGACCGCGCGCTGAGCTGTA-----CA 2184
Db 2161 AGACCGCGCGCTGAGCTGTA-----CA 2184
QY 2185 TCCCCAGAGCAGGCTCAGAGGTATCGCCAGCATCAAAACCCAGAACAGTACT 2244
Db 2221 TCCCCAGAGCAGGCTCAGAGGTATCGCCAGCATCAAAACCCAGAACAGTACT 2280
QY 2245 GCGTGCCTGATGCGGTGCTGCAAGAGCGCGCCCAATGGGCACTCCGCAAGCGCTCA 2304
Db 2281 GCGTGCCTGATGCGGTGCTGCAAGAGCGCGCCCAATGGGCACTCCGCAAGCGCTCA 2340
QY 2305 AGA----- 2307
Db 2341 AGAGCCAGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGCTCAC 2400
QY 2308 ----- 2307
Db 2401 TGACAGAGACAGCGCGCTGAGGAGTGCCTGCTCATCGACAGAGCTCCTCCGTAATG 2460
QY 2308 ----- 2307
Db 2461 AGGCCAGAGTGCGCTCTTCAAGCTCTTCTACGCTTCACTGCGCACACGCGGTGCGCA 2520
QY 2308 -----GCAAGTCTTACGTCAGTGCCAGGGAGTCCCGCAGGCTCCATCTTCAAGC 2362
Db 2521 TCAAGGCAAGTCTTACGTCAGTGCCAGGGAGTCCCGCAGGCTCCATCTTCAAGC 2580
QY 2363 TGCTCTGACGCTGTGTCACGCGGACATGAGAGACAGCTGTTGCGGGGATTCGCGGG 2422
Db 2581 TGCTCTGACGCTGTGTCACGCGGACATGAGAGACAGCTGTTGCGGGGATTCGCGGG 2422
QY 2423 ACGGCTGCTCTGCTGCTTGTGATGATTTCTTGTGTGACACCTCACTTCAACCCAG 2482
Db 2641 ACGGCTGCTCTGCTGCTTGTGATGATTTCTTGTGTGACACCTCACTTCAACCCAG 2700
QY 2483 CGAAACCTTCTCAGAGACCTGTGTCGAGGTGCTTCCAGATGCTGCTGCTGCTGCTG 2542
Db 2701 CGAAACCTTCTCAGAGACCTGTGTCGAGGTGCTTCCAGATGCTGCTGCTGCTGCTG 2760
QY 2543 TGGGGAAGACAGTGTGAATCTTCCCTGTGAAGACAGAGCGCTGCTGCTGCTGCTT 2602
Db 2761 TGGGGAAGACAGTGTGAATCTTCCCTGTGAAGACAGAGCGCTGCTGCTGCTGCTT 2820
QY 2603 TTCAAGTCCGCGCCACGCGCTATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2662
Db 2821 TTCAAGTCCGCGCCACGCGCTATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2880
QY 2663 TGGAGGTGACAGGCACTACTCAGCTATGCGCGGACCTCCATCAGAGGCACTTCACT 2722
Db 2881 TGGAGGTGACAGGCACTACTCAGCTATGCGCGGACCTCCATCAGAGGCACTTCACT 2940
QY 2723 TCAACCGCGCTTCAAGGCTGGAGGAACATGCGTGCMAACTCTTGGGGTCTTGGCG 2782
Db 2941 TCAACCGCGCTTCAAGGCTGGAGGAACATGCGTGCMAACTCTTGGGGTCTTGGCG 3000
QY 2783 TGAAGTGTACAGCTGTTCTGATTTGCAAGGTGAACAGGCTTCAAGCGGTGACCA 2842
Db 3001 TGAAGTGTACAGCTGTTCTGATTTGCAAGGTGAACAGGCTTCAAGCGGTGACCA 3060
QY 2843 ACATCTACAAGATCTCTGCTGACGCGGTACAGGTTTACGCAATGTGTGCTGACGCTCC 2902

Dp	3061	ACATCTACAAGATCCTCCTGCTGCAGGCGGTACAGGTTTCAACGATGTGTGCTGCAGCTCC	3120
QY	2903	CATTTCATCAGCAAGTTTGGAGAAGAACCCACATTTTTCCTGCGCGTCATCTGTGACACGG	2962
Dp	3121	CATTTCATCAGCAAGTTTGGAGAAGAACCCACATTTTTCCTGCGCGTCATCTGTGACACGG	3180
QY	2963	CCTCCCTCTGCTACTCCATCTCTGAAGCCAGAAGCAGGATGTGCTGGGGCCAAAG	3022
Dp	3181	CCTCCCTCTGCTACTCCATCTCTGAAGCCAGAAGCAGGATGTGCTGGGGCCAAAG	3240
QY	3023	GCGCCGCGGCGCCTCTGCGCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGC	3082
Dp	3241	GCGCCGCGGCGCCTCTGCGCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGC	3300
QY	3083	TCAAGCTGACTGCACACCGGTGTCACTACGTGCCACTCTGGGGTCACTCAGACAGCCC	3142
Dp	3301	TCAAGCTGACTGCACACCGGTGTCACTACGTGCCACTCTGGGGTCACTCAGACAGCCC	3360
QY	3143	AGACGCACTGAGTCGGAAGCTCCGGGAGCAGCGCTGACTGCCCTGAGGCGCCAGCCA	3202
Dp	3361	AGACGCACTGAGTCGGAAGCTCCGGGAGCAGCGCTGACTGCCCTGAGGCGCCAGCCA	3420
QY	3203	ACCCGCACTGCGCCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCCCAAGCC	3262
Dp	3421	ACCCGCACTGCGCCTCAGACTTCAAGACCATCTGGACTGATGGCCACCGCCCAAGCC	3480
QY	3263	AGGCCGAGACAGACACCAAGCAGCCCTGTCAAGCCCGGCTCTACGTCCCAAGGAGGAGG	3322
Dp	3481	AGGCCGAGACAGACACCAAGCAGCCCTGTCAAGCCCGGCTCTACGTCCCAAGGAGGAGG	3540
QY	3323	GCGCGCCCAACACCCAGGCGCCGCAACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCCG	3382
Dp	3541	GCGCGCCCAACACCCAGGCGCCGCAACCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCCG	3600
QY	3383	AGGCTGCAATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCC	3442
Dp	3601	AGGCTGCAATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGGAGTGTCCAGCC	3660
QY	3443	AAGGCTGAGTGTCCAGCAACCTGCGCTTCACTTCCCAAGGCTGCGCTCGGCTC	3502
Dp	3661	AAGGCTGAGTGTCCAGCAACCTGCGCTTCACTTCCCAAGGCTGCGCTCGGCTC	3720
QY	3503	CACCCAGGCGCAGCTTTTCTCACAGAGAGCCGGCTTCACTCCCAATAGGAATAG	3562
Dp	3721	CACCCAGGCGCAGCTTTTCTCACAGAGAGCCGGCTTCACTCCCAATAGGAATAG	3780
QY	3563	TCCATCCCCAGATTGCGCATTTGTCACCCCTGCGCTCCTTGTGCTTCAACCCCC	3622
Dp	3781	TCCATCCCCAGATTGCGCATTTGTCACCCCTGCGCTCCTTGTGCTTCAACCCCC	3840
QY	3623	ACCATCCAGGTGAGAACCTTGAGAAGAGACCCTGGAGCTCTGGGAATTTGAGTGAACCA	3682
Dp	3841	ACCATCCAGGTGAGAACCTTGAGAAGAGACCCTGGAGCTCTGGGAATTTGAGTGAACCA	3900
QY	3683	AGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAAA	3742
Dp	3901	AGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAAA	3960
QY	3743	TTGGGGGAGGAGTGTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAA	3802
Dp	3961	TTGGGGGAGGAGTGTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAAGAAA	4020
QY	3803	AAAAAAAAAAAAAAAAAAAAA 3824	
Dp	4021	AAAAAAAAAAAAAAAAAAAAA 4042	

RESULT	10		
E36819			
LOCUS	E36819	4037 bp	DNA
DEFINITION	Human telomerase catalytic subunit		linear
ACCESSION	E36819		PAT 18-JUN-2001
			promoter.

[illegible]

QY	428	CCTGCCCAACACGGTGAACCGACGACTGCGGGGAGCGGGGGCGTGGGGCTGCTGTCG	487
Db	421	CCTGCCCAACACGGTGAACCGACGACTGCGGGGAGCGGGGGCGTGGGGCTGCTGTCG	480
QY	488	CCGCGTGGGCGACGACGCTGTGTTCACTGTGGCAAGCTGCGGCTTTTGTGTGT	547
Db	481	CCGCGTGGGCGACGACGCTGTGTTCACTGTGGCAAGCTGCGGCTTTTGTGTGT	540
QY	548	GGCTTCCAGCTGCGCCTACCAGTGTGCGGGCGCGCTGTACAGCTCGGCGTGCCAC	607
Db	541	GGCTTCCAGCTGCGCCTACCAGTGTGCGGGCGCGCTGTACAGCTCGGCGTGCCAC	600
QY	608	TCAGGCCCCGCCCCCGCCACACGCTAGTGAACCCCGAAGCGCTTGGGATGCCAACGGG	667
Db	601	TCAGGCCCCGCCCCCGCCACACGCTAGTGAACCCCGAAGCGCTTGGGATGCCAACGGG	660
QY	668	CTGGAAACCATAGCGTCAGGAGGCGCGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAG	727
Db	661	CTGGAAACCATAGCGTCAGGAGGCGCGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCGAG	720
QY	728	GAGGCGCGGGGGCAGTGCACGCCAGTCTGCCGTTGCCAAGAGCCCAAGGCGTGCGC	787
Db	721	GAGGCGCGGGGGCAGTGCACGCCAGTCTGCCGTTGCCAAGAGCCCAAGGCGTGCGC	780
QY	788	TGCCCTGAGCCCGAGCGGACGCCCGTTGGGCAAGGGTCTTGCGGCCCAACCCGGGCAAGAC	847
Db	781	TGCCCTGAGCCCGAGCGGACGCCCGTTGGGCAAGGGTCTTGCGGCCCAACCCGGGCAAGAC	840
QY	848	GCGTGAACCGAGTGACCGTGTGTTCTGTGTGTCACTGCGCAGACCCGCGAAGAAGC	907
Db	841	GCGTGAACCGAGTGACCGTGTGTTCTGTGTGTCACTGCGCAGACCCGCGAAGAAGC	900
QY	908	CACCTCTTTGAGAGGTGCGCTCTGTGGCACGCGCACTCCCAATCCGTGGGCGGCCA	967
Db	901	CACCTCTTTGAGAGGTGCGCTCTGTGGCACGCGCACTCCCAATCCGTGGGCGGCCA	960
QY	968	GCAACACGCGGGCCCCCATCCACATCGCGCCACCAAGTCCCTGGGACACGCTTGTCC	1027
Db	961	GCAACACGCGGGCCCCCATCCACATCGCGCCACCAAGTCCCTGGGACACGCTTGTCC	1020
QY	1028	CCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGAGCAGTGC	1087
Db	1021	CCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCCTCAGGCGACAAGAGCAGTGC	1080
QY	1088	GCCCTCCTTCTACTCAGCTCTGTAGGCCAGCCTGATGCGGCTCGGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTACTCAGCTCTGTAGGCCAGCCTGATGCGGCTCGGAGGCTCGTGA	1140
QY	1148	GACCATCTTCTGAGTTCCAGGCGCTGATGCCAGGACCTCCCGAGGTTGCCCGCCT	1207
Db	1141	GACCATCTTCTGAGTTCCAGGCGCTGATGCCAGGACCTCCCGAGGTTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGGCGCCCTGTCTTCTGAGAGCTTGGGAACCAACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGGCGCCCTGTCTTCTGAGAGCTTGGGAACCAACGCGCA	1260
QY	1268	GTGCCCCCTACGGGCTGCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGC	1327
Db	1261	GTGCCCCCTACGGGCTGCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGCGCCCCCGAGGAGGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGCGCCCCCGAGGAGGAGGA	1380
QY	1388	CACAGACCCCCCGTGGCTGTGTGTCAGCTGCTCCGCGACAGACAGACGCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCCGTGGCTGTGTGTCAGCTGCTCCGCGACAGACAGACGCCCCCTGGCAGGTGA	1440
QY	1448	CGGCTTGTGCGGGCGTGTGCGCGCGCTGTGTGCCCCCAAGGCTCTGCGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGCGGGCGTGTGCGCGCGCTGTGTGCCCCCAAGGCTCTGCGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCTTCTCTCAGGAACAACCAAGATTCATCTCCCTGGGGAAGCATGCCAA	1567

[illegible]

Dp	2581	CAGCTGTGCTACGGCGACATGAGAA	CAAGCTGTTTGGGGGATT	CGCGGACGGGCT	2640
QY	2430	GCTCCTGCGTTTGGTGATGATTTCTGTTGGTGACACACTCACTCA	CAACCCACGGAAAC		2489
Dp	2641	GCTCCTGCGTTTGGTGATGATTTCTGTTGGTGACACACTCACTCA	CAACCCACGGAAAC		2700
QY	2490	CTTCTCAAGAACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGGTGTA	CTTGCGGA		2549
Dp	2701	CTTCTCAAGAACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGGTGTA	CTTGCGGA		2760
QY	2550	GACAGTGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGACGG	CTTTGTTCAGAT		2609
Dp	2761	GACAGTGTGAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGACGG	CTTTGTTCAGAT		2820
QY	2610	GCGGCGCCACGGCCTATTTCCCTGGTGGCGGCTGTGCTGAATA	CCCGGACCCCTGAGGT		2669
Dp	2821	GCGGCGCCACGGCCTATTTCCCTGGTGGCGGCTGTGCTGAATA	CCCGGACCCCTGAGGT		2880
QY	2670	GCAGAGGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGT	CTCACTTCAACCG		2729
Dp	2881	GCAGAGGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGT	CTCACTTCAACCG		2940
QY	2730	CGGCTTCAAGGCTGGGAGGAAACATGCGTCGCAAACTCTTTGGGGT	CTTGGCGCTGAAGTG		2789
Dp	2941	CGGCTTCAAGGCTGGGAGGAAACATGCGTCGCAAACTCTTTGGGGT	CTTGGCGCTGAAGTG		3000
QY	2790	TCACAGCCTGTTTCTGGAATTGGAGGTGAACAGCCTCCAGACGGT	GTGCACCAACATCTA		2849
Dp	3001	TCACAGCCTGTTTCTGGAATTGGAGGTGAACAGCCTCCAGACGGT	GTGCACCAACATCTA		3060
QY	2850	CAAGATCCTCCTGCTGCAGGCGGTACAGGTTCAACGATGTGTGCT	GCAGCTCCCATTTCA		2909
Dp	3061	CAAGATCCTCCTGCTGCAGGCGGTACAGGTTCAACGATGTGTGCT	GCAGCTCCCATTTCA		3120
QY	2910	TCAGCAAGTTTGAAGAACCACCATTTTTCCTGCGCTCATCTGACA	CGGCTCCT		2969
Dp	3121	TCAGCAAGTTTGAAGAACCACCATTTTTCCTGCGCTCATCTGACA	CGGCTCCT		3180
QY	2970	CTGCTACTCCATCCTGAAAGCCAAAGAACGACGAGGATGCTGGGG	CCAAAGGCGCCGC		3029
Dp	3181	CTGCTACTCCATCCTGAAAGCCAAAGAACGACGAGGATGCTGGGG	CCAAAGGCGCCGC		3240
QY	3030	CGGCCCTCTGCCCCCGGAGGCGGTGCAGTGGCTGTGCCAACATTC	CTGCTCAAGCT		3089
Dp	3241	CGGCCCTCTGCCCCCGGAGGCGGTGCAGTGGCTGTGCCAACATTC	CTGCTCAAGCT		3300
QY	3090	GACTCGACACCGGTACCTACGTGCCACTCCTGGGGTCACTCAGACA	GGCCAGCGCA		3149
Dp	3301	GACTCGACACCGGTACCTACGTGCCACTCCTGGGGTCACTCAGACA	GGCCAGCGCA		3360
QY	3150	GCTGAGTGGAAAGCTCCGGGGGACGACGCTGACTGCCCTGGAAG	CGCCAGCCAAACCCGGC		3209
Dp	3361	GCTGAGTGGAAAGCTCCGGGGGACGACGCTGACTGCCCTGGAAG	CGCCAGCCAAACCCGGC		3420
QY	3210	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGACCAACCC	GGCCACAGCCAGGCCGA		3269
Dp	3421	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGACCAACCC	GGCCACAGCCAGGCCGA		3480
QY	3270	GAGCAGACACCAAGCAGCCTGTCAAGCCGGGCTCTACGTCCCA	GGAAGGAGGGGCGGCC		3329
Dp	3481	GAGCAGACACCAAGCAGCCTGTCAAGCCGGGCTCTACGTCCCA	GGAAGGAGGGGCGGCC		3540
QY	3330	CACACCCAGGCCCCGCAACCGCTGGGAGTCTGAGGCTGAGTGT	TTTGGCCGAGGCCCTG		3389
Dp	3541	CACACCCAGGCCCCGCAACCGCTGGGAGTCTGAGGCTGAGTGT	TTTGGCCGAGGCCCTG		3600
QY	3390	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTTGAAGGT	TTCCAGGCTCAAGGCT		3449
Dp	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTTGAAGGT	TTCCAGGCTCAAGGCT		3660
QY	3450	GAGTGTCCAGACACACTGCGCTTCACTTCCCCACAGGCTGGCG	CTCGGCTTCAACCCCA		3509
Dp	3661	GAGTGTCCAGACACACTGCGCTTCACTTCCCCACAGGCTGGCG	CTCGGCTTCAACCCCA		3720

QY	3510	GGGCCAGCTTTTCTCTCAACCAGGAGCCCGGCTTCACTCCCAATAGATGTCATCC	3569
Dp	3721	GGGCCAGCTTTTCTCTCAACCAGGAGCCCGGCTTCACTCCCAATAGATGTCATCC	3780
QY	3570	CCAGATTGGCCATTGTTCAACCCCTGCGCCCTGCTCCTTGGCTTCCACCCCAATCC	3629
Dp	3781	CCAGATTGGCCATTGTTCAACCCCTGCGCCCTGCTCCTTGGCTTCCACCCCAATCC	3840
QY	3630	AGGTGAGAGCCCTGAGAGGACCCCTGGAGCTCTGGGAATTTGAGTGACCAAGGTGTG	3689
Dp	3841	AGGTGAGAGCCCTGAGAGGACCCCTGGAGCTCTGGGAATTTGAGTGACCAAGGTGTG	3900
QY	3690	CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGTCAAAATTGGGGG	3749
Dp	3901	CCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGTCAAAATTGGGGG	3960
QY	3750	GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTGTGAAAAA	3809
Dp	3961	GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTGTGAAAAA	4020
QY	3810	AAAAAAAAAAAAAAAA 3824	
Dp	4021	AAAAAAAAAAAAAAAA 4035	

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RESULT 11
AR390496
LOCUS      AR390496              4037 bp      mRNA
DEFINITION Sequence 343 from patent US 6610839.
ACCESSION  AR390496
VERSION     AR390496.1
KEYWORDS   GI:40112420
SOURCE      .
ORGANISM   Unknown.
            Unknown.
REFERENCE   1 (bases 1 to 4037)
AUTHORS    Morin,G.B. and Andrews,W.H.
TITLE       Promoter for telomerase reverse transcriptase
JOURNAL     Patent: US 6610839-A 343 26-AUG-2003;
FEATURES    Location/Qualifiers
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             /organism="unknown"
             /mol_type="mRNA"

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Query Match	93.4%;	Score 3572.6;	DB 6;	Length 4037;
Best Local Similarity	94.4%;	Pred. No. 0;		
Matches 3810;	Conservative	4;	Mismatches 3;	Indels 218; Gaps 2;
QY	8	GCAGCGCTGCGTCTCTGCTGCGCAGTGGGAAGCCCTTGCCCCGGCCACCCCGCATGCC	67	
Db	1	GCAGCGCTGCGTCTCTGCTGCGCAGTGGGAAGCCCTTGCCCCGGCCACCCCGCATGCC	60	
QY	68	GCGCGCTCCCGCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTTACCGGAGGTCT	127	
Db	61	GCGCGCTCCCGCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTTACCGGAGGTCT	120	
QY	128	GCCGCTGGCCACGTTCTGTGCGGCGCTTGGGGCCCCCAGGGCTGGCGGCTGTGACGCGGG	187	
Db	121	GCCGCTGGCCACGTTCTGTGCGGCGCTTGGGGCCCCCAGGGCTGGCGGCTGTGACGCGGG	180	
QY	188	GGACCCGGCGGCTTTCGCGCGCGCTGTGGCCCAAGTGCTGTGTGCGTGCCCTTGGGACGC	247	
Db	181	GGACCCGGCGGCTTTCGCGCGCGCTGTGGCCCAAGTGCTGTGTGCGTGCCCTTGGGACGC	240	
QY	248	ACGGCGCGCCCCCGCGCGCCCCCTTCTTCGCCCAGGTGTCTGCTGAAGGAGCTGTGGC	307	
Db	241	ACGGCGCGCCCCCGCGCGCCCCCTTCTTCGCCCAGGTGTCTGCTGAAGGAGCTGTGGC	300	
QY	308	CCGAGTGTGACAGAGGCTGTGCGACGCGCGCGGAGGAACGTGTGCGCTTGGCTTGC	367	
Db	301	CCGAGTGTGACAGAGGCTGTGCGACGCGCGCGGAGGAACGTGTGCGCTTGGCTTGC	360	

QY	368	GCTGCTGGACGGGGCCCCGGGGGGCCCCCCCCCGAGGCTTTCACCAACAGCTGCGCAGCTA	427
Db	361	GCTGCTGGACGGGGCCCCGGGGGGCCCCCCCCCGAGGCTTTCACCAACAGCTGCGCAGCTA	420
QY	428	CCTGCCCCAACACGGGTGACCCGACGACTGCGGGGAGCGGGGCGTGGGGGCTGCTGTCGCG	487
Db	421	CCTGCCCCAACACGGGTGACCCGACGACTGCGGGGAGCGGGGCGTGGGGGCTGCTGTCGCG	480
QY	488	CCGCGTGGGGCGACGACGCTGCTGTTCACTGCTGGCAGCTGCGGCTCTTGTGCTGCT	547
Db	481	CCGCGTGGGGCGACGACGCTGCTGTTCACTGCTGGCAGCTGCGGCTCTTGTGCTGCT	540
QY	548	GGCTCCCAAGCTGCGCTTACAGGTGTGCGGGCCGGCGCTGTACAGCTCGCGCTGCCAC	607
Db	541	GGCTCCCAAGCTGCGCTTACAGGTGTGCGGGCCGGCGCTGTACAGCTCGCGCTGCCAC	600
QY	608	TCAGGCCCCGGCCCCCGCCACACGCTAGTGAACCCGGAAGCGCTGGGATGCGAACGGGC	667
Db	601	TCAGGCCCCGGCCCCCGCCACACGCTAGTGAACCCGGAAGCGCTGGGATGCGAACGGGC	660
QY	668	CTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCCCTGGGCTGCGAGCCCCGGGTGCGAG	727
Db	661	CTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCCCTGGGCTGCGAGCCCCGGGTGCGAG	720
QY	728	GAGGCGGGGGGCGAGTGCACGCCGAAGTCTGCCGTTGCCAAGAGCCCCAGGCGTGGCGC	787
Db	721	GAGGCGGGGGGCGAGTGCACGCCGAAGTCTGCCGTTGCCAAGAGCCCCAGGCGTGGCGC	780
QY	788	TGCCCCCTGAGCCGAGCGGACGCCCGCTTGGGCAAGGGGTCTTGGGCCCAACCCGGGCAAGAC	847
Db	781	TGCCCCCTGAGCCGAGCGGACGCCCGCTTGGGCAAGGGGTCTTGGGCCCAACCCGGGCAAGAC	840
QY	848	GCGTGAACCGAGTGACCGTGTGTTCTGTGTGTGTCACTGCGAAGCCCGCGAAGAAC	907
Db	841	GCGTGAACCGAGTGACCGTGTGTTCTGTGTGTGTCACTGCGAAGCCCGCGAAGAAC	900
QY	908	CACCTCTTTGGAGGGGTGCGCTCTTGCCACGCGCCACTCCCAACCATCCGTGGGCGGCCA	967
Db	901	CACCTCTTTGGAGGGGTGCGCTCTTGCCACGCGCCACTCCCAACCATCCGTGGGCGGCCA	960
QY	968	GCAACACGCGGGGGCCCCCATCCACATCGCGGGCCACCAAGTCCCTGGGAACAGCCTTGTCC	1027
Db	961	GCAACACGCGGGGGCCCCCATCCACATCGCGGGCCACCAAGTCCCTGGGAACAGCCTTGTCC	1020
QY	1028	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGGCGCAAGAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGGCGCAAGAGAGCAGCTGCG	1080
QY	1088	GCCCTCCTTCTCTACTCTAGCTCTCTGAGGGCCAGCCTGACTGGGCGCTCGGAAGCTCGTGA	1147
Db	1081	GCCCTCCTTCTCTACTCTAGCTCTCTGAGGGCCAGCCTGACTGGGCGCTCGGAAGCTCGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCCCCCTGGATGCCAGGAGCTCCCCGAGGTTGCCCGGCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCCCCCTGGATGCCAGGAGCTCCCCGAGGTTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAAATGCGGGCCCCCTGTTTCTGAGCTGCTTGGGAACCAACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAAATGCGGGCCCCCTGTTTCTGAGCTGCTTGGGAACCAACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTACCCCCAGC	1327
Db	1261	GTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTACCCCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCCCGGAGAAAGCCCCAGGGGCTCTGTGCGGGCCCCCGAGGAGAGAA	1387
Db	1321	AGCCGGTGTCTGTGCCCCCGGAGAAAGCCCCAGGGGCTCTGTGCGGGCCCCCGAGGAGAGAA	1380
QY	1388	CACAGACCCCCGCTGCGCTGCTGTGCAAGCTGCTCCGCGCAGCAGCAGCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCGCTGCGCTGCTGTGCAAGCTGCTCCGCGCAGCAGCAGCCCCCTGGCAGGTGA	1440

QY	1448	CGGCTTCGTGCGGGCTGCCTGCGCCGGCTGGTGGCCCCAGGCGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGGCTGCCTGCGCCGGCTGGTGGCCCCAGGCGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCCCGCTTCTCTCAGGAACACCAAGAACTTCATCTCCCTGGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCCCGCTTCTCTCAGGAACACCAAGAACTTCATCTCCCTGGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGGTGCGGAACTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTCGCTGCAGAGAGCTGACGTGGAAGATGAGCGGTGCGGAACTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAAGAAATCCTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAAGAAATCCTGGC	1680
QY	1688	CAAGTTCCTGCATGAGCTGATGAGTGTGTACGTCTGAGCTGCTCAGTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCATGAGCTGATGAGTGTGTACGTCTGAGCTGCTCAGTCTTCTTTTA	1740
QY	1748	TGTACGAGAGACACGTTTCAAAAGAACAGGCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTACGAGAGACACGTTTCAAAAGAACAGGCTTTTCTACCGCGCGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGGCAGCATCGGGAAGCCAGCCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGGCAGCATCGGGAAGCCAGCCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACCGGGCTGCGGCGGATTTGTGAACATGAGACTGCTGTGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACCGGGCTGCGGCGGATTTGTGAACATGAGACTGCTGTGGAGC	1980
QY	1988	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCTAACTACGAGCGGGCGCGGCGCCCGGCTCTGGGCGCTGTGTGCTGGG	2107
Db	2041	CAGCGTGTCTAACTACGAGCGGGCGCGGCGCCCGGCTCTGGGCGCTGTGTGCTGGG	2100
QY	2108	CCTGAGCAGATATCCACAGGGCCTGCGGCACTTCTGTGCTGCGTGTGCGGCGCCAGGACCC	2167
Db	2101	CCTGAGCAGATATCCACAGGGCCTGCGGCACTTCTGTGCTGCGTGTGCGGCGCCAGGACCC	2160
QY	2168	GCCGCGTGAAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCGTGAAGCTGTACTTTGTCAAGTGAATGTGACGGCGGCTAGACACCATCCCCCA	2220
QY	2192	GGACAGGCTCACGGAAGTCAATCGCCAGCATCATCAAAACCCAGAACACAGTAATGCGTGGC	2251
Db	2221	GGACAGGCTCACGGAAGTCAATCGCCAGCATCATCAAAACCCAGAACACAGTAATGCGTGGC	2280
QY	2252	TGCGTATGCCGTGGTCCAGAAAGCCGCCCATGGGCAAGTCCCGCAAGGCTTCAAGA----	2307
Db	2281	TGCGTATGCCGTGGTCCAGAAAGCCGCCCATGGGCAAGTCCCGCAAGGCTTCAAGAAGCCA	2340
QY	2308	-----	2307
Db	2341	CGTCTTACCTTGAACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACCTGACAGGA	2400
QY	2308	-----	2307
Db	2401	GACCAAGCCCGCTGAGGGATGCCCGTGTCTATCGAGCAAGAGTCTCTCCCTGAATGAGGCCAG	2460
QY	2308	-----GG	2309
Db	2461	CAGTGGCTCTTGACGCTCTTCTTACGCTTCATGTGCCACACGCGGTGCGCATCAGGGG	2520
QY	2310	CAAGTCTTACGCTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGTCTG	2369

Dp	2521	CAAGTCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATTCCTCCACGCTGCTTG	2580
QY	2370	CAGCCTGTGCTACGGCGCATGAGAAACAAGCTGTTTGGCGGATTCGGCGGACGGGCT	2429
Dp	2581	CAGCCTGTGCTACGGCGCATGAGAAACAAGCTGTTTGGCGGATTCGGCGGACGGGCT	2640
QY	2430	GCTCCTGCGTTTGGTGGATGATTTCTTGTGTGTGACACCTCACTCACCCACGCGAAAC	2489
Dp	2641	GCTCCTGCGTTTGGTGGATGATTTCTTGTGTGTGACACCTCACTCACCCACGCGAAAC	2700
QY	2490	CTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCCGTGTGACTTGGGAA	2549
Dp	2701	CTTCCTCAGGACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCCGTGTGACTTGGGAA	2760
QY	2550	GACAGTGTGAACCTCCCTGTAGAGAAGAGAGGCCCTGGGTGGCAACGGCTTTTGTACAT	2609
Dp	2761	GACAGTGTGAACCTCCCTGTAGAGAAGAGAGGCCCTGGGTGGCAACGGCTTTTGTACAT	2820
QY	2610	GCCGCCCCACGGCCTATTCCCTGTGTCGGGCTGCTGCTGATACCCGGAACCTTGAAGT	2669
Dp	2821	GCCGCCCCACGGCCTATTCCCTGTGTCGGGCTGCTGCTGATACCCGGAACCTTGAAGT	2880
QY	2670	GCAGAGCGACTACTCTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACG	2729
Dp	2881	GCAGAGCGACTACTCTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACG	2940
QY	2730	CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGCTCTTGGCGTGAAGTG	2789
Dp	2941	CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGCTCTTGGCGTGAAGTG	3000
QY	2790	TCACAGCCTGTTTCTGGAATTGACAGGTGAACAGCCTCCAGACGGTGTGCACCACTTA	2849
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QY	2850	CAAGATCCTCCTGCTGACGGCGTACAGGTTTCAACGCAATGTGTGCTGACGCTCCATTCA	2909
Dp	3061	CAAGATCCTCCTGCTGACGGCGTACAGGTTTCAACGCAATGTGTGCTGACGCTCCATTCA	3120
QY	2910	TCAGCAAGTTTGAAGAACCCCACTTTTCTGCGCGTCACTCTGACACGGCCTCCCT	2969
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QY	2970	CTGCTACTCCATCCTGAAGCCAAGACGCAAGGATGTGCTGGGGGCCAAGGGCGCCG	3029
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Dp	3301	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAAGCGCA	3360
QY	3150	GCTGAGTCGGAAGCTTCCCGGGGACGACGCTGACTTGCCTGGAGCGCGCAGCCAA	3209
Dp	3361	GCTGAGTCGGAAGCTTCCCGGGGACGACGCTGACTTGCCTGGAGCGCGCAGCCAA	3420
QY	3210	ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACAGCGCGCGA	3269
Dp	3421	ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACAGCGCGCGA	3480
QY	3270	GAGCAGACACCAAGACCCCTGTACAGCCGGGCTTACGTCCAGGGAGGAGGGCGGGC	3329
Dp	3481	GAGCAGACACCAAGACCCCTGTACAGCCGGGCTTACGTCCAGGGAGGAGGGCGGGC	3540
QY	3330	CACACCCAGGCCCCGCAACCGCTGGAGTCTGAGGCTGAGTGAATGTTTGGCGAGGCTG	3389
Dp	3541	CACACCCAGGCCCCGCAACCGCTGGAGTCTGAGGCTGAGTGAATGTTTGGCGAGGCTG	3600
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Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTTGAGCCGAGTGTCCAGCCAAAGGCT	3660
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Db	3661	GAGTGTCCAGCACACCTGCGGCTTCTCACTTCCCCACAGGCTGGCGCTCCACCCCA	3720
QY	3510	GGGCCAGCTTTTCTCTCACAGGAGCCCGGCTTCACTCCCCACATAGGAATAGTCCATCC	3569
Db	3721	GGGCCAGCTTTTCTCTCACAGGAGCCCGGCTTCACTCCCCACATAGGAATAGTCCATCC	3780
QY	3570	CCAGATTGCGCAATGTTCACCCGCTGCGCCTGCCCTCCTTTGCCCTTCCACCCCAACATCC	3629
Db	3781	CCAGATTGCGCAATGTTCACCCGCTGCGCCTGCCCTCCTTTGCCCTTCCACCCCAACATCC	3840
QY	3630	AGGTGAGACCCCTGAGAGAAGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG	3689
Db	3841	AGGTGAGACCCCTGAGAGAAGACCCCTGGAGCTCTGGGAATTTGGAGTGACCAAGGTGTG	3900
QY	3690	CCCTGTACACAGGCGAGGACCCCTGCACCTGTGATGGGGGCTCCCTGTGGGTCAAAATTGGGGG	3749
Db	3901	CCCTGTACACAGGCGAGGACCCCTGCACCTGTGATGGGGGCTCCCTGTGGGTCAAAATTGGGGG	3960
QY	3750	GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAA	3809
Db	3961	GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGGAAAAA	4020
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DEFINITION	Sequence 343 from patent US 6617110.
ACCESSION	AR393110
VERSION	AR393110.1 GI:40116392
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ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 4037) Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B., Harley,C.B. and Andrews,W.H. Cells immortalized with telomerase reverse transcriptase for use in drug screening Patent: US 6617110-A 343 09-SEP-2003; Location/Qualifiers 1 . 4037 /organism="unknown" /mol_type="mRNA"
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QY	68	GCGCGTCCCCCGCTGCGCGAGCCGTGCGTCCCTGCTGCGCAGCCACTACCGCGAGTCT	127	
Dp	61	GCGCGTCCCCCGCTGCGCGAGCCGTGCGTCCCTGCTGCGCAGCCACTACCGCGAGTCT	120	
QY	128	GCCGCTGGCAGCTTCGTGCGGCGCCTGGGGCCCCAGGGCTGCGGCTGTGTGACGCGCG	187	
Dp	121	GCCGCTGGCAGCTTCGTGCGGCGCCTGGGGCCCCAGGGCTGCGGCTGTGTGACGCGCG	180	
QY	188	GGACCCGCGCGCTTCCGCGCGCTGTGGGCCAGTGCCCTGTGTGCTGTGCCCTGGGACGC	247	
Dp	181	GGACCCGCGCGCTTCCGCGCGCTGTGGGCCAGTGCCCTGTGTGCTGTGCCCTGGGACGC	240	

QY		248	ACGAGCCGCCCGCCCCCGCCCCCTCCTTCCGCACAGGTGTCTTGCTGAAGAGCTGTGGC	307
Db		241	ACGAGCCGCCCGCCCCCGCCCCCTCCTTCCGCACAGGTGTCTTGCTGAAGAGCTGTGGC	300
QY		308	CCGAGTGTCTGACAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGTGGCTTCGGCTTCGC	367
Db		301	CCGAGTGTCTGACAGAGGCTGTGCGAGCGCGGCGCGAAGAACGTGTGGCTTCGGCTTCGC	360
QY		368	GCTGCTGACCGGGGGCCCCGGGGGGCCCCCGAGGCTTCAACCACGATGCGCAGCTA	427
Db		361	GCTGCTGACCGGGGGCCCCGGGGGGCCCCCGAGGCTTCAACCACGATGCGCAGCTA	420
QY		428	CCTGCCCAACAACGCTGACCGACGCACTGCGGGGGAAGCGGGCGTGGGGCTGCTGTGCG	487
Db		421	CCTGCCCAACAACGCTGACCGACGCACTGCGGGGGAAGCGGGCGTGGGGCTGCTGTGCG	480
QY		488	CCGCGTGGCGGACGACGCTGTGTTTCACTGTGGCACGCTGCGGCTTTGTGTGTGT	547
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QY		548	GGCTCCCAAGCTGCGCCTAACAGGTGTGGGGCGCGCGTGTACCACTCGCGCTGCCAC	607
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QY		608	TCAAGCCCGGCCCCCGCCACACGCTAATGGAACCCCGAAGCGCTTGGGATGCGAACGGGC	667
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QY		668	CTGGAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCCAG	727
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QY		728	GAGGCGCGGGGGGCAAGTGCAGCCGAAATGTCCCGTTGCCCAAGAGGCCAAGCGTGGCGC	787
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QY		788	TGCCCTTAGCCCGGAGCGGACGCCCCGTGGGACAGGGGTCTTGCGGCCACCCGGGCAAGAC	847
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QY		848	GCGTGGACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCGCAGACCCCGCGAAGAGC	907
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QY		908	CACCTCTTGGAGGGGTGCGCTCTGTGCAACGCGCCACTCCACCCATCCGTGGGCGGCCA	967
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QY		968	GCAACACGCGGGCCCCCCCATTCCAATCGCGGCCACCAAGTCCCTGGGACACAGCCTTGTCC	1027
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QY		1028	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGCGGCAAGAGAGAGCTGCG	1087
Db		1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGCGGCAAGAGAGAGCTGCG	1080
QY		1088	GCCCTCTCTTCTACTACGCTCTGTAGGCCCCAGCCTGACTGGGCTCGGAGCTCGTGA	1147
Db		1081	GCCCTCTCTTCTACTACGCTCTGTAGGCCCCAGCCTGACTGGGCTCGGAGCTCGTGA	1140
QY		1148	GACCATCTTCTGTGGTTCCAAGCCCTGATGCCAAGGACTCCCCGAGGTTGCCCGCCT	1207
Db		1141	GACCATCTTCTGTGGTTCCAAGCCCTGATGCCAAGGACTCCCCGAGGTTGCCCGCCT	1200
QY		1208	GCCCCAGCGCTACTGGCAAATGGGGCCCCCTGTTTCTGAGTGTCTTGGGAACCAACGCGCA	1267
Db		1201	GCCCCAGCGCTACTGGCAAATGGGGCCCCCTGTTTCTGAGTGTCTTGGGAACCAACGCGCA	1260
QY		1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTCACCCCAGC	1327
Db		1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTCACCCCAGC	1320
QY		1328	AGCCGGTGTCTGTGCCCGGGAAGAGCCCCAGGGCTCTGTGCGCGGCCCCCGAGGAGGAGA	1387

Db	1321	AGCCGGTGTCTGTGCCCCGGAGAAAGCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGAGGA	1380
QY	1388	CACAGACCCCGCTGCGCTGGTGACAGCTGCTCCGCCAGCACACAGACAGCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCGCTGCGCTGGTGACAGCTGCTCCGCCAGCACACAGACAGCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCGTGCGGCGCTGCTGCGCGCGGCTGTGTGCCCCAGGCGCTGTGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGCGCTGCTGCGCGCGGCTGTGTGCCCCAGGCGCTGTGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCCGCTTCTCTCAGGAACACCAAGAATTCATCTCCCTGGGGAAGCATGCCAA	1567
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Db	1621	GAGCCCAAGGGGTGGCTGTGTTCCCGCGCCAGAGCACCGTCTGCGTGAAGAGATCCTGGC	1680
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RESULT 13

AX810378

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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AX810378 4037 bp mRNA linear PAT 25-NOV-2003

Sequence 343 from Patent EP1333094.

AX810378

AX810378.1 GI:38523892

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1

Cech, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Morin, G.B.,

Harley, C.B. and Andrews, W.H.

Human telomerase catalytic subunit

Patent: EP 1333094-A 343 06-Aug-2003;

Geron Corporation (US); University Technology Corporation (US)

location/Qualifiers

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SOURCE
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QY	1746	TATGTACGAGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCCGGAAGATGTCTGG	1805
Db	1759	TATGTACGAGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCCGGAAGATGTCTGG	1818
QY	1806	AGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGAGCTG	1865
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Job time : 9652.49 secs

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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 19:58:33 ; Search time 833.593 Seconds
(without alignment)

16548.779 Million cell updates/sec

Title: US-09-424-686F-10

Perfect score: 3824

Sequence: 1 gttcagcagcagcgtcgtc.....aaaaaaaaaaaaaaaaa 3824

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2353733 seqs, 1803733377 residues 4707466

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	3767.8	98.5	3855	14 US-10-044-692-4	Sequence 4, Appli
2	3767.8	98.5	3855	14 US-10-044-539-4	Sequence 4, Appli
3	3559	93.1	4015	9 US-09-733-294A-3	Sequence 3, Appli
4	3559	93.1	4015	9 US-09-990-080-1	Sequence 1, Appli
5	3559	93.1	4015	9 US-09-843-676-224	Sequence 224, App
6	3559	93.1	4015	9 US-09-953-052-1	Sequence 1, Appli
7	3559	93.1	4015	14 US-10-053-758-224	Sequence 224, App
8	3559	93.1	4015	14 US-10-208-243-1	Sequence 1, Appli
9	3559	93.1	4015	14 US-10-054-295-224	Sequence 224, App
10	3559	93.1	4015	14 US-10-054-611-224	Sequence 224, App
11	3559	93.1	4015	14 US-10-105-963-1	Sequence 1, Appli
12	3559	93.1	4015	14 US-10-044-692-1	Sequence 1, Appli
13	3559	93.1	4015	14 US-10-044-539-1	Sequence 1, Appli
14	3557	93.0	4027	15 US-10-385-882-1	Sequence 1, Appli
15	3414.8	89.3	4029	9 US-09-843-676-173	Sequence 173, App

16	3414.8	89.3	4029	10 US-09-438-486-173	Sequence 173, App
17	3414.8	89.3	4029	14 US-10-053-758-173	Sequence 173, App
18	3414.8	89.3	4029	14 US-10-054-295-173	Sequence 173, App
19	3414.8	89.3	4029	14 US-10-054-611-173	Sequence 1, Appli
20	2944	77.0	3453	14 US-10-205-629-1	Sequence 1, Appli
21	2944	77.0	13766	14 US-10-105-616-1	Sequence 32, Appli
22	2940	76.9	3396	9 US-09-749-728B-32	Sequence 6, Appli
23	2932	76.7	8742	14 US-10-105-616-6	Sequence 3, Appli
24	2087.2	54.6	2176	14 US-10-044-692-3	Sequence 100, App
25	2087.2	54.6	2176	14 US-10-044-539-3	Sequence 100, App
26	2004	52.4	2171	9 US-09-843-676-100	Sequence 100, App
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32	1522.8	39.8	4200	14 US-10-044-692-6	Sequence 6, Appli
33	1522.8	39.8	4200	14 US-10-044-539-6	Sequence 1, Appli
34	1522.8	39.8	15418	9 US-09-783-203-1	Sequence 1, Appli
35	1522.8	39.8	15418	9 US-09-994-427A-1	Sequence 1, Appli
36	1522.8	39.8	15418	10 US-09-995-419A-1	Sequence 1, Appli
37	1522.8	39.8	15418	14 US-10-141-220-1	Sequence 1, Appli
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39	1522.8	39.8	15418	14 US-10-206-447-1	Sequence 1, Appli
40	1521.2	39.8	51552	9 US-09-733-294A-30	Sequence 30, Appli
41	1367	35.7	1866	14 US-10-294-778-11	Sequence 11, Appli
42	814	21.3	1314	14 US-10-294-778-9	Sequence 9, Appli
43	798	20.9	1311	14 US-10-294-778-1	Sequence 1, Appli
44	586.8	15.3	873	14 US-10-282-960-1	Sequence 1, Appli
45	519	13.6	519	14 US-10-282-960-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-044-692-4

Sequence 4, Application US/10044692
Publication No. US20030096344A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044, 692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912, 951
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854, 050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997

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QY 1328 AGCGGCTGTCTGTGCGCGGAGAAAGCCCCAGGCTCTGTGCGGCGCCCCGAGAGAGAGA 1387
Db 1321 AGCGGCTGTCTGTGCGCGGAGAAAGCCCCAGGCTCTGTGCGGCGCCCCGAGAGAGAGA 1380
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QY 1868 GGAAGCAGAGGTCAGGAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG 1927
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QY 1928 CTTCACTCCCAAGGCTGACGCGGCTGCGGCGCATTTGTGAACATGACTACGTCTGGAGC 1987
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QY 2792 ACAGCTGTTCTGATTTGAGGTGAAGAGCTCCAGACGCTGACCAACATCTACA 2851
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QY	2970	CTGCTACTCCATCCTGTAAGCCCAAGAACGCAGGGATGTTCCTGGGGGCCAAGGGCGCC	3029
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QY	3030	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCCAAGCATTCCTGCTCAAGCT	3089
Db	3241	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCCAAGCATTCCTGCTCAAGCT	3300
QY	3090	GACTGCACACCGGTGTCACTACGTGCCACTCCTGGGGTCACTCAGSACAGCCCAAGCGCA	3149
Db	3301	GACTGCACACCGGTGTCACTACGTGCCACTCCTGGGGTCACTCAGSACAGCCCAAGCGCA	3360
QY	3150	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTCTGGAGGCCGACGCCAACCCGGC	3209
Db	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTCTGGAGGCCGACGCCAACCCGGC	3420
QY	3210	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3269
Db	3421	ACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3270	GAGCAGACACCAAGCAGCCCTGTCAACGCCGGGCTTACGTCCAGGGAGGAGGGCGGCC	3329
Db	3481	GAGCAGACACCAAGCAGCCCTGTCAACGCCGGGCTTACGTCCAGGGAGGAGGGCGGCC	3540
QY	3330	CACACCCAGGCCCGCAACCGCTGGAGTCTGAGGCCCTGAGTGAAGTGTTCGCCAGGCCCTG	3389
Db	3541	CACACCCAGGCCCGCAACCGCTGGAGTCTGAGGCCCTGAGTGAAGTGTTCGCCAGGCCCTG	3600
QY	3390	CATGTCCGGCTGAAGCTGAAGTGTCCGGCTGAGGCTTGAAGCGAGTGTCCAGCCAAAGGCT	3449
Db	3601	CATGTCCGGCTGAAGCTGAAGTGTCCGGCTGAGGCTTGAAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3450	GAGTGTCCAGCAACCTGCGCTTCACTTCCCAACAGGCTGGCGTCCGCCCAACCCCA	3509
Db	3661	GAGTGTCCAGCAACCTGCGCTTCACTTCCCAACAGGCTGGCGTCCGCCCAACCCCA	3720
QY	3510	GGGCCAGCTTTTCCCTCACCAAGAGCCCGGCTTCACTCCCCACATAGGAATAGTCCATCC	3569
Db	3721	GGGCCAGCTTTTCCCTCACCAAGAGCCCGGCTTCACTCCCCACATAGGAATAGTCCATCC	3780
QY	3570	CCAGATTGCAATTGTTCAACCCCTGCGCTGCCCTCCTTGGCTTCCACCCCAACCATCC	3629
Db	3781	CCAGATTGCAATTGTTCAACCCCTGCGCTGCCCTCCTTGGCTTCCACCCCAACCATCC	3840
QY	3630	AGGTGAGAACCTGAGAAGAACCCCTGGAGCTTGGGAATTTGAGTGACCAAAAGTGTG	3689
Db	3841	AGGTGAGAACCTGAGAAGAACCCCTGGAGCTTGGGAATTTGAGTGACCAAAAGTGTG	3900
QY	3690	CCCTGTACACAGGCGAGAACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAATTGGGGG	3749
Db	3901	CCCTGTACACAGGCGAGAACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAAATTGGGGG	3960
QY	3750	GAGGTGCTGTGGAGTAATAATCTGAATATATGACTTTTTCAGTTTGTGAAAAAAA 3804	
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RESULT 4
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; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; PRIORITY FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIORITY FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0

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; SEQ ID NO 1
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; LENGTH: 4015
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; TYPE: DNA
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; ORGANISM: Homo sapiens
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; FEATURE:
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; NAME/KEY: CDS
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; LOCATION: (56)..(3454)
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; OTHER INFORMATION: human telomerase reverse transcriptase (hTRT) cDNA
US-09-990-080-1

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Query Match	93.14;	Score 3559;	DB 9;	Length 4015;
Best Local Similarity	94.68;	Pred. No. 0;		
Matches 3797;	Conservative	0;	Mismatches	0;
			Indels	218;
			Gaps	22;

QY	8	GCAGCGGTGCGTCTGTGCGGACGTGGGAAGCCCTGGCCCCCGGCACACCCCGGATGCC	67
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QY	128	GCCGCTGGCCACGTTTCGTGCGGCGCCTTGGGGCCCCCAAGGCTGGCGGCTGTGTGACGCGG	187
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QY	188	GGACCCGGCGGCTTTCGCGCGGCTGTGTGCCCCAGTGTCTGTGTGCGTGCCTTGGGACGC	247
Db	181	GGACCCGGCGGCTTTCGCGCGGCTGTGTGCCCCAGTGTCTGTGTGCGTGCCTTGGGACGC	240
QY	248	ACGGCGGCCCCCGCGCGCCCTCTCTTCGCGCAGGTGTCTGCTGAAGGAGCTGGTGCC	307
Db	241	ACGGCGGCCCCCGCGCGCCCTCTCTTCGCGCAGGTGTCTGCTGAAGGAGCTGGTGCC	300
QY	308	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGACGTGCTGGCCTTGCGCTTGC	367
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGCGAAGACGTGCTGGCCTTGCGCTTGC	360
QY	368	GCTGTGGAACGGGGCCCGCGGGGGCCCCCGAGGCTTCAACACAGCGTGGCAGCTA	427
Db	361	GCTGTGGAACGGGGCCCGCGGGGGCCCCCGAGGCTTCAACACAGCGTGGCAGCTA	420
QY	428	CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGCTGTGCTGCG	487
Db	421	CCTGCCCAACACGGTGACCGACGCACTGCGGGGAGCGGGCGTGGGGCTGTGCTGCG	480
QY	488	CCGCGTGGGCGAGCAGTGTGTTTACCTGTGCGACGCTGCGGCTCTTGTGTGCTGT	547
Db	481	CCGCGTGGGCGAGCAGTGTGTTTACCTGTGCGACGCTGCGGCTCTTGTGTGCTGT	540
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[illegible]

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Db	2281	TCGGTATGCCGTGTCTCAGAAAGCCGCCCATGCGGCACTCCGCAAGGCTTCAAGAGCCA	2340
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Db	2341	CGTCTTACCTTGAAGACCTCCAGCCGTACATGCGACAGTTCTGTGGCTCACTGCAGGA	2400
QY	2308	-----	2307
Db	2401	GACCAGCCCGCTGAGGGATGCCGTCTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2308	-----GG	2309
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Db	2521	CAAGTCCTACGTCACAGTGGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCAAGCTGCTG	2580
QY	2370	CAGCCTGTGCTACGGCGACATGAGAACAAAGCTGTTGCGGGGATTCGGCGGGACGGGCT	2429
Db	2581	CAGCCTGTGCTACGGCGACATGAGAACAAAGCTGTTGCGGGGATTCGGCGGGACGGGCT	2640
QY	2430	GCTCCTGCGTTTGTGTGATGATTTCTTGTGTGACACCTCACTCAACCCACGCGAAAAAC	2489
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QY	2490	CTTCTCTAGGACCCCTGTGTCCGAGGTGTCCCTGAGTATGCTGCGTGTGAACCTTGCAGAA	2549
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QY	2550	GACAGTGTGAACCTTCCCTGTAGAAAGCAGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2609
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QY	2790	TCACAGCCTGTTTCTGGATTTGCAAGGTGAACAGCCTCCAGACCGGTGTGCAACCAATCTA	2849
Db	3001	TCACAGCCTGTTTCTGGATTTGCAAGGTGAACAGCCTCCAGACCGGTGTGCAACCAATCTA	3060
QY	2850	CAAGATCTCTCTGCTGACAGGCGTACAGGTTTCAACGCATGTGTGCTGACGCTCCCAATTCA	2909

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Dp	3301	GACTCGAACCCGTGTACCTACCTACGTCCACTCCTGGGGTCACTCAGACAGCCAGCGCA	3360
QY	3150	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCCGACCAACCCGCGC	3209
Dp	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGCCGACCAACCCGCGC	3420
QY	3210	ACTGCCCTCAGACTTCAAGACCAATCCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3269
Dp	3421	ACTGCCCTCAGACTTCAAGACCAATCCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3270	GAGCAGACACCAGACAGCCCTGTCAACGCCGGGCTCTACGTCCAGGAGGGAGGGCGGCC	3329
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Dp	3541	CACACCCAGGCGCCGACCCGCTGGGAGTCTGAGGCGCTGAGTGTGTTGGCCGAGGCTG	3600
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Dp	3601	CATGTCGGGCTGAAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
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Dp	3901	CCCTGTACACAGGCGGAGAACCTTGCACTGGATGGGGTCCCTGTGGGTCAAAATTGGGGG	3960
QY	3750	GAGGTGCTGTGGGAGTAATACTGAATATATGAGTTTTCAGTTTGAATAAAA 3804	
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RESULT 5
US-09-843-676-224
; Sequence 224, Application US/09843676
; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
;

	93.1%;	Score 3559;	DB 9;	Length 4015;	
	Best Local Similarity	94.6%;	Pred. No. 0;		
	Matches 3797;	Conservative	0;	Mismatches	0; Indels 218; Gaps 2

US-09-843-676-224

SEQUENCE DESCRIPTION: SEQ ID NO: 224:

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      / /note= "human telomerase reverse
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      / NAME/KEY: CDS
      / FEATURE:
      / MOLECULE TYPE: CDNA
      / TOPOLOGY: linear
      / STRANDEDNESS: single
      / TYPE: nucleic acid
      / LENGTH: 4015 base pairs
      / SEQUENCE CHARACTERISTICS:
      / INFORMATION FOR SEQ ID NO: 224:
      / TELEFAX: (415) 576-0300
      / TELEPHONE: (415) 576-0200
      / REGISTRATION NUMBER: 36,429
      / REFERENCE/DOCKET NUMBER: 015389-002930US
      / TELECOMMUNICATION INFORMATION:
      / ATTORNEY/AGENT INFORMATION:
      / FILING DATE: 01-OCT-1996
      / APPLICATION NUMBER: US 08/724,643
      / FILING DATE: 18-APR-1997
      / APPLICATION NUMBER: US 08/844,419
      / FILING DATE: 25-APR-1997
      / APPLICATION NUMBER: US 08/846,017
      / FILING DATE: 09-MAY-1997
      / APPLICATION NUMBER: US/08/854,050
      / PRIOR APPLICATION DATA:
      / CLASSIFICATION: 536
      / FILING DATE: 26-Apr-2001
      / CURRENT APPLICATION DATA:
      / SOFTWARE: Patent Release #1.0, Version #1.30
      / OPERATING SYSTEM: PC-DOS/MS-DOS
      / COMPUTER: IBM PC compatible
      / MEDIUM TYPE: Floppy disk
      / COMPUTER READABLE FORM:
      / ZIP: 94111
      / COUNTRY: United States of America
      / STATE: California
      / CITY: San Francisco
      / STREET: Two Embarcadero Center, 8th Floor
      / ADDRESS: Townsend and Townsend and Crew LLP
      / CORRESPONDENCE ADDRESSES:
      / NUMBER OF SEQUENCES: 225
      / TITLE OF INVENTION: No. US20020164786A1el Telomerase
      / Andrews, Calvin H.
      / Morin, Gregg B.
    
```

QY	248	ACGAGCCGCCCCCGCCGCCCCCTCTCTTCCGACAGGTGTCTGCTGAAGAGACTGTGAC	307
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QY	788	TGCCCCTGAGCCGAGCGGACGCCCCGTTGGGCAAGGGTCTTGGGCCCCACCCGGGCAAGAC	847
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QY	848	GCGTGAACCGAGTGACCGTGTCTCTGTGTGTCTCACTGCGCAGACCCGCGGAAGAGC	907
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Db	961	GCAACCAAGCGGGCCCCCCCATCCACATCGCGGGCAACCAAGTCCCTGGGACACGCTTGTCC	1020
QY	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGCAAGAGGACAGCTGCG	1087
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGCAAGAGGACAGCTGCG	1080
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QY	1328	AGCCGGTGTCTGTGCCCCGGAGAAAGCCCCCAGGGCTCTGTGGCGCCCCCCGAGGAGGAGGA	1387
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Db	1621	GAGCCAGAGGGTGTGCTGTGTTCCGGCCGACAGAACCGTCTGCTGAGGAGATCCTGGC	1680
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Db	2101	CCTGAGCATATCCACAGGGCCTGCGCACCTTCTGTGCTGCTGTGCGGGCCAGGACCC	2160
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RESULT 6
US-09-953-052-1
; Sequence 1, Application US/09953052
; Patent No. US20020173476A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,052
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (hTRT)"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1
Query Match 93.1%; Score 3559; DB 9; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

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QY 2430 GCTCTCGCTTTGGTGGATGATTTCTTGTGTGACACCTCACTCACCACGCGAAAC 2489
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RESULT 7
US-10-053-758-224

Sequence 224, Application US/10053758
Publication No. US20030032075A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224

Query Match 93.1%; Score 3559; DB 14; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCGTCTGCTGCGCACAGTGGAGAGCCCTGGCCCCGCCACCCCGCATGCC 67
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QY 68 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCACAGTACCCGAGTGTCT 127
DB 61 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCACAGTACCCGAGTGTCT 120
QY 128 GCGCGCTGCGCACAGTTCGTCGCGGCGCGCTGCGGCGCCCGACAGGCTGGCGCTGTGACAGCGCG 187
DB 121 GCGCGCTGCGCACAGTTCGTCGCGGCGCGCTGCGGCGCCCGACAGGCTGGCGCTGTGACAGCGCG 180
QY 188 GGAACCCGCGGCTTTCGCGCGCGCTGTGTGCGCCAGTGCCTGTGTGCGCTGGGAGCGC 247
DB 181 GGAACCCGCGGCTTTCGCGCGCGCTGTGTGCGCCAGTGCCTGTGTGCGCTGGGAGCGC 240
QY 248 ACGGCGCGCGCGCGCGCGCGCGCTCTTCCGCGAGTGTCTGCTGAGAGAGTGTGTGC 307
DB 241 ACGGCGCGCGCGCGCGCGCGCGCTCTTCCGCGAGTGTCTGCTGAGAGAGTGTGTGC 300
QY 308 CCGAGTGTGACAGAGCTGTGTGCGAGCGCGCGCGAGAGAGAGTGTGTGTGCGCTTGC 367
DB 301 CCGAGTGTGACAGAGCTGTGTGCGAGCGCGCGCGAGAGAGAGTGTGTGTGCGCTTGC 360
QY 368 GCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCAACCAAGCGTGCAGCTA 427
DB 361 GCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCAACCAAGCGTGCAGCTA 420
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DB 541 GCGTCCAGCTGCGCTTACAGGTGTGCGGCGCGCGCGCTGTACCAAGCTGCGCGCTGCCAC 600
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DB 601 TCAGGCGCGCGCGCGCGCGCGCGCGCTAGTGAACCCGAGAGCGTCTGGAGTGCAGACGGGC 660
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QY 848 GCGTGACCGAGTGAACCGTGGTTTCTGTGTGTGTACCTGCGCAGACCCGCGAAGAGC 907
DB 841 GCGTGACCGAGTGAACCGTGGTTTCTGTGTGTGTGTACCTGCGCAGACCCGCGAAGAGC 900
QY 908 CACCTCTTTGAGAGGTGCGCTCTCTGCAAGCGCCACTCCCAACCACTCGTGAGCGGCA 967
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DB 961 GCACCAAGCGGCG 1020
QY 1028 CCGCGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAGCGGCAAGAGAGAGCTGCG 1087
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QY 1088 GCGCTCTCTCTACTACTAGCTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1147
DB 1081 GCGCTCTCTCTACTACTAGCTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
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DB 1261 GTGCGCGCTACGCGGTTGCTCTCTCAAGACGCACTGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1328 AGCGCGTGTGTGTGCG 1387
DB 1321 AGCGCGTGTGTGTGCG 1380
QY 1388 CACAGACCG 1447
DB 1381 CACAGACCG 1440
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DB 1441 CGGCTCTGTGCG 1500
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DB 1681 CAGGTTCTGTGCACTGGCTGATGATGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTA 1740
QY 1748 TGTCAAGGAGCAACGTTTCAAAAGACAGGCTCTTTTCTAACGGAAGAGTGTGTAG 1807
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Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3270 GAGCAGACACCGAGCGCTGTACGCGCGGCTCTACGTCGCCAGAGGAGGAGGCGCGG 3329
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RESULT 8

US-10-208-243-1
; Sequence 1, Application US/10208243
; Publication No. US20030044394A1
; GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.

APPLICANT: Geron Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
FILE REFERENCE: 015389-003500PC
CURRENT APPLICATION NUMBER: US/10/208,243
PRIOR FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/675,321
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/112,006
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: WO PCT/US99/06898
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

Query Match 93.1%; Score 3559; DB 14; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCTCTGCTGCGACAGTGGAGAGCCCTGGCCCGGACCCCGGATGCC 67
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QY 608 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 667
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QY	788	TGCCCCGTAGCCGGAGCGGACGCGCGGTGGGCGAGGGGTCTTGCGCCACCCGGCGAGGAC	847
Db	781	TGCCCCGTAGCCGGAGCGGACGCGCGGTGGGCGAGGGGTCTTGCGCCACCCGGCGAGGAC	840
QY	848	GCGTGACCCGAGTGACCGTGTTTCTGTGTGTGTCACTGCGCAGACCCGCGGAAGAGC	907
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QY	908	CACCTCTTTGGAGGGGTGCGCTCTCTGGCAGCGCCACTCCACCCATCCGTGGCGGCCA	967
Db	901	CACCTCTTTGGAGGGGTGCGCTCTGGCAGCGCCACTCCACCCATCCGTGGCGGCCA	960
QY	968	GCACCAAGCGGGCCCCCATCAATCGCGGCCACCAAGTCCCTGGGACACGCGTTGTCC	1027
Db	961	GCACCAAGCGGGCCCCCATCAATCGCGGCCACCAAGTCCCTGGGACACGCGTTGTCC	1020
QY	1028	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCTCAGGCGCACAAAGAGCAAGTCCG	1087
Db	1021	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCTCAGGCGCACAAAGAGCAAGTCCG	1080
QY	1088	GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGCGCTCGGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGCGCTCGGAGGCTCGTGA	1140
QY	1148	GACCATCTTCTGAGTTCAGAGCCCTGAGTCCAGGGACTCCCCGAGGTGCCCCCGCT	1207
Db	1141	GACCATCTTCTGAGTTCAGAGCCCTGAGTCCAGGGACTCCCCGAGGTGCCCCCGCT	1200
QY	1208	GCCCCAGCGTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACCAAGCGCA	1267
Db	1201	GCCCCAGCGTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACCAAGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCAACCCAGC	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCAACCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCGGAGAAAGCCCCAGGGCTGTGTGCGGCCCCCGAGAGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCGGAGAAAGCCCCAGGGCTGTGTGCGGCCCCCGAGAGAGGA	1380
QY	1388	CACAGACCCCGTGGCTGTGTCAGCTGCTCCGACAGCAGCAGCCCCCTGGCAGGTGA	1447
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QY	1448	CGGCTTCTGTGCGGGCTGCGCTGCGCGCGCTGTGTGCCCCAGAGGCTCTGGGCTCCAGGA	1507
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QY	1508	CAACGAACGCGCTTCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAAGCATGCCA	1567
Db	1501	CAACGAACGCGCTTCTCAGGAACACCAAGAAGTTCACTCCCTGGGGAAGCATGCCA	1560
QY	1568	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGCTGCGCAG	1627
Db	1561	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTGCTGCGCAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCGGCGCGCAGAGCACCGTCTGCGTGAAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTTCGGCGCGCAGAGCACCGTCTGCGTGAAGAGATCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1740
QY	1748	TGTACGGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1807

Db	1741	TGTACGGAGACCA	CGTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCA	AAGCATTTGGAATCAGACAGACACTTGAAGAGGGTGACGTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCA	AAGCATTTGGAATCAGACAGACACTTGAAGAGGGTGACGTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGT	CAGGACGATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGT	CAGGACGATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCA	AGCCTGACGGGCTGCGGCGAATTGTGAACATGACTACGTCTGGAGAC	1987
Db	1921	CTTCATCCCCA	AGCCTGACGGGCTGCGGCGAATTGTGAACATGACTACGTCTGGAGAC	1980
QY	1988	CAGAACGTTCC	GCAGAGAAAGAGGCGCCAGCGTCTCACCTCGAGGCTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCC	GCAGAGAAAGAGGCGCCAGCGTCTCACCTCGAGGCTGAAGGCACTGTT	2040
QY	2048	CAGCGTCTCA	ACTACGAGCGGCGCGCGCCCGGCTCTGGCGGCTCTGTGCTGGG	2107
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QY	2168	GCCGCGCTG	AGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCGCTG	AGCTGTA-----CATCCCCCA	2220
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Db	2221	GGACAGGCTCA	CGGAGGTCATCGCCAGCATCATCAAAACCCCAAGAACAGTACTGCGTGG	2280
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QY	2310	CAAGTCTCA	AGTCCAGTGCAGGGGATCCCGAGGGCTCCATCCTTCCACGCTGCTTG	2369
Db	2521	CAAGTCTCA	AGTCCAGTGCAGGGGATCCCGAGGGCTCCATCCTTCCACGCTGCTTG	2580
QY	2370	CAGCCTGTG	CTACGGCAGATGGAACAAGCTGTTTGGCGGGGATTCGGCGGGACGGGCT	2429
Db	2581	CAGCCTGTG	CTACGGCAGATGGAACAAGCTGTTTGGCGGGGATTCGGCGGGACGGGCT	2640
QY	2430	GCTCCTGG	TTTGGTGATGATTTCTTGTGTGTGACACTCACTCAACCCACGCAAAAAC	2489
Db	2641	GCTCCTGG	TTTGGTGATGATTTCTTGTGTGTGACACTCACTCAACCCACGCAAAAAC	2700
QY	2490	CTTCCTAG	GGAACCTGTCCGAGGCTGCTGAGTATGGCTGCGTGGTGAACCTTGCGGAA	2549
Db	2701	CTTCCTAG	GGAACCTGTCCGAGGCTGCTGAGTATGGCTGCGTGGTGAACCTTGCGGAA	2760
QY	2550	GACAGTGTG	AACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAGAT	2609
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QY 2730 CGGCTTCAAGGCTGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGGCGGCTGAAGTG 2789
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DB 3061 CAAGATCCTCCTGCTGACAGGCGGTACAGGTTTCAAGCATGTGTGTGCAAGCTCCCATTTCA 3120
QY 2910 TCAGCAAGTTGGAAGAACCCCAATTTTCTGCGGCTCATCTTGACACGGGCTCCCT 2969
DB 3121 TCAGCAAGTTGGAAGAACCCCAATTTTCTGCGGCTCATCTTGACACGGGCTCCCT 3180
QY 2970 CTGCTACTCCTCATCTGAAAGCCCAAGAACGCGATGTGCTGGGGGCCAAGGCGCGC 3029
DB 3181 CTGCTACTCCTCATCTGAAAGCCCAAGAACGCGATGTGCTGGGGGCCAAGGCGCGC 3240
QY 3030 CGGCTCTGCTGCTGCGAGGCGGCTGACGTGCTGCGACCAAGCATTTCTGCTCAAGCT 3089
DB 3241 CGGCTCTGCTGCTGCGAGGCGGCTGACGTGCTGCGACCAAGCATTTCTGCTCAAGCT 3300
QY 3090 GACTGACACCGGTGTCACTTACGTGCGCACTCTGGGGTCACTCAGAGACAGCCAGACGCA 3149
DB 3301 GACTGACACCGGTGTCACTTACGTGCGCACTCTGGGGTCACTCAGAGACAGCCAGACGCA 3360
QY 3150 GCTGAGTGGAGAGCTCCCGGGGACGAGCGTGAAGTCCCTGAGAGCGGCAACCCGCGC 3209
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QY 3390 CATGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGGCT 3449
DB 3601 CATGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAGGGCT 3660
QY 3450 GAGTGTCAAGACACCTGCGCTTCACTTCCCAAGGCTGGCGCTCGGCTCCACCCCA 3509
DB 3661 GAGTGTCAAGACACCTGCGCTTCACTTCCCAAGGCTGGCGCTCGGCTCCACCCCA 3720
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DB 3721 GGGCCAGCTTTTCTCACCAGAGAGCCGCGCTTCCACTCCCAATAGGAATAGTCCATCC 3780
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QY 3750 GAGTGCTGTGGAGTAATACTGATATATGAGTTTTCAAGTTTGAAGAAA 3804
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RESULT 9

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TITLE OF INVENTION: No. US20030044953A1el Telomerase

NUMBER OF SEQUENCES: 225

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CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

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CLASSIFICATION: 536

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APPLICATION NUMBER: US 08/846,017

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APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

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INFORMATION FOR SEQ ID NO: 224:

SEQUENCE CHARACTERISTICS:

LENGTH: 4015 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "hTRT"

/note= "human telomerase reverse

transcriptase (hTRT) catalytic protein

component"

SEQUENCE DESCRIPTION: SEQ ID NO: 224:

US-10-054-295-224

Query Match 93.1%; Score 3559; DB 14; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;
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QY 128 GCGGCTGCGCAGCTTCTGCGCGCGCTGGGGCCCCAGGGCTGGCGGTGTCAGCGCG 187
Db 121 GCGGCTGCGCAGCTTCTGCGCGCGCTGGGGCCCCAGGGCTGGCGGTGTCAGCGCG 180
QY 188 GGACCCGCGGCTTTCGCGCGCTGCGCGCCAGTGCTGCTGCTGCTGCGCGCC 247
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QY 248 ACGGCG 307
Db 241 ACGGCG 300
QY 308 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
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QY 368 GCTGTGCAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
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QY 488 CCGGCTGGGCGACGAGCTGTGTTCACTGTGCAAGCTGCGCGCTCTTGTGCTGT 547
Db 481 CCGGCTGGGCGACGAGCTGTGTTCACTGTGCAAGCTGCGCGCTCTTGTGCTGT 540
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QY 728 GAGGCG 787
Db 721 GAGGCG 780
QY 788 TGCCCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 781 TGCCCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
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Db 961 GCACCAACG 1020
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QY 1268 GTGCGCGCTACGCGGCTGCTCTCAAGACGCACTGCGCGCGCGCGCGCGCGCGCGCGCG 1327
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Db 1561 GCTCTGCTGCAAGAGCTGAAGATGAGCGTGGCGGAGCTGCGCTTGGCTGCGCAG 1620
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QY 1748 TGTCAAGGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTCTGAG 1807
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QY 1868 GGAAGCAGAGGTCAGGACAGCATCGGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1927
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QY	2252	TCGGTATGCGGTGCTCCAGAAAGCCGCCCATGGGCACGTCCGCAAGGCCCTTCAAGA----	2307
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Db	2341	CGTCTTAACTTGACAGACCTCCAGCCGTACATGCGACAGATTCTGGCTCACTGCAGAGA	2400
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QY	2308	-----CG 2309	2309
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QY	2430	GCTCCTGCGTTTGGTGATGATTTCTGTTGGTGACACCTCACTCAACCCACGCAAAAC	2489
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QY	2490	CTTCCTCAGGACCCCTGCTCCGAGGTGTCCTGATGATGCTGCTGGTGAACCTTGCAGAA	2549
Db	2701	CTTCCTCAGGACCCCTGCTCCGAGGTGTCCTGATGATGCTGCTGGTGAACCTTGCAGAA	2760
QY	2550	GACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2609
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QY	2610	GCCGGCCACAGGCTATTCCCTGTGTGCGGCTGTGCTGATATACCCGGAACCTGAGGT	2669
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Db	3241	CGGCCCTCTGCCCTCCAGAGCCGTGCAGTGGCTGTGCCACCAAGCATTTCTGTCTCAAGCT	3300

QY	3090	GACTCGACACCGGTGTCACTTACGTGCCACTCTGGGGTCACTCAGACAGCCCAAGCGCA	3149
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QY	3270	GAGCAGACACCAAGCAGCCCTGTCAACGCCGGGCTTACGTCCAGGAGGAGGGGGGGCC	3329
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Db	3541	CACACCCAGGCCCCGACACCGCTGGAGTCTGAGGCTGAGTGTGTTGGCCGAGCCTG	3600
QY	3390	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGGCT	3449
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGGCT	3660
QY	3450	GAGTGTCCAGCACACTGCGCTTCACTTCCCAACAGGCTGGCGCTGGCTCCACCCCA	3509
Db	3661	GAGTGTCCAGCACACTGCGCTTCACTTCCCAACAGGCTGGCGCTGGCTCCACCCCA	3720
QY	3510	GGGCCAGCTTTTCTCTCACACGAGGCCCGCTTCACTCCCAATAGGAATGTCATCC	3569
Db	3721	GGGCCAGCTTTTCTCTCACACGAGGCCCGCTTCACTCCCAATAGGAATGTCATCC	3780
QY	3570	CCAGATTGCACTGTTCACCCCTGACCTGCGCTCCTTGGCTTCCACCCCAACCATCC	3629
Db	3781	CCAGATTGCACTGTTCACCCCTGACCTGCGCTCCTTGGCTTCCACCCCAACCATCC	3840
QY	3630	AGGTGAGACCTTGAGAAGGACCTGGAGCTCTGGGAATTTGAGTGACCAAGAAGTGTG	3689
Db	3841	AGGTGAGACCTTGAGAAGGACCTGGAGCTCTGGGAATTTGAGTGACCAAGAAGTGTG	3900
QY	3690	CCCTGTACACAGGCGAGGACCTGCACTGATGGGGGTCCCTGTGGGTCAATTTGGGGG	3749
Db	3901	CCCTGTACACAGGCGAGGACCTGCACTGATGGGGGTCCCTGTGGGTCAATTTGGGGG	3960
QY	3750	GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAAAA 3804	
Db	3961	GAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAAAAA 4015	

RESULT 10
US-10-054-611-224
; Sequence 224, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1e1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/054,611
/ FILING DATE: 18-Jan-2002
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/854,050
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph T.
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002930US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 224:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4015 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 56..3454
/ OTHER INFORMATION: /product= "hTERT"
/ /note= "human telomerase reverse
/ transcriptase (hTERT) catalytic protein
/ component"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 224:

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QY	1568	GCTCTCGCTGACGAGCTGACGTGGAAGATGACCGTGGCGGACTGCGCTTGCGCTGCGCAG	1627
Db	1561	GCTCTCGCTGACGAGCTGACGTGGAAGATGACCGTGGCGGACTGCGCTTGCGCTGCGCAG	1620
QY	1628	GAGCCCAAGGCGTTGCGCTGTGTTCCGGCCGACAGACACCGTCTGCGGTGAGAGATCCTGGC	1687
Db	1621	GAGCCCAAGGCGTTGCGCTGTGTTCCGGCCGACAGACACCGTCTGCGGTGAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1740
QY	1748	TGTACGAGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1807
Db	1741	TGTACGAGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1800
QY	1808	CAAGTTCCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGACGTGCGGAGCTGTC	1867
Db	1801	CAAGTTCCAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGACGTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACCGGGCTGCCGCCGATTGTGAAACATGGACTACGTGCTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACCGGGCTGCCGCCGATTGTGAAACATGGACTACGTGCTGGAGC	1980
QY	1988	CAGAACGTTCCGCGACAGAAAGAGGGCCGAGCGTCTACCTCGAAGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCGACAGAAAGAGGGCCGAGCGTCTACCTCGAAGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCACTACGAGCGGGCGCGCGCCCGCCCTCTCTGCGCTGCTGCTGGG	2107
Db	2041	CAGCGTGTCACTACGAGCGGGCGCGCGCCCGCCCTCTCTGCGCTGCTGCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGAACCC	2167
Db	2101	CCTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGAACCC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCCGCTGAGCTGTA-----CATCCCCCA	2220
QY	2192	GGAACAGGCTCACGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGG	2251
Db	2221	GGAACAGGCTCACGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTACTGCGTGG	2280
QY	2252	TCCGTATGCCGTGTTCCAGAAAGCCGCCCATGGGCAAGTCCGCAAGGCTTTCAGA-----	2307
Db	2281	TCCGTATGCCGTGTTCCAGAAAGCCGCCCATGGGCAAGTCCGCAAGGCTTTCAGA-----	2340
QY	2308	-----	2307
Db	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTTGTGCTCACCTGACAGGA	2400
QY	2308	-----	2307
Db	2401	GACCAGCCCGCTGAGGAGATGCCGTGCTCATCGACAGAGCTCCTCCTGAATGAGGCCAG	2460
QY	2308	-----GG	2309
Db	2461	CAGTGGCCTCTTCGACGTCTTCTCTACGCTTCAATGTGCCACCAAGCCGTGCCATCAGGGG	2520
QY	2310	CAAGTCTTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTTCCACGCTGCTCTG	2369
Db	2521	CAAGTCTTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTTCCACGCTGCTCTG	2580
QY	2370	CAGCCTGTGCTACGCGGACATGAGAACCAAGCTGTTTTCGGGGATTTCGGCGGAGACGGGCT	2429
Db	2581	CAGCCTGTGCTACGCGGACATGAGAACCAAGCTGTTTTCGGGGATTTCGGCGGAGACGGGCT	2640

QY	2430	GCTCTGCGCTTTGGTGGATGATTTCTTGTGGTGACACCTCACTCACCACGGCAAAAC	2489
Db	2641	GGTCTGCGCTTTGGTGGATGATTTCTTGTGGTGACACCTCACTCACCACGGCAAAAC	2700
QY	2490	CTTCTCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGAGCTGCGTGTGAACCTTGCAGAA	2549
Db	2701	CTTCTCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGAGCTGCGTGTGAACCTTGCAGAA	2760
QY	2550	GACAGTGTGTAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2609
Db	2761	GACAGTGTGTAACCTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGAT	2820
QY	2610	GCGGGCCCCACGGCCCTATTCCCTGTGTGGCGCCTGTCTGTGATACCCGGACCTTGAGAGT	2669
Db	2821	GCGGGCCCCACGGCCCTATTCCCTGTGTGGCGCCTGTCTGTGATACCCGGACCTTGAGAGT	2880
QY	2670	GCAAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAACCTTCAACCG	2729
Db	2881	GCAAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAACCTTCAACCG	2940
QY	2730	CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAACTCTTTGGGGTCTTGCGGCTGAAGTG	2789
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCCGAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
QY	2790	TCACAGCCTGTTCTGGAATTGACAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	2849
Db	3001	TCACAGCCTGTTCTGGAATTGACAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTA	3060
QY	2850	CAAGATCCTCCTGCTGCGAGGGCTACAGGTTTCAACGCAATGTGTCTGCAGCTCCCATTTCA	2909
Db	3061	CAAGATCCTCCTGCTGCGAGGGCTACAGGTTTCAACGCAATGTGTCTGCAGCTCCCATTTCA	3120
QY	2910	TCAGCAAGTTTGGAGAACCACCAATTTTCTGCGCGTCACTCTGACACAGGCTCCCT	2969
Db	3121	TCAGCAAGTTTGGAGAACCACCAATTTTCTGCGCGTCACTCTGACACAGGCTCCCT	3180
QY	2970	CTGCTACTCCATCCTGGAAGCCAAAGACGACGGATGTGCTGGGGGCCAAGGGCGCCGC	3029
Db	3181	CTGCTACTCCATCCTGGAAGCCAAAGACGACGGATGTGCTGGGGGCCAAGGGCGCCGC	3240
QY	3030	CGGCCCTCTGCCCCCTCCGAGGGCCGTGACGTGGCTGTGCCACCAAGCATTCCTCAAGCT	3089
Db	3241	CGGCCCTCTGCCCCCTCCGAGGGCCGTGACGTGGCTGTGCCACCAAGCATTCCTCAAGCT	3300
QY	3090	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGACAGCCACGACGCA	3149
Db	3301	GACTCGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGACAGCCACGACGCA	3360
QY	3150	GCTGAGTCGAGACTCCCGGGGACGACGCTGACTGCCCTGAGGCCGACCAACCCGGC	3209
Db	3361	GCTGAGTCGAGACTCCCGGGGACGACGCTGACTGCCCTGAGGCCGACCAACCCGGC	3420
QY	3210	ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3269
Db	3421	ACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3270	GAGCAGACACCAAGCCCTGTCAACGCCGGGCTCTACGTCCCAAGGAGGAGGGGGCGCC	3329
Db	3481	GAGCAGACACCAAGCCCTGTCAACGCCGGGCTCTACGTCCCAAGGAGGAGGGGGCGCC	3540
QY	3330	CACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGGCCTGAGTGAATTTGGCCGAGGCCCTG	3389
Db	3541	CACACCCAGGCCCCGACCCGCTGGGAGTCTGAGGGCCTGAGTGAATTTGGCCGAGGCCCTG	3600
QY	3390	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3449
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3450	GAGTGTCCAGACACCTGCGCTTTCATTTCCCAACAGGCTGGCGCTCGGCTCCACCCCA	3509
Db	3661	GAGTGTCCAGACACCTGCGCTTTCATTTCCCAACAGGCTGGCGCTCGGCTCCACCCCA	3720
QY	3510	GGGCGACGTTTTTCTCACCAAGAGCCCGGCTTCCACTCCCCCATAGGAATAGTCCATCC	3569

Db 3721 GGGCCAGCTTTTCCCTCAACCAGGAGCCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC 3780

QY 3570 CCAGATTGCCATTGTTTCACCCCCTGCCCCCTGCCCTCTTTGCTTCCACCCCCCACCATCC 3629

Db 3781 CCAGATTGCCATTGTTTCACCCCCTGCCCCCTGCCCTCTTTGCTTCCACCCCCCACCATCC 3840

QY 3630 AGGTGAGACCCTGAAGAAGACCCTGGAGCTCTGGGAATTTGAGTGACCCAAAGGTGTG 3689

Db 3841 AGGTGAGAGACCCTGAAGAAGACCCTGGAGCTCTGGGAATTTGAGTGACCCAAAGGTGTG 3900

QY 3690 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3749

Db 3901 CCCTGTACACAGGCGGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGG 3960

QY 3750 GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 3804

Db 3961 GAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAA 4015

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RESULT 11
US-10-105-963-1
; Sequence 1, Application US/10105963
; Publication No. US20030068818A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Denning, Chris
; APPLICANT: Clark, A. John
; APPLICANT: Schief, J. Michael
; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human
; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System
; FILE REFERENCE: 731/002
; CURRENT APPLICATION NUMBER: US/10/105,963
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/277,811
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION:
US-10-105-963-1

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	Query Match	93.1%;	Score 3559;	DB 14;	Length 4015;	
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	Matches 3797;	Conservative	0;	Mismatches	0;	Indels 218; Gaps 2
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DB	1	GCAGCGTGCCTGCTGCGCAGTGGGAAGCCCTGGCCCCCGCCACCCCGCATGCC	60			
QY	68	GCGCGTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGCT	127			
DB	61	GCGCGTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGCT	120			
QY	128	GCGCGTGGCCACGTTCTGTGCGGCGCTTGGGGCCCCCAGGGCTGGCGGCTGTGTGACGCGGG	187			
DB	121	GCGCGTGGCCACGTTCTGTGCGGCGCTTGGGGCCCCCAGGGCTGGCGGCTGTGTGACGCGGG	180			
QY	188	GGAACCCGCGGCTTCCGCGCGCTGTGGCCCAAGTGCTGTGTGCGTGCCCTGGGACGC	247			
DB	181	GGAACCCGCGGCTTCCGCGCGCTGTGGCCCAAGTGCTGTGTGCGTGCCCTGGGACGC	240			
QY	248	ACGCGCGCCCCCGCGCGCCCTTCTTCCGCCAGGTGTCTGCTGAAGAGACTGTGTGC	307			
DB	241	ACGCGCGCCCCCGCGCGCCCTTCTTCCGCCAGGTGTCTGCTGAAGAGACTGTGTGC	300			

QY	308	CCGAGTGTCTGACAGAGGCTGTGCCAGCGCGCGCGAAGAACGTGTCTGGCTTCGGCTTCGC	367
Db	301	CCGAGTGTCTGACAGAGGCTGTGCCAGCGCGCGCGAAGAACGTGTCTGGCTTCGGCTTCGC	360
QY	368	GCTGCTGGACGGGGCCCCCGGGGGGGCCCCCCCCCGAGGCCCTTACCAACCAAGCGTGCAGACTA	427
Db	361	GCTGCTGGACGGGGCCCCCGGGGGGGCCCCCCCCCGAGGCCCTTACCAACCAAGCGTGCAGACTA	420
QY	428	CCTGCCCAACACCGGTACCGGACGCACTGCGGGGAGCGGGGGCGTGGGGGCTGTCTGCTCG	487
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QY	488	CCGCGTGGGGCGACGACGTGTGTTCACTGTGTGACAGCTGCGCGCTCTTGTGTGTGT	547
Db	481	CCGCGTGGGGCGACGACGTGTGTTCACTGTGTGACAGCTGCGCGCTCTTGTGTGTGT	540
QY	548	GGCTCCCAAGCTGCGCTTACCAAGTGTGCGGGCGCGCGCTGTACCAAGCTCGGCGCTGCCAC	607
Db	541	GGCTCCCAAGCTGCGCTTACCAAGTGTGCGGGCGCGCGCTGTGTACCAAGCTCGGCGCTGCCAC	600
QY	608	TCAGCCCCGGCCCCCGCCACACGCTAGTGAACCCCGAAGGCGTCTGGGATGCCAAGGGG	667
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QY	668	CTGGAACCATAGCGTCAAGGAGGCGCGGGGTCCCCCTGTGGGCTGCCAGCCCCGGGTGCCAG	727
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QY	728	GAGCGCGGGGGCAGTGCACAGCCGGAAGTCTGCCGTTGCCAAGAGGCCCCAAGGCGTGGCG	787
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QY	788	TGCCCCGTAGCCCGGAGCGGACGCCCCGTGGGCAAGGGGCTCTGGGCCCAACCCGGGCAAGAC	847
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QY	848	GCGTGAACCGAGTGAACCGTGGTTTCTGTGTGTGTGTCACTGCCAGAACCCGCGGAAGAGC	907
Db	841	GCGTGAACCGAGTGAACCGTGGTTTCTGTGTGTGTGTCACTGCCAGAACCCGCGGAAGAGC	900
QY	908	CACCTCTTTGAGGGGTGCGCTCTCTGGCAGCGGCTACTCCACCCCATCCGTGGGCGGCCA	967
Db	901	CACCTCTTTGAGGGGTGCGCTCTCTGGCAGCGGCTACTCCACCCCATCCGTGGGCGGCCA	960
QY	968	GCACCAAGCGGGCCCCCCCCCATCCACATCGCGGCCAACAGTCCCTGGGACACGCTTGTCC	1027
Db	961	GCACCAAGCGGGCCCCCCCCCATCCACATCGCGGCCAACAGTCCCTGGGACACGCTTGTCC	1020
QY	1028	CCCGGTGTACGCGCGAGAACCAAGCACTTCTCTACTCTCTCAGGCGACMAAGAGCAGCTGC	1087
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QY	1088	GCCCTCTTCTTACTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCTGGA	1147
Db	1081	GCCCTCTTCTTACTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGGCTCTGGA	1140
QY	1148	GACCATCTTCTGTGGTTCCAGGCCCTGATGCGAAGGACTCCCCGAGGTTGCCCGCT	1207
Db	1141	GACCATCTTCTGTGGTTCCAGGCCCTGATGCGAAGGACTCCCCGAGGTTGCCCGCT	1200
QY	1208	GCCCCAGCGCTACTGSCAAATGCGGCCCTGTCTGTGAGCTGCTTGGAAACACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGSCAAATGCGGCCCTGTCTGTGAGCTGCTTGGAAACACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCACGC	1327
Db	1261	GTGCCCCCTACGGGGGTGCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTACCCACGC	1320
QY	1328	AGCCGGTGTCTGTGCCCGGAGAGGCCCGAGGGCTCTGTGGCGGCCCCCGAGAGAGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCGGAGAGGCCCGAGGGCTCTGTGGCGGCCCCCGAGAGAGAGGA	1380
QY	1388	CACAGACCCCGCTGCGCTGTGACGCTGTCCGACAGCAGCAGCCCTTGACAGGTGT	1447

Db	1381	CACAGACCCCCGCTGCGCTGGTGAGTGTCTCCGCCAGCAGACAGCCCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTGGTGGGGGCTGCGCTGCGCGCGCTGGTGGCCCCCAGGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTGGTGGGGGCTGCGCTGCGCGCGCTGGTGGCCCCCAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAAGCGCGCTTCTCTCAGGAACAACGAAGTTCACTCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAAGCGCGCTTCTCTCAGGAACAACGAAGTTCACTCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTGCTGCAAGAGCTGACCGTGAAGATGAGCGTGGGGAATGCGCTTGGCTGGCGAG	1627
Db	1561	GCTCTGCTGCAAGAGCTGACCGTGAAGATGAGCGTGGGGAATGCGCTTGGCTGGCGAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTGTTCGGGCGCAGAGACACCGTCTGCGTGAAGAGATCCTGGC	1687
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCGGGCGCAGAGACACCGTCTGCGTGAAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGATGTGTACGTTCGTCAGCTGCTCAGGTCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGATGTGTACGTTCGTCAGCTGCTCAGGTCTTTCTTTTA	1740
QY	1748	TGTCAAGGAGACCAAGCTTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTGTCTGGAG	1807
Db	1741	TGTCAAGGAGACCAAGCTTTCAAAAGACAGGCTCTTTTCTACCGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTCGAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGGGGAAGCTGTC	1867
Db	1801	CAAGTTCGAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGGGGAAGCTGTC	1860
QY	1868	GGAAGCAGAGGTGAGGCAAGTCGGGAAGCCAGGCGCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTGAGGCAAGTCGGGAAGCCAGGCGCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACGGGCTGCGCGCATTTGTGAACATGACATCCTCGTGGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACGGGCTGCGCGCATTTGTGAACATGACATCCTCGTGGGAGC	1980
QY	1988	CAGAAAGTTCCGAGAGAAAAGAGGGCCGAGCGCTCTCACTCGAGGGTGAAGCACTGTT	2047
Db	1981	CAGAAAGTTCCGAGAGAAAAGAGGGCCGAGCGCTCTCACTCGAGGGTGAAGCACTGTT	2040
QY	2048	CAGCGTCTCACTACGAGCGGGGCGCGCGCGCGCCCTCTCTGGGCGCTCTGTGTGGG	2107
Db	2041	CAGCGTCTCACTACGAGCGGGGCGCGCGCGCGCCCTCTCTGGGCGCTCTGTGTGGG	2100
QY	2108	CCTGCAAGATATCCACAGGGGCTGGCGCACTTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	2167
Db	2101	CCTGCAAGATATCCACAGGGGCTGGCGCACTTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	2160
QY	2168	GCGCGCTGAGCTGTA-----CATCCCCCA	2191
Db	2161	GCGCGCTGAGCTGTA-----CATCCCCCA	2220
QY	2192	GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGG	2251
Db	2221	GGACAGGCTCAGGAGGTATCGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGG	2280
QY	2252	TGCGTATGCGGTGTTCAGAAAGCGCGCCCATGGGCAAGTCCGCAAGGCTTCAAGAGCA	2307
Db	2281	TGCGTATGCGGTGTTCAGAAAGCGCGCCCATGGGCAAGTCCGCAAGGCTTCAAGAGCA	2340
QY	2308	-----	2307
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCGGTACATGCGACAGTTGCTGGCTCACTGACAGA	2400
QY	2308	-----	2307
Db	2401	GACCAGCCCGCTGAGGAGTCCGTCTCATGAGCAGAGCTCTCTCTGAATGAGGCGAG	2460
QY	2308	-----CG	2309

QY 3390 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGGCT 3449
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGGCT 3660
QY 3450 GAGTGTCCAGCAGCCTGCGCTCTTCACTTCCCAAGGCTGCGGCTCGGCTCCAGCCCA 3509
Db 3661 GAGTGTCCAGCAGCCTGCGCTCTTCACTTCCCAAGGCTGCGGCTCGGCTCCAGCCCA 3720
QY 3510 GGGCCAGCTTTCTCAACAGAGAGCGCGCTTCCACTCCCAATAGGAATAGTCCATCC 3569
Db 3721 GGGCCAGCTTTCTCAACAGAGAGCGCGCTTCCACTCCCAATAGGAATAGTCCATCC 3780
QY 3570 CCAGATTCGCCATTTGTTCACCCCTGCGCTGCGCTCTTCTTCCACCCCGCAGCCATCC 3629
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QY 3630 AGGTGAGACCTCTGAGAGAGACCCCTGGAGCTCTGGGAATTGGAGTGAACCAAGGTGTG 3689
Db 3841 AGGTGAGACCTCTGAGAGAGACCCCTGGAGCTCTGGGAATTGGAGTGAACCAAGGTGTG 3900
QY 3690 CCCTGTACACAGGCGAGGACCCCTGACCTGGATGGGGGTCCCTGTGGGTCAAAATTGGGGG 3749
Db 3901 CCCTGTACACAGGCGAGGACCCCTGACCTGGATGGGGGTCCCTGTGGGTCAAAATTGGGGG 3960
QY 3750 GAGGTGCTGTGGAGTAATAATCTGATATATGAGTTTTCAGTTTGAAGAAAAA 3804
Db 3961 GAGGTGCTGTGGAGTAATAATCTGATATATGAGTTTTCAGTTTGAAGAAAAA 4015

RESULT 12

US-10-044-692-1

Sequence 1, Application US/10044692

Publication No. US2003009634A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1

Query Match 93.1%; Score 3559; DB 14; Length 4015;
Best Local Similarity 94.6%; Pred. No. 0;
Matches 3797; Conservative 0; Mismatches 0; Indels 218; Gaps 2;

QY 8 GCAGCGCTGCGCTCTGCTGCGCAGCTGGAGAGCCCTGCGCCCGGCGCCACCCCGCGATGCC 67
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QY 68 GCGCGCTCCCGCTGCGCGAGCGCGCTGCTGCTGCTGCGCGAGCCACTACCGCGAGTGTCT 127
Db 61 GCGCGCTCCCGCTGCGCGAGCGCGCTGCTGCTGCTGCGCGAGCCACTACCGCGAGTGTCT 120
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RESULT 13
US-10-044-539-1

Sequence 1, Application US/10044539
Publication No. US2003010093A1

GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Martin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4015 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 56..3454

OTHER INFORMATION: /product= "hTERT"

/note= "human telomerase reverse

transcriptase (hTERT) catalytic protein

component"

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-044-539-1

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QY	2252	TGCGTATGCCGTGTTCCAGAGGCCGCCCATGGGCACTTCGCAAGGCTTCAAGA----	2307
Db	2281	TGCGTATGCCGTGTTCCAGAGGCCGCCCATGGGCACTTCGCAAGGCTTCAAGACCA	2340
QY	2308	-----	2307
Db	2341	CGTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCACCTGCAAGA	2400
QY	2308	-----	2307
Db	2401	GACCAAGCCCGCTGAGGAGTCCGTGCTCATGACGACAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2308	-----GG	2309
Db	2461	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCACCAAGCCGTGCGCATCAGGG	2520
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Db	2521	CAAGTCTACGTCCAGTCCAGGAGATCCCGCAGAGGCTCCATCCTCCACAGCTGCTTG	2580
QY	2370	CAGCCTGTGCTACGCGGCATGAGAACAAAGCTGTTGCGGGATTGCGCGGACGGGCT	2429
Db	2581	CAGCCTGTGCTACGCGGCATGAGAACAAAGCTGTTGCGGGATTGCGCGGACGGGCT	2640
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Db	2641	GCTCCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGAAAC	2700
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Db	3061	CAAGATCCTCCTGCTGCAAGGCTACAGGTTTCAAGCATGTGTGCTGACGCTCCCATTTCA	3120
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Db	3181	CTGCTACTCCATCCTCTGAAAGCCCAAGAACCGCAGGAATGTGCTGGGGGGCCCAAGGGCGCCGC	3240
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Db	3241	CGGCCCTCTGCCCCCTCCGAGGCCGTGCGAGTGGCTGTGCCACCAAGCATTTCTGTCTCAAGCT	3300
QY	3090	GACTCGACACCGTGTCACTTAAGTGCACCTCTGGGGTCACTCAGSACAGCCCAAGCGCA	3149
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Db	3361	GCTAGTCCGAGAGCTCCCGGGGAGCGACGCTGACTGCCCCCTGAGAGCCGCAAGCCCGGC	3420
QY	3210	ACTGCCCTCAGACTTTCAAGAACCATCCTTGACTGATGCCCCACCCGCCCAAGCCAGGCCGA	3269
Db	3421	ACTGCCCTCAGACTTTCAAGAACCATCCTTGACTGATGCCCCACCCGCCCAAGCCAGGCCGA	3480
QY	3270	GAGCAGACACCAGCAGCCCTGTCAACGCCGGGCTTAAGTCCCAAGGAGGAGGGGGCC	3329
Db	3481	GAGCAGACACCAGCAGCCCTGTCAACGCCGGGCTTAAGTCCCAAGGAGGAGGGGGCC	3540
QY	3330	CACACCCAGGCCCGCACCCGCTGGGAGTCTGAAGCCTGAGTGAAGTGTGGCCGAGGCCCTG	3389
Db	3541	CACACCCAGGCCCGCACCCGCTGGGAGTCTGAAGCCTGAGTGAAGTGTGGCCGAGGCCCTG	3600
QY	3390	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAAGCCTGAAGCAGTGTCCAGGCCCAAGGCT	3449
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAAGCCTGAAGCAGTGTCCAGGCCCAAGGCT	3660
QY	3450	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGAGCTGGCGCTCGGCTCCACCCCA	3509
Db	3661	GAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGAGCTGGCGCTCGGCTCCACCCCA	3720
QY	3510	GGGCCAGCTTTTCTCAACCAAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCC	3569
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RESULT 14
US-10-385-882-1
? Sequence 1, Application US/10385882
? Publication No. US20030232409A1
? GENERAL INFORMATION:
? APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
? APPLICANT: FARRIS, James
? APPLICANT: FOSTER, Douglas
? APPLICANT: O'GRADY, Scott
? TITLE OF INVENTION: IMMORTAL PORCINE CELLS
? FILE REFERENCE: 110.01700101
? CURRENT APPLICATION NUMBER: US/10/385,882
? CURRENT FILING DATE: 2003-03-11
? PRIOR APPLICATION NUMBER: 60/363,129
? PRIOR FILING DATE: 2002-03-11
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 1

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LENGTH: 4027
TYPE: DNA
ORGANISM: ARTIFICIAL
FEATURE:
OTHER INFORMATION: Nucleotide sequence encoding telomerase reverse transcriptase
US-10-385-882-1

Query Match 93.0%; Score 3557; DB 15; Length 4027;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 3798; Conservative 0; Mismatches 5; Indels 218; Gaps 2;

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OY	2675	GCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAATCTACCTTCAACCGCGGCT	2734
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OY	2735	TCAAAGCTGGGAGGAACATGCGTCCCAAACTCTTTGGGGCTTTGCGGCTGAAGTGTACA	2794
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OY	2795	GCGCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGGGTGTGACCAACATCTACAGA	2854
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OY	2855	TCCTCTGCTGCAGGCGGTACAGGTTTCAACGCATGTGTGCTGACGCTCCCATTTCAATCAGC	2914
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QY	3035	CTCTGCCCTCCGAGGCGCTGCAGTGGCTGTGTGCCACCAAGCATTTCTGTCTCAAGTGA	3094
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QY	3095	GACACCGTGTCACTTACGTGCCACTCCTGTGGGTCACTCAGGACAGCCAGACGACTGA	3154
Db	3307	GACACCGTGTCACTTACGTGCCACTCCTGTGGGTCACTCAGGACAGCCAGACGACTGA	3366
QY	3155	GTTGGGAAGCTCCCGGGGACGACGCTGACTGTGCCCTGAGAGCCGACAGCCAACCCGGCA	3214
Db	3367	GTTGGGAAGCTCCCGGGGACGACGCTGACTGTGCCCTGAGAGCCGACAGCCAACCCGGCA	3426
QY	3215	CCTCAGACTTCAAGACCATCCTTGACTGATGAGCCACCCGCCACAGCCAGCGCAGAGCA	3274
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QY	3275	GACACCCAGCAGCCCTGTCA CGCCGGGCTTAAGTCCAGGAGGAGGGGCGGCCACAC	3334
Db	3487	GACACCCAGCAGCCCTGTCA CGCCGGGCTTAAGTCCAGGAGGAGGGGCGGCCACAC	3546
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Db	3547	CCAGGCCCGCACCGCTGGAGTCTGAGGCGCTGAAGTGTGTTGGCCGAGGCTGCATGT	3606
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QY	3515	AGCTTTTCTTCAACGAGAGCCCGGCTTCCACTTCCCAATAGGAATAGTCCATCCCCAGA	3574
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QY	3575	TTGCGCATTTGTCAACCCCTCGCCCTGCCCTCCTTTGCTTCCACCCCAACCATCCAGGTG	3634
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QY	3635	GAGACCCCTGAGAAGAACCTGGAGCTCTGGGAATTTGAGTGAACCAAGGTGTGCCCTG	3694
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QY	3695	TACACAGGCGAGAACCTGCACCTGATGGGGGTCCCTGTGGGTCAATTTGGGGGAGGT	3754
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QY	3755	GCTGTGGAGTAATAATACTGAATATAGATTTTTCAGTTTGGAAAAAATTTTAAAAA	3814
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; Patent No. US20020164786A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru

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QY	1926	CGCTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGTGGGA	1985
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OM nucleic - nucleic search, using SW model

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3778	98.8	3860	20	US-09-424-686F-8
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4	3767.8	98.5	3855	13	US-08-911-312A-18
5	3767.8	98.5	3855	13	US-08-974-524E-122
6	3767.8	98.5	3855	13	US-08-974-549-4
7	3767.8	98.5	3855	13	US-08-974-584C-122
8	3767.8	98.5	3855	20	US-09-432-503-4
9	3767.8	98.5	3855	31	US-09-721-477-4
10	3767.8	98.5	3855	31	US-09-721-506-4
11	3767.8	98.5	3855	43	US-10-044-539-4
12	3767.8	98.5	3855	43	US-10-044-692-4
13	3767.8	98.5	3855	49	US-10-325-810-4
14	3632	95.0	4006	20	US-09-424-686F-9
15	3586	93.8	4042	20	US-09-424-686B-1
16	3586	93.8	4042	20	US-09-424-686F-1
17	3586	93.8	4042	24	US-09-582-246-2
18	3572.6	93.4	4037	13	US-08-974-549-343
19	3572.6	93.4	4037	20	US-09-432-503-343
20	3572.6	93.4	4037	31	US-09-721-477-343
21	3572.6	93.4	4037	31	US-09-721-506-343
22	3572.6	93.4	4037	49	US-10-325-810-343
23	3572.6	93.4	4038	13	US-08-974-524E-117
24	3572.6	93.4	4038	13	US-08-974-584C-117
25	3563.8	93.2	4023	14	US-09-026-981-35
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27	3559.4	93.1	7029	13	US-08-911-312A-1
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29	3559	93.1	4015	1	PCT-US02-14867-1
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37	3559	93.1	4015	14	US-09-052-864-1
38	3559	93.1	4015	20	US-09-432-503-1
39	3559	93.1	4015	25	US-09-601-645-10
40	3559	93.1	4015	25	US-09-601-645A-10
41	3559	93.1	4015	31	US-09-721-477-1
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44	3559	93.1	4015	39	US-09-949-016-455
45	3559	93.1	4015	42	US-09-990-080-1

ALIGNMENTS

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RESULT 1
US-09-424-686F-10
; Sequence 10, Application US/09424686F
; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Siegmund, Hans-Ulrich
; APPLICANT: Weichel, Walter
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Therag
; TITLE OF INVENTION: Use
; FILE REFERENCE: Bayer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686F
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/EP98/03468
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft word
; SEQ ID NO 10

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? LENGTH: 3824
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (1)..(3824)
? OTHER INFORMATION: Nucleotides 2184 to 2219 and 2345 to 2526 of SEQ ID NO. 1 were
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Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3824; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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Db	241	GGACGCAACG	300
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QY	3361	GGCTTGAGTGAAGTGTGTTGGCCAGGCTGTGATGTCCGGCTGAAAGCTGAAGTGTCCGGCTG	3420
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QY	3421	AGGCTTGAGCGAGTGTCCAGCCAAAGGCTGAGTGTCCAGCACACCTGCCGCTTCACTTC	3480
Dp	3421	AGGCTTGAGCGAGTGTCCAGCCAAAGGCTGAGTGTCCAGCACACCTGCCGCTTCACTTC	3480
QY	3481	CCCCAGGCTGGCGCTCGGCTTCCACCCCAAGGCGCAAGCTTTCTCAACAGAGGCCGCT	3540
Dp	3481	CCCCAGGCTGGCGCTCGGCTTCCACCCCAAGGCGCAAGCTTTCTCAACAGAGGCCGCT	3540
QY	3541	TCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCCGCAATTGTCAACCCCTCGCCCTG	3600
Dp	3541	TCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCCGCAATTGTCAACCCCTCGCCCTG	3600
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Dp	3601	CCCTCCTTTGGCTTCCACCCCAACCATCCAGGTGAGAACCTGAGAAGGACCCCTGGGAGC	3660
QY	3661	TCTGGGAATTTGGAGTGACCAAAAGTGTGCCCTGTACACAGCGAGGACCCCTGCACCTGG	3720
Dp	3661	TCTGGGAATTTGGAGTGACCAAAAGTGTGCCCTGTACACAGCGAGGACCCCTGCACCTGG	3720
QY	3721	ATGGGGGTCCCTGTGGGTCAAAATTGGGGGGAGGTGCTGTGGAGTAAATATCTGAATATA	3780
Dp	3721	ATGGGGGTCCCTGTGGGTCAAAATTGGGGGGAGGTGCTGTGGAGTAAATATCTGAATATA	3780
QY	3781	TGAGTTTTCAGTTTGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3824	
Dp	3781	TGAGTTTTCAGTTTGAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3824	

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RESULT 2
US-09-424-686F-8
; Sequence 8, Application US/09424686F
; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Slegmund, Hans-Ulrich
; APPLICANT: Weichel, Walter
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Therap
; TITLE OF INVENTION: Use
; FILE REFERENCE: Bayer 10, 203
; CURRENT APPLICATION NUMBER: US/09/424, 686F
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/EP98/03468
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Word
; SEQ ID NO 8
; LENGTH: 3860
; TYPE: DNA
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; ORGANISM: Human
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3860)
; OTHER INFORMATION: Nucleotides 2345 to 2526 of SEQ ID NO 1 were deleted to provide
; OTHER INFORMATION: this sequence.
US-09-424-686F-8

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Best Local Similarity	99.1%;	Pred. No. 0;		
Matches 3824; Conservative	0;	Mismatches	0;	Indels 36; Gaps 1;

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QY		121 AGGTGCTGCGCGCTGAGCCACTGTTGTCGGCGCGCTGGGGGCCCCCAAGGCTGCGCGCTGTGC	180
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QY		181 AGCGCGGGGACCCCGCGGCTTTCGCGCGCTGTTGGGCCAAGTGCTGTGTGCGTGCCCT	240
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QY		241 GGGACGCACGGCGCGCCCCCGCGCCCCCTCCTTCCGCCAAGTGTCTGCTGAAAGAGC	300
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QY		301 TGGTGCGCCCGAGTGTGTGACAAGCTGTGCGAGCGCGCGCGAGAAGACGTGCTGGCCTTCG	360
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QY		481 TGCTGCGCGCGGTGGGCCACGACGTGCTTCACTGCTGSCACGCTGCGCGCTCTTTG	540
Db	481	TGCTGCGCGCGGTGGGCCACGACGTGCTTCACTGCTGSCACGCTGCGCGCTCTTTG	540
QY		541 TGCTGTGTGCTCCCAAGCTGCGGCTTAACAGGTGTGCGGGCGCGCTGTACCAAGCTCGGG	600
Db	541	TGCTGTGTGCTCCCAAGCTGCGGCTTAACAGGTGTGCGGGCGCGCTGTACCAAGCTCGGG	600
QY		601 CTGCCACTCAGGCGCGCGCGCGCGCCACACAGCTAGTGGAACCCCGAAGGCGTCTGGGATTGC	660
Db	601	CTGCCACTCAGGCGCGCGCGCGCGCCACACAGCTAGTGGAACCCCGAAGGCGTCTGGGATTGC	660
QY		661 AACGGGCTTGAAACCATAGCGTCAAGGAGGCCGGGCTCCCTCTGGGCTTGCCAGCCCCGG	720
Db	661	AACGGGCTTGAAACCATAGCGTCAAGGAGGCCGGGCTCCCTCTGGGCTTGCCAGCCCCGG	720
QY		721 GTGCGAAGAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGGCCCAAGAGGCCCAAGG	780
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QY		781 GTGGCGCTGCCCCCTGAGCCGGAGCGGACGCCGTTGGGCAAGGGTCTGGGCCCAACCCGG	840
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QY		841 GCAGGACGCGTGAACCAAGTAGACCGTGGTTTTCTGTGTGTGTCACTTGCCAGACCCGGCG	900
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QY		901 AAGAAGCCACCTCTTTGAGAGGTGCGCTCTCTGSGCACGCGCCAATCCCAACCATCCGTGG	960

Db 901 AAGAGCCACCTCTTTGGAGGGTGGCTCTCTGCGACGCGCCACTCCACCCATCCGTGG 960
QY 961 GCCGCCAGCACCGCGGGGCCCCCATTCACATCGCGGCCACCAAGTCTCTGGACACGC 1020
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QY 1021 CTTGTCCCCGGGTGAGCGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGGAGC 1080
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QY 1081 AGCTGCGGCCCTCTCTCTACTCTCAGCTCTCTGAGGCCCGAGCTGAGCTGCGAGGC 1140
Db 1081 AGCTGCGGCCCTCTCTCTACTCTCAGCTCTCTGAGGCCCGAGCTGAGCTGCGAGGC 1140
QY 1141 TCGTGAGAGCACTTTCTGGGTTCCAGGCCCTGAGTGCAGGAGCACTCCCGCAGGTTC 1200
Db 1141 TCGTGAGAGCACTTTCTGGGTTCCAGGCCCTGAGTGCAGGAGCACTCCCGCAGGTTC 1200
QY 1201 CCGGCTGCCCCAGCGCTACTGCGAATGCGGCCCTGTTCTGAGCTGTTGGAACC 1260
Db 1201 CCGGCTGCCCCAGCGCTACTGCGAATGCGGCCCTGTTCTGAGCTGTTGGAACC 1260
QY 1261 ACGCGAGTGCCTCTAAGGGGTGCTCTCTCAAGACGCACTGCGCGCTGCGAGTGCATCA 1320
Db 1261 ACGCGAGTGCCTCTAAGGGGTGCTCTCTCAAGACGCACTGCGCGCTGCGAGTGCATCA 1320
QY 1321 CCCCAGCAGCGGCTGTGTGCCCCGAGAGAGCCCGAGGCTGTGGCGGGCCCCCGAGG 1380
Db 1321 CCCCAGCAGCGGCTGTGTGCCCCGAGAGAGCCCGAGGCTGTGGCGGGCCCCCGAGG 1380
QY 1381 AGAGAGACACAGACCCCGCTGCGCTGTGAGTGTCTCCGACAGACAGACAGCCCTGGC 1440
Db 1381 AGAGAGACACAGACCCCGCTGCGCTGTGAGTGTCTCCGACAGACAGACAGCCCTGGC 1440
QY 1441 AGGTGTACGGCTTGTGGGGGCTGCTGCTGCGCGGCTGTGCCCCAGGCTCTGGGGCT 1500
Db 1441 AGGTGTACGGCTTGTGGGGGCTGCTGCTGCGCGGCTGTGCCCCAGGCTCTGGGGCT 1500
QY 1501 CCAGGACACAGACCGCGCTTCTCAGAGACCAAGAGTTCATCTCCCTGGGGAAGC 1560
Db 1501 CCAGGACACAGACCGCGCTTCTCAGAGACCAAGAGTTCATCTCCCTGGGGAAGC 1560
QY 1561 ATGCCAAGCTCTCGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
Db 1561 ATGCCAAGCTCTCGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1620
QY 1621 TGGCGAGAGAGCCAGGGGTTGGCTGTGTCCGCGCGCAGAGCACTGCTGCGTGAAGAGA 1680
Db 1621 TGGCGAGAGAGCCAGGGGTTGGCTGTGTCCGCGCGCAGAGCACTGCTGCGTGAAGAGA 1680
QY 1681 TCCTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTAAGTGTGAGCTGCTCAGGTCTT 1740
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QY 1741 TCTTTTATGTACCGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTAACCGGAAGAGTG 1800
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QY 1801 TCTGAGCAAGTTGCAAGCATTTGAATCAGACACTTGAAGAGGTTGCAAGTGCAGG 1860
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QY 1861 AGCTGTGGAAGAGAGTCAAGGAGCATCGGGAAGCCAGGCGCGCTGCTGACGTCCA 1920
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QY 1921 GACTCCGCTTCATCCCAAGCCTGACGGGCTGCGCGCGATTTGTAACATGGACTACGTG 1980
Db 1921 GACTCCGCTTCATCCCAAGCCTGACGGGCTGCGCGCGATTTGTAACATGGACTACGTG 1980
QY 1981 TGGGAGCCAGAACGTTCCGACAGAGAAAGAGGCGCGCTCTCAGCTGAGGGTGAAGG 2040

Db 1981 TGGGAGCCAGAACGTTCCGACAGAGAAAGAGGCGCGCTCTCAGCTGAGGGTGAAGG 2040
QY 2041 CACTGTTACGGTGTCAACTACGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCTG 2100
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QY 2101 TGCTGGGCTGAGCAATATCCACAGAGGCGCTGGCGCACTTCTGCTGCTGCTGCGGGCCC 2160
Db 2101 TGCTGGGCTGAGCAATATCCACAGAGGCGCTGGCGCACTTCTGCTGCTGCTGCGGGCCC 2160
QY 2161 AGAAGCCGCGCGCTGAGCTGTA-----CA 2184
Db 2161 AGAAGCCGCGCGCTGAGCTGTA-----CA 2184
QY 2185 TCCCCAGAGACAGGCTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAGGAGTCAAG 2244
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QY 2245 GCGTGGCTGGTATGCGCGTGTGTCAGAGAGCGCGCCCATGAGGACAGTCCGCAAGGCTTCA 2304
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QY 2305 AGAGGCAAGTCTTACGTCAGTGCAGAGGAGTCCCGCAGAGGCTCCATCTCTCCACGCTG 2364
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QY 2341 AGAGGCAAGTCTTACGTCAGTGCAGAGGAGTCCCGCAGAGGCTCCATCTCTCCACGCTG 2400
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QY 2365 CTCTGAGCGCTGTGCTACGCGGACATGAGAGAACAGCTGTTGCGGGGATTCGCGGGAGC 2424
Db 2365 CTCTGAGCGCTGTGCTACGCGGACATGAGAGAACAGCTGTTGCGGGGATTCGCGGGAGC 2424
QY 2401 CTCTGAGCGCTGTGCTACGCGGACATGAGAGAACAGCTGTTGCGGGGATTCGCGGGAGC 2460
Db 2401 CTCTGAGCGCTGTGCTACGCGGACATGAGAGAACAGCTGTTGCGGGGATTCGCGGGAGC 2460
QY 2425 GGGCTGCTCTGCGCTTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAAGGAGC 2484
Db 2425 GGGCTGCTCTGCGCTTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAAGGAGC 2484
QY 2461 GGGCTGCTCTGCGCTTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAAGGAGC 2520
Db 2461 GGGCTGCTCTGCGCTTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAAGGAGC 2520
QY 2485 AAAACCTTCTCAGAGACCTGTCAGAGTGTCTCTGATGATGCTGCTGCTGCTGCTGCTG 2544
Db 2485 AAAACCTTCTCAGAGACCTGTCAGAGTGTCTCTGATGATGCTGCTGCTGCTGCTGCTG 2544
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Db 2881 ATCTACAAGATCTCTCTGCTGAGGCTGACAGGTTTCAAGCATGTGTGCTGAGTCCCA 2940
QY 2905 TTTATCAGCAAGTTTGAAGAACCCCACTTTTCTGCGGCTGATCTGACACGCGC 2964
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QY	3085	AAGCTGACTGCACACCCGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAAG	3144
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QY	3145	ACGCACTGAGTCGGAAGCTCCCGGGGACGACGCGTGACTGCGCCTGGAGGCCGACGCCAAC	3204
Db	3181	ACGCACTGAGTCGGAAGCTCCCGGGGACGACGCGTGACTGCGCCTGGAGGCCGACGCCAAC	3240
QY	3205	CCGGCACTGCCCCCTCAGACTTCAAGACCATCCTGACTGATATGGCCACCCGCCACAGCCAG	3264
Db	3241	CCGGCACTGCCCCCTCAGACTTCAAGACCATCCTGACTGATATGGCCACCCGCCACAGCCAG	3300
QY	3265	GCCGAGAGCAGACACACGACGACCCCTGTCAAGCCGGGCTTAAGTCCCAAGGAGGAGGGG	3324
Db	3301	GCCGAGAGCAGACACACGACGACCCCTGTCAAGCCGGGCTTAAGTCCCAAGGAGGAGGGG	3360
QY	3325	CGGCCACACACCCAGGCCCGCACCCGCTGGAGTCTGAGGCGCTGAGTGAAGTGTGGCCGAG	3384
Db	3361	CGGCCACACACCCAGGCCCGCACCCGCTGGAGTCTGAGGCGCTGAGTGAAGTGTGGCCGAG	3420
QY	3385	GCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAAGCCTGACGAGTGTCCAGCCAA	3444
Db	3421	GCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAAGCCTGACGAGTGTCCAGCCAA	3480
QY	3445	GGGCTGAGTGTCCAGACACACTGCCGTCTTCACTTCCCAACAGGCTGGCGCTGGCTCCA	3504
Db	3481	GGGCTGAGTGTCCAGACACACTGCCGTCTTCACTTCCCAACAGGCTGGCGCTGGCTCCA	3540
QY	3505	CCCCAGGGCCAGCTTTTCTCTCAACAGAGACCCGGCTTCCACTCCCACATAGAAATAGTC	3564
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QY	3565	CATCCCCAGATTGCGCAATTGTTCACCCCTCGCCCTGCGCCTCTTGGCCTTCCACCCCAAC	3624
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QY	3625	CATCCAGGTGAGACCCCTGAGAAAGAACCCCTGGAGCTCTGGAAATTGGAGTGAACCAAG	3684
Db	3661	CATCCAGGTGAGACCCCTGAGAAAGAACCCCTGGAGCTCTGGAAATTGGAGTGAACCAAG	3720
QY	3685	GTTGTGCCCTGTACACAGGCGAGAGAACCCCTGCACCTGGAATGGGGGTCCCTGTGGGTCAAATT	3744
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QY	3745	GGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAAAAAAAA	3804
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RESULT 3
 US-08-911-312-18
 ; Sequence 18, Application US/08911312
 ; GENERAL INFORMATION:
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 ; APPLICANT: Cech, Thomas R.
 ; APPLICANT: Lingner, Joachim
 ; APPLICANT: Nakamura, Toru
 ; APPLICANT: Chapman, Karen B.
 ; APPLICANT: Morin, Gregg B.
 ; APPLICANT: Harley, Calvin B.
 ; APPLICANT: Andrews, William
 ; TITLE OF INVENTION: Telomerase Reverse Transcriptase
 ;
 ; NUMBER OF SEQUENCES: 170
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA

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1  ZIP: 94111-3834
2
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: Floppy disk
5  COMPUTER: IBM PC compatible
6  OPERATING SYSTEM: PC-DOS/MS-DOS
7  SOFTWARE: Patentin Release #1.0, Version #1.30
8  CURRENT APPLICATION DATA:
9  APPLICATION NUMBER: US/08/911,312
10 FILING DATE: 14-AUG-1997
11 CLASSIFICATION: 536
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 08/724,643
14 FILING DATE: 01-OCT-1996
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/844,419
17 FILING DATE: 18-APR-1997
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/846,017
20 FILING DATE: 25-APR-1997
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/851,843
23 FILING DATE: 06-MAY-1997
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 08/854,050
26 FILING DATE: 09-MAY-1997
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 08/912,951
29 FILING DATE: 14-AUG-1997
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 08/915,503
32 FILING DATE: 14-AUG-1997
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Einhorn, Gregory P.
35 REGISTRATION NUMBER: 38,440
36 REFERENCE/DOCKET NUMBER: 015389-002500US
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (415) 576-0200
39 TELEFAX: (415) 576-0300
40 INFORMATION FOR SEQ ID NO: 18:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 3855 base pairs
43 TYPE: nucleic acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: cDNA
47 FEATURE:
48 NAME/KEY: CDS
49 LOCATION: 56..2476
50 OTHER INFORMATION: /product= "hTfT"
51 OTHER INFORMATION: /note= "clone #712562"
52
53 US-08-911-312-18
54
55 Query Match 98.5%; Score 3767.8; DB 13; Length 3855;
56 Best Local Similarity 99.0%; Pred. No. 0;
57 Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1
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5      ; GENERAL INFORMATION:
6      ;
7      ; APPLICANT: Cech, Thomas R.
8      ; APPLICANT: Lingner, Joachim
9      ; APPLICANT: Nakamura, Toru
10     ; APPLICANT: Chapman, Karen B.
11     ; APPLICANT: Morin, Gregg B.
12     ; APPLICANT: Harley, Calvin B.
13     ; APPLICANT: Andrews, William
14     ; TITLE OF INVENTION: Telomerase Reverse Transcriptase
15     ;
16     ; NUMBER OF SEQUENCES: 171
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18     ; CORRESPONDENCE ADDRESS:
19     ;
20     ; ADDRESSEE: Townsend and Townsend and Crew LLP
21     ;
22     ; STREET: Two Embarcadero Center, Eighth Floor
23     ;
24     ; CITY: San Francisco
25     ;
26     ; STATE: California
27     ;
28     ; COUNTRY: USA
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44     ; APPLICATION NUMBER: US/08/911,312A
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46     ; FILING DATE: 14-AUG-1997
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48     ; CLASSIFICATION: 536
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51     ;
52     ; APPLICATION NUMBER: US 08/724,643
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54     ; FILING DATE: 01-OCT-1996
55     ;
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58     ; APPLICATION NUMBER: US 08/844,419
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84     ; FILING DATE: 14-AUG-1997
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86     ; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..2476
OTHER INFORMATION: /product= "hprt"
OTHER INFORMATION: /note= "clone #712562"
US-08-911-312A-18

Query Match 98.5%; Score 3767.8; DB 13; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

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QY 1088 GCGCTCTCTCTACTCTAGCTCTGTAGGCGCGCAAGCTGTAGGCGCTCGGAGCTGTGGA 1147
DB 1081 GCGCTCTCTCTACTCTAGCTCTGTAGGCGCGCAAGCTGTAGGCGCTCGGAGCTGTGGA 1140
QY 1148 GACCATCTTTCTGGGTTCAGGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1207
DB 1141 GACCATCTTTCTGGGTTCAGGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
QY 1208 GCGCCAGCGCTACTGGCAATGCGCGCGCGCTTCTGTGAGCTGTGTGGAACCAAGCGCG 1267
DB 1201 GCGCCAGCGCTACTGGCAATGCGCGCGCGCTTCTGTGAGCTGTGTGGAACCAAGCGCG 1260
QY 1268 GTGCCCTTACCGGGTGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1327
DB 1261 GTGCCCTTACCGGGTGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1320
QY 1328 AGCGGTGTGTGTGCGCGGAGAGCGCGCGCGCTGTGTGCGCGCGCGCGCGCGCGCGCG 1387
DB 1321 AGCGGTGTGTGTGCGCGGAGAGCGCGCGCGCTGTGTGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCGCGCTGCTGTGTGAGCTGCTCGCGAGCAAGAGAGCGCGCGCGCGCGCGCG 1447
DB 1381 CACAGACCGCGCTGCTGTGTGAGCTGCTCGCGAGCAAGAGAGCGCGCGCGCGCGCGCG 1440
QY 1448 CCGCTTGTGCGGGCGCTGCTGCGCGCGCGCGCTGTGTGCGCGCGCGCGCGCGCGCGCG 1507
DB 1441 CCGCTTGTGCGGGCGCTGCTGCGCGCGCGCGCTGTGTGCGCGCGCGCGCGCGCGCGCG 1500
QY 1508 CAACGAAGCGCGCTTCTCTCAAGAACCAAGAGTTTCTCTCTGGGGAAGCATGCGCA 1567
DB 1501 CAACGAAGCGCGCTTCTCTCAAGAACCAAGAGTTTCTCTCTGGGGAAGCATGCGCA 1560
QY 1568 GCTCTGCTGAGAGCTGACGTGAGAGAGTGTGAGCGGTGCGGAGCTGCGCTTGGCTGCGAG 1627
DB 1561 GCTCTGCTGAGAGCTGACGTGAGAGAGTGTGAGCGGTGCGGAGCTGCGCTTGGCTGCGAG 1620
QY 1628 GAGCCAGAGGGTGTGCTGTGTTCCGCGCGAGAGCAACCGTGTGAGAGAGATCTGGC 1687
DB 1621 GAGCCAGAGGGTGTGCTGTGTTCCGCGCGAGAGCAACCGTGTGAGAGAGATCTGGC 1680
QY 1688 CAAGTCTGTCACTGCTGATGATGTGTACGTGTGAGAGCTGCTAGGTCTTTCTTTA 1747
DB 1681 CAAGTCTGTCACTGCTGATGATGTGTACGTGTGAGAGCTGCTAGGTCTTTCTTTA 1740
QY 1748 TGTACGAGAGACAGTTTCAAAAGAACAGAGCTTTTCTTCAACGGAAGAGTGTCTGAG 1807
DB 1741 TGTACGAGAGACAGTTTCAAAAGAACAGAGCTTTTCTTCAACGGAAGAGTGTCTGAG 1800

QY 1808 CAAGTTCAGACATTTGGAATCAGACGACTTGAAGAGGTCAGCTGCGGAGCTGTC 1867
DB 1801 CAAGTTCAGACATTTGGAATCAGACGACTTGAAGAGGTCAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCGCCCTGTCAGCTCCAGACTCCG 1927
DB 1861 GGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCGCCCTGTCAGCTCCAGACTCCG 1920
QY 1928 CTTATCCCAAGCCTGACGCGCTGCGCGCATTTGTAAACATGACTACGTCTGGAGC 1987
DB 1921 CTTATCCCAAGCCTGACGCGCTGCGCGCATTTGTAAACATGACTACGTCTGGAGC 1980
QY 1988 CAGAACGTTCCGACAGAGAAAGAGGCGAGCGCTCTACCTCGAGGTCAGGCACTGTT 2047
DB 1981 CAGAACGTTCCGACAGAGAAAGAGGCGAGCGCTCTACCTCGAGGTCAGGCACTGTT 2040
QY 2048 CAGCGTCTCACTACAGAGCGGCGCGCGCGCGCGCGCGCTCTGCGCGCTCTGTCGGG 2107
DB 2041 CAGCGTCTCACTACAGAGCGGCGCGCGCGCGCGCGCGCTCTGCGCGCTCTGTCGGG 2100
QY 2108 CTTGACGATATCCACAGAGGCGCTGCGCGCATTTGTCGTGCTGTGCGGCGCGCGCAC 2167
DB 2101 CTTGACGATATCCACAGAGGCGCTGCGCGCATTTGTCGTGCTGTGCGGCGCGCGCAC 2160
QY 2168 GCGCGCTGAGCTGTA-----CATCCCCCA 2191
DB 2161 GCGCGCTGAGCTGTA-----CATCCCCCA 2220
QY 2192 GGACAGGCTCAAGAGGTCATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTCCG 2251
DB 2221 GGACAGGCTCAAGAGGTCATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTCCG 2280
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QY 2312 AGTCTACGTCAGTGCAGAGGAGTCCCGCAGAGGCTCCATCTCTCCAGCGCTGCTGCA 2371
DB 2341 CGTCTACGTCAGTGCAGAGGAGTCCCGCAGAGGCTCCATCTCTCCAGCGCTGCTGCA 2400
QY 2372 GCGTGTGTCAGGCGGACATGAGAAACAAGCTGTTGCGGAGATTGCGGCGGAGCGGCTGC 2431
DB 2401 GCGTGTGTCAGGCGGACATGAGAAACAAGCTGTTGCGGAGATTGCGGCGGAGCGGCTGC 2460
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DB 2461 TCCTGCGTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAACCT 2520
QY 2492 TCCTCAGAGCCTGTCGCGAGGTCCTGATGATGCTGCTGCTGTAACCTGCGGAAAG 2551
DB 2521 TCCTCAGAGCCTGTCGCGAGGTCCTGATGATGCTGCTGCTGTAACCTGCGGAAAG 2580
QY 2552 CAGTGTGAACTTCCCTGTAGAGACGAGGCGCTGGTGCAAGCTTTTGTTCAGATGC 2611
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QY 2612 CGGCGCAGCGCTATTTCCCTGTCGCGGCGCTGCTGCTGTAACCCGAGCCTGAGAGTGC 2671
DB 2641 CGGCGCAGCGCTATTTCCCTGTCGCGGCGCTGCTGCTGTAACCCGAGCCTGAGAGTGC 2700
QY 2672 AGAGCGACTATCCAGCTATGCGCGGACCTCCATCAGAGCAGTCTCACTTCAACCGCG 2731
DB 2701 AGAGCGACTATCCAGCTATGCGCGGACCTCCATCAGAGCAGTCTCACTTCAACCGCG 2760
QY 2732 GCTTCAAGGCTGGAGGAAACATGCGTCAAACTCTTGGGCTCTTGGGCTGAAGTGC 2791
DB 2761 GCTTCAAGGCTGGAGGAAACATGCGTCAAACTCTTGGGCTCTTGGGCTGAAGTGC 2820
QY 2792 ACAGCCTGTTTCTGATTTGAGGTGAACAGCCTCCAGAGGCTGACACCAACATCTACA 2851
DB 2821 ACAGCCTGTTTCTGATTTGAGGTGAACAGCCTCCAGAGGCTGACACCAACATCTACA 2880

QY 2852 AGATCTCTCTGCTGACGCGCTACAGGTTTACAGCATGTGCTGACGCTCCCATTTGATC 2911
DB 2881 AGATCTCTCTGCTGACGCGCTACAGGTTTACAGCATGTGCTGACGCTCCCATTTGATC 2940
QY 2912 AGCAAGTTGGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGCGCTCCCTCT 2971
DB 2941 AGCAAGTTGGAAGAACCCACATTTTCTGCGCGTCACTCTGACACGCGCTCCCTCT 3000
QY 2972 GCTACTCATCTGAAAGCCAGAAACGAGGATGTGCTGGGGGCAAGGGCGCGCGCG 3031
DB 3001 GCTACTCATCTGAAAGCCAGAAACGAGGATGTGCTGGGGGCAAGGGCGCGCGCG 3060
QY 3032 GCGCTCTGCGCTCCGAGGCGCTGACGCTGCTGTCACCAAGCATTTCTGCTCAAGCTGA 3091
DB 3061 GCGCTCTGCGCTCCGAGGCGCTGACGCTGCTGTCACCAAGCATTTCTGCTCAAGCTGA 3120
QY 3092 CTCGACCGTGTACCTACGTCGCACTCTGCGGTCCTCAAGACAGCCAGAGCGAGC 3151
DB 3121 CTCGACCGTGTACCTACGTCGCACTCTGCGGTCCTCAAGACAGCCAGAGCGAGC 3180
QY 3152 TGAGTGGAGACTCCCGGAGCAGCCTGACTGACCTGAGAGCGCGCAACCGCGCAC 3211
DB 3181 TGAGTGGAGACTCCCGGAGCAGCCTGACTGACCTGAGAGCGCGCGCAACCGCGCAC 3240
QY 3212 TGCCCTGAGACTTCAAGACCATCTGAGTATGAGGCGCACCCGCGCACAGCCAGCGGAGA 3271
DB 3241 TGCCCTGAGACTTCAAGACCATCTGAGTATGAGGCGCACCCGCGCACAGCCAGCGGAGA 3300
QY 3272 GCAGACACGACGAGCCCTGTACGCGCGGCTCTACGTCAGAGGAGGAGGCGCGCGCA 3331
DB 3301 GCAGACACGACGAGCCCTGTACGCGCGGCTCTACGTCAGAGGAGGAGGCGCGCGCA 3360
QY 3332 CACCCAGCGCGCAGCCGCTGGAGTCTGAGGCGCTGAGTGTGCGCGGAGCGCTGCA 3391
DB 3361 CACCCAGCGCGCAGCCGCTGGAGTCTGAGGCGCTGAGTGTGCGCGGAGCGCTGCA 3420
QY 3392 TGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGGAGTGTGCGCGGAGCGCTGA 3451
DB 3421 TGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCGCTGAGGAGTGTGCGCGGAGCGCTGA 3480
QY 3452 GTGTCCAGACACCTGCGCTTCTCACTTCCCAAGGCTGCGCTCCACCCAGG 3511
DB 3481 GTGTCCAGACACCTGCGCTTCTCACTTCCCAAGGCTGCGCTCCACCCAGG 3540
QY 3512 GCCAGCTTTTCTCACCAGAGGCGCGGCTTCCACTCCCAATAGGAATGCTCACTCCC 3571
DB 3541 GCCAGCTTTTCTCACCAGAGGCGCGGCTTCCACTCCCAATAGGAATGCTCACTCCC 3600
QY 3572 AGATTCCGCAATGTTCAACCCCTGCGCTGCGCTGCGCTTGTGCTTCCACCCCAACCTCAG 3631
DB 3601 AGATTCCGCAATGTTCAACCCCTGCGCTGCGCTGCGCTTGTGCTTCCACCCCAACCTCAG 3660
QY 3632 GTGAGACCTTGAGAGGAGCCTGAGAGCTCTGAGAAATTTGAGTGAACCAAGGTCGCC 3691
DB 3661 GTGAGACCTTGAGAGGAGCCTGAGAGCTCTGAGAAATTTGAGTGAACCAAGGTCGCC 3720
QY 3692 CTGTACACAGGCGAGGACCTTGACACTTGATGGGGGTCCTGCGTCAAAATTTGGGGGGA 3751
DB 3721 CTGTACACAGGCGAGGACCTTGACACTTGATGGGGGTCCTGCGTCAAAATTTGGGGGGA 3780
QY 3752 GGTGCTGTGGGAGTAAATATGATATATGATTTTCAAGTTTGAAGGAGGAGGAGGAGG 3811
DB 3781 GGTGCTGTGGGAGTAAATATGATATATGATTTTCAAGTTTGAAGGAGGAGGAGGAGG 3840
QY 3812 AAAAAAAAAA 3824
DB 3841 AAAAAAAAAA 3853

RESULT 5
US-08-974-524E-122
; Sequence 122, Application US/08974524E
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 477
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,524E
FILING DATE: 19-Nov-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002950US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single.
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..2479
OTHER INFORMATION: /product= "hTERT"
SEQUENCE DESCRIPTION: SEQ ID NO: 122:
US-08-974-524E-122
Query Match 98.5%; Score 3767.8; DB 13; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;
QY 8 GCAGCGTGCCTGCTGCGCAGCGTGGAGAGCCCTGGCCCCCGCCACCCCGCATGCC 67
|||||

Db 1 GCAGCGTGCCTGCTGCGCAGTGGAGAGCCCTGGCCCCCGCCACCCCGCATGCC 60
QY 68 GCGCGTCCCGCTGCGCAGCGTGGAGAGCCCTGCTGCGCAGCGTGGAGAGTGT 127
Db 61 GCGCGTCCCGCTGCGCAGCGTGGAGAGCCCTGCTGCGCAGCGTGGAGAGTGT 120
QY 128 GCGCGTGGCCAGTTCGTGCGCGCTGGGAGCCCGCCAGCGTGGCGCTGTGAGCGCG 187
Db 121 GCGCGTGGCCAGTTCGTGCGCGCTGGGAGCCCGCCAGCGTGGCGCTGTGAGCGCG 180
QY 188 GGAACCGCGCGCTTCCTGCGCGCTGGGAGCCCGCCAGCGTGGCGCTGTGAGCGCG 247
Db 181 GGAACCGCGCGCTTCCTGCGCGCTGGGAGCCCGCCAGCGTGGCGCTGTGAGCGCG 240
QY 248 ACGCGCGCGCGCTTCCTGCGCGCTGGGAGCCCGCCAGCGTGGCGCTGTGAGCGCG 307
Db 241 ACGCGCGCGCGCTTCCTGCGCGCTGGGAGCCCGCCAGCGTGGCGCTGTGAGCGCG 300
QY 308 CCGAGTGTGAGAGCGTGTGCGAGCGCGCGCGCGAGAGAGTGTGAGCGCGTGTGAG 367
Db 301 CCGAGTGTGAGAGCGTGTGCGAGCGCGCGCGCGAGAGAGTGTGAGCGCGTGTGAG 360
QY 368 GCTGCTGAGACGGGCG 427
Db 361 GCTGCTGAGACGGGCG 420
QY 428 CTTGCCCAACACGAGTGCAGCGAGCGAGTGCAGCGAGCGAGCGAGCGAGCGAGCG 487
Db 421 CTTGCCCAACACGAGTGCAGCGAGCGAGTGCAGCGAGCGAGCGAGCGAGCGAGCG 480
QY 488 CCGCGTGGCGCGAGCGAGTGTGCTTACCTGCTGCGAGCGAGCGAGCGAGCGAGCG 547
Db 481 CCGCGTGGCGCGAGCGAGTGTGCTTACCTGCTGCGAGCGAGCGAGCGAGCGAGCG 540
QY 548 GGTCTCCAGCTGCGCTTACAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Db 541 GGTCTCCAGCTGCGCTTACAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCAGCG 667
Db 601 TCAGCG 660
QY 668 CTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Db 661 CTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGCG 787
Db 721 GAGCG 780
QY 788 TGCCCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 781 TGCCCCCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GCGTGAACCGAGTGAAGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 907
Db 841 GCGTGAACCGAGTGAAGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 900
QY 908 CACTCTTTGAGGCTGCGCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
Db 901 CACTCTTTGAGGCTGCGCTCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 968 GCACCAAGCG 1027
Db 961 GCACCAAGCG 1020
QY 1028 CCGCGTGTACGCGCGAGAGCAAGCACTTCTCTACTCTCTCAGGCGAGAGAGAGCTGCG 1087
Db 1021 CCGCGTGTACGCGCGAGAGCAAGCACTTCTCTACTCTCTCAGGCGAGAGAGAGCTGCG 1080
QY 1088 GCGCTCTTCTACTAGCTCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGA 1147
Db 1081 GCGCTCTTCTACTAGCTCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGGA 1140

QY	1148	GACCATCTTTCTGGGTTCCAGGCGCTTGATGCCAGGACATCCCGAGGTTGCCCGCCT	1207
Db	1141	GACCATCTTTCTGGGTTCCAGGCGCTTGATGCCAGGACATCCCGAGGTTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCTGTGTTCTTGAGCTGCTTGGAAACCACGGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTGTGTTCTTGAGCTGCTTGGAAACCACGGCA	1260
QY	1268	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTACCCACG	1327
Db	1261	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTACCCACG	1320
QY	1328	AGCCGGTGTCGTGCCCCGGGAGAAAGCCCCAGGGCTCTGCGCGCCCCCGAGAGAGGA	1387
Db	1321	AGCCGGTGTCGTGCCCCGGGAGAAAGCCCCAGGGCTCTGCGCGCCCCCGAGAGAGGA	1380
QY	1388	CACAGACCCCCGTGCGCTGTGTGACGTGCTCCGACAGACAGACCCCTGCAAGTGA	1447
Db	1381	CACAGACCCCCGTGCGCTGTGTGACGTGCTCCGACAGACAGACCCCTGCAAGTGA	1440
QY	1448	CGGCTTCGTGCGGGCTGCGCTGCGCGCGGCTGTGTGCCCCCAGGCTCTGCGGCTCCAGCA	1507
Db	1441	CGGCTTCGTGCGGGCTGCGCTGCGCGCGGCTGTGTGCCCCCAGGCTCTGCGGCTCCAGCA	1500
QY	1508	CAACGAACGCGCCTTCTCTAGAAACACCAAGAATTCACTCCCTGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCCTTCTCTAGAAACACCAAGAATTCACTCCCTGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGACGAGCTACGTTGAAGATGAGCGTGCGGACTGCGCTTGCTGCGCAG	1627
Db	1561	GCTCTCGCTGACGAGCTACGTTGAAGATGAGCGTGCGGACTGCGCTTGCTGCGCAG	1620
QY	1628	GAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGAGATCCTGGC	1687
Db	1621	GAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGTCTTCTTTTA	1740
QY	1748	TGTACGAGAGACCACTTTCAAAGAACAAGGCTCTTTTCTACCGGAAGATGCTGAG	1807
Db	1741	TGTACGAGAGACCACTTTCAAAGAACAAGGCTCTTTTCTACCGGAAGATGCTGAG	1800
QY	1808	CAAGTTGCAAGCATTTGNAATCAGACGACCTTGAAGAGGTGCACTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAGCATTTGNAATCAGACGACCTTGAAGAGGTGCACTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGSTCAGGACGATCGGGAAGCCAGGCCCGCTGTGACGTCACAGACTCCG	1927
Db	1861	GGAAGCAGAGSTCAGGACGATCGGGAAGCCAGGCCCGCTGTGACGTCACAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTGCTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTGCTGGAGC	1980
QY	1988	CAGAAGCTTCCGCAAGAAAAAGAGGGCCGAGCGTCTCACTCGAAGGTGAAGCACTGTT	2047
Db	1981	CAGAAGCTTCCGCAAGAAAAAGAGGGCCGAGCGTCTCACTCGAAGGTGAAGCACTGTT	2040
QY	2048	CAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCGCTCTTGAGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCGCTCTTGAGCGCTCTGTGCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCTTGCGCACTTTCGTGCTGCGTGTGCGGGGCCAGGACCC	2167
Db	2101	CCTGACGATATCCACAGGGCTTGCGCACTTTCGTGCTGCGTGTGCGGGGCCAGGACCC	2160
QY	2168	GCCGCTGAGCTGA-----CATCCCCCA 2191	
Db	2161	GCCGCTGAGCTGACTTTGTCAAGGTGATGTGACGGGCGCGTACGACCATCCCCCA 2220	

QY	2192	GGA	CAGGCTC	ACG	GAGGTCA	TCC	GCAGCAT	CA	TCAA	CCCCA	GAA	CAC	GTACTG	CGTGG	2251								
Db	2221	GGA	CAGGCTC	ACG	GAGGTCA	TCC	GCAGCAT	CA	TCAA	CCCCA	GAA	CAC	GTACTG	CGTGG	2280								
QY	2252	TCC	GTATGCC	GTG	TCC	GAA	GGCCG	CCCAT	TGGG	CAGTCC	CGA	AGG	CCCTT	CAAGAGCA	2311								
Db	2281	TCC	GTATGCC	GTG	TCC	GAA	GGCCG	CCCAT	TGGG	CAGTCC	CGA	AGG	CCCTT	CAAGAGCA	2340								
QY	2312	AGT	CCATACG	TCC	AGT	GCC	AGGGG	ATCC	CGC	AGGG	CTCC	ATCCT	CTCC	ACGCTG	CTGCA	2371							
Db	2341	CGT	CTACGT	CCAGT	GCC	AGGGG	ATCC	CGC	AGGG	CTCC	ATCCT	CTCC	ACGCTG	CTGCA	2400								
QY	2372	GCT	GTGCTAC	CGG	CGA	CAT	TGAG	AACA	AGCTG	TTT	GCGGG	ATT	TGCG	CGGAG	CGGGCTGC	2431							
Db	2401	GCT	GTGCTAC	CGG	CGA	CAT	TGAG	AACA	AGCTG	TTT	GCGGG	ATT	TGCG	CGGAG	CGGGCTGC	2460							
QY	2432	TCCT	GCGTTT	GTGTA	TGATTT	CTG	TGTGTG	TGACA	CTCA	CTCA	CCCA	CGCG	AAAA	CCT		2491							
Db	2461	TCCT	GCGTTT	GTGTA	TGATTT	CTG	TGTGTG	TGACA	CTCA	CTCA	CCCA	CGCG	AAAA	CCT		2520							
QY	2492	TCCT	CAGAAC	CCCTG	TCGAG	GTGT	CCCTG	AGTAT	TGGCT	GCTG	TGAA	CTTG	CGG	AAGA		2551							
Db	2521	TCCT	CAGAAC	CCCTG	TCGAG	GTGT	CCCTG	AGTAT	TGGCT	GCTG	TGAA	CTTG	CGG	AAGA		2580							
QY	2552	CAGT	GTGA	CTTCC	CTGT	AGAA	GACG	AGGCC	CTGGG	TGG	CA	CGG	CTTT	GTTC	GATGC	2611							
Db	2581	CAGT	GTGA	CTTCC	CTGT	AGAA	GACG	AGGCC	CTGGG	TGG	CA	CGG	CTTT	GTTC	GATGC	2640							
QY	2612	CGG	CCACG	GCCTA	TTC	CCCT	TG	TGCGG	CCCTG	CTG	ATAC	CCG	GA	CCCT	TGAG	TGC	2671						
Db	2641	CGG	CCACG	GCCTA	TTC	CCCT	TG	TGCGG	CCCTG	CTG	ATAC	CCG	GA	CCCT	TGAG	TGC	2700						
QY	2672	AGAG	CGACTAC	TCC	CAGCTA	TGCC	CGG	ACCTT	CAG	AGCC	AGTCT	CA	ACCTT	CA	ACCGG	2731							
Db	2701	AGAG	CGACTAC	TCC	CAGCTA	TGCC	CGG	ACCTT	CAG	AGCC	AGTCT	CA	ACCTT	CA	ACCGG	2760							
QY	2732	GCTT	CAAGG	CTGG	GAGAA	CAT	GCGT	CG	AAA	CTCTT	TGGGG	CTTG	CGG	CTG	AA	TGTC	2791						
Db	2761	GCTT	CAAGG	CTGG	GAGAA	CAT	GCGT	CG	AAA	CTCTT	TGGGG	CTTG	CGG	CTG	AA	TGTC	2820						
QY	2792	ACAG	CCGTG	TTCTG	GAATTT	TG	CAGGT	GAA	CAG	CCCTC	CAG	ACGG	TGTG	CAC	CA	ATCT	2851						
Db	2821	ACAG	CCGTG	TTCTG	GAATTT	TG	CAGGT	GAA	CAG	CCCTC	CAG	ACGG	TGTG	CAC	CA	ATCT	2880						
QY	2852	AGAT	CCCTC	TGCTG	CAGG	CGTAC	AG	TTT	CA	CGCAT	TGTG	CTG	CAG	CTCC	CA	TTT	2911						
Db	2881	AGAT	CCCTC	TGCTG	CAGG	CGTAC	AG	TTT	CA	CGCAT	TGTG	CTG	CAG	CTCC	CA	TTT	2940						
QY	2912	AGCA	AGTTT	GGA	GAAC	CCCA	CATTTT	CT	GCG	GT	CATCT	CTG	ACA	CGG	CT	CCCT	2971						
Db	2941	AGCA	AGTTT	GGA	GAAC	CCCA	CATTTT	CT	GCG	GT	CATCT	CTG	ACA	CGG	CT	CCCT	3000						
QY	2972	GCT	ACTCC	ATCCT	GAAA	GC	CAAG	AA	CGG	AG	TGTC	GCTG	G	GGG	CC	AA	GGG	CGCCG	3031				
Db	3001	GCT	ACTCC	ATCCT	GAAA	GC	CAAG	AA	CGG	AG	TGTC	GCTG	G	GGG	CC	AA	GGG	CGCCG	3060				
QY	3032	GCC	CTTG	CCCTC	CGAG	GC	CGT	CAG	TG	GTG	TCC	CA	CCA	AG	CA	TTCT	G	CT	CA	AG	CT	G	3091
Db	3061	GCC	CTTG	CCCTC	CGAG	GC	CGT	CAG	TG	GTG	TCC	CA	CCA	AG	CA	TTCT	G	CT	CA	AG	CT	G	3120
QY	3092	CTG	AC	ACCG	TGTCA	CA	CTAC	GTG	CCA	CTCT	CTG	GGG	TCA	CT	CA	GGA	CA	AG	CC	CA	CG	CAG	3151

[illegible]

RESULT 6
US-08-974-549-4
; Sequence 4, Application US/08974549
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 726
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549
; FILING DATE: 19-NOV-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; PRIOR APPLICATION DATA:
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	APPLICATION NUMBER:	US 08/844,419
/	FILING DATE:	18-APR-1997
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER:	US 08/846,017
/	FILING DATE:	25-APR-1997
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER:	US 08/851,843
/	FILING DATE:	06-MAY-1997
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER:	US 08/854,050
/	FILING DATE:	09-MAY-1997
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER:	US 08/911,312
/	FILING DATE:	14-AUG-1997
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER:	US 08/912,951
/	FILING DATE:	14-AUG-1997
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/	APPLICATION NUMBER:	US 08/915,503
/	FILING DATE:	14-AUG-1997
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER:	WO PCT/US97/17618
/	FILING DATE:	01-OCT-1997
/	PRIOR APPLICATION DATA:	
/	APPLICATION NUMBER:	WO PCT/US97/17885
/	FILING DATE:	01-OCT-1997
/	ATTORNEY/AGENT INFORMATION:	
/	NAME:	Apple, Randolph Ted
/	REGISTRATION NUMBER:	36,429
/	REFERENCE/DOCKET NUMBER:	015389-002610US
/	TELECOMMUNICATION INFORMATION:	
/	TELEPHONE:	(415) 576-0200
/	TELEFAX:	(415) 576-0300
/	INFORMATION FOR SEQ ID NO:	4:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	3855 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	linear
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/	FEATURE:	
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/	LOCATION:	1..3855
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QY	1268	GTGCCCCCTACGGGGGTGTCTCTCAAGAAGCACTGCCCCGTGCGAGCTGCGGTCAACCCACG	1327
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QY	1328	AGCCGGTGTCTGTGCCCCGGAGAGAAGCCCCCAGGGCTCTGTGCGCGGCCCCCCCGAGAGAGAGA	1387

Db	1321	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGGCTCTGTGGCGGCCCCGAGAGAGAGA	1380
QY	1388	CACAGACCCCCGTGCGCTGTGTGACAGTGTCTCCGCCAGCACAGCAGCCCTGTGACGTGTA	1447
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US-08-974-584C-122
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GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Telomerase Reverse Transcriptase
NUMBER OF INVENTIONS: 479
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,584C
FILING DATE: 19-Nov-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618

FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002950US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-974-584C-122

Query Match 98.5%; Score 3767.8; DB 13; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

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QY	1808	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGTTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTGTTGGAGC	1980
QY	1988	CAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTT	2047
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QY	2048	CAGCGTGTCAACTACGAGCGGGCGCGGCCGCCGCTCTGGGGCCTCTGTGTGGG	2107
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Db	2101	CCTGACGATATCCACAGGGCCTGCGCACCTTCGTGTCGCTGTGCGGGCCAGAACCC	2160
QY	2168	GCCGCTGAGCTGTA-----CATCCCCA	2191
Db	2161	GCCGCTGAGCTGTACTTTGTCAAAGTGGATGTGACGGGCGCGTACGACACCATCCCCA	2220
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Db	2221	GACACAGGCTCACGGAGTCAATCGCCAGCATCATCAAACCCAGAACACAGTACTGCGTGC	2280
QY	2252	TCGGTATGCCGTGTTCCAGAAGCGGCCCATGGGACCGTCCGCAAGGCTTCAAGAGGCA	2311
Db	2281	TCGGTATGCCGTGTTCCAGAAGCGGCCCATGGGACCGTCCGCAAGGCTTCAAGAGGCA	2340
QY	2312	AGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATTCCTCTCCAAGCTGCTGTGCA	2371
Db	2341	CGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATTCCTCTCCAAGCTGCTGTGCA	2400
QY	2372	GCCTGTGCTACGGCGCATGTGAAGAACAAAGCTGTTTGGGGGATTGGCGGGAACGGGCTGC	2431
Db	2401	GCCTGTGCTACGGCGCATGTGAAGAACAAAGCTGTTTGGGGGATTGGCGGGAACGGGCTGC	2460
QY	2432	TCCTGCGTTTGGTGGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGGGAAAACCT	2491
Db	2461	TCCTGCGTTTGGTGGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGGGAAAACCT	2520
QY	2492	TCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTGGGAGA	2551
Db	2521	TCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAACCTTGGGAGA	2580
QY	2552	CAGTGTGAACTTCCCTGTAGAAACAAGAGGCCCTGGGTGAGACGGCTTTTGTTCAGATGC	2611
Db	2581	CAGTGTGAACTTCCCTGTAGAAACAAGAGGCCCTGGGTGAGACGGCTTTTGTTCAGATGC	2640
QY	2612	CGGCCCAACGGCCTATTTCCCTGTGTGCGGCTGCTGCTGTGAATACCCGGAACCTGAGGTGC	2671
Db	2641	CGGCCCAACGGCCTATTTCCCTGTGTGCGGCTGCTGCTGTGAATACCCGGAACCTGAGGTGC	2700
QY	2672	AGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCACTTCAACCGCG	2731
Db	2701	AGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCACTTCAACCGCG	2760
QY	2732	GCTTCAAGGCTGGAGAGAAATGCGTGCAGAACTCTTTGGGGTCTTGGCGCTGAAGTGC	2791
Db	2761	GCTTCAAGGCTGGAGAGAAATGCGTGCAGAACTCTTTGGGGTCTTGGCGCTGAAGTGC	2820
QY	2792	ACAGCCTGTTTCTGGATTGCAAGTGAACAAGCCTCCAGACGGTGTGCAACCAACATCTACA	2851
Db	2821	ACAGCCTGTTTCTGGATTGCAAGTGAACAAGCCTCCAGACGGTGTGCAACCAACATCTACA	2880

QY	2852	AGATCCTCCTGCTGCAGGCGGTACAGATTTCACGCATGTGTGCTGCAGCTCCCATTTTCATC	2911
Db	2881	AGATCCTCCTGCTGCAGGCGGTACAGATTTCACGCATGTGTGCTGCAGCTCCCATTTTCATC	2940
QY	2912	AGCAAGTTTGGAAGAACCCCAACATTTTTCTCGCGGTATCTCTGACACGGCTCCCTCT	2971
Db	2941	AGCAAGTTTGGAAGAACCCCAACATTTTTCTCGCGGTATCTCTGACACGGCTCCCTCT	3000
QY	2972	GCTACTCCATCCTGAAGACCAAGAACGCAAGGATGTGCTGGGGCCAAAGGCGCCGCCG	3031
Db	3001	GCTACTCCATCCTGAAGACCAAGAACGCAAGGATGTGCTGGGGCCAAAGGCGCCGCCG	3060
QY	3032	GCCCTCTGCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3091
Db	3061	GCCCTCTGCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3120
QY	3092	CTGCACACCGTGTCACTAAGTGCCTCTGGGGTCACTCAAGACAGCCACGACG	3151
Db	3121	CTGCACACCGTGTCACTAAGTGCCTCTGGGGTCACTCAAGACAGCCACGACG	3180
QY	3152	TGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAACCCGGCAC	3211
Db	3181	TGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAACCCGGCAC	3240
QY	3212	TGCCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACAGCCAGGCCGAGA	3271
Db	3241	TGCCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACAGCCAGGCCGAGA	3300
QY	3272	GCAGACACCCAGACCCCTGTCAACGCCGGGCTCTACGTCGCCAGGGAGGGAGGGCGGCCCA	3331
Db	3301	GCAGACACCCAGACCCCTGTCAACGCCGGGCTCTACGTCGCCAGGGAGGGAGGGCGGCCCA	3360
QY	3332	CACCCAGGCGCCGACCCGCTGGAGTCTGAGGCTGAGTGAAGTTTGGCCGAGGCTGCA	3391
Db	3361	CACCCAGGCGCCGACCCGCTGGAGTCTGAGGCTGAGTGAAGTTTGGCCGAGGCTGCA	3420
QY	3392	TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGGCTGA	3451
Db	3421	TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGGCTGA	3480
QY	3452	GTGTCCAGCACCTGCGCTTCTCACTTCCCAACAGGCTGGCGCTCGCTCCACCCACAG	3511
Db	3481	GTGTCCAGCACCTGCGCTTCTCACTTCCCAACAGGCTGGCGCTCGCTCCACCCACAG	3540
QY	3512	GCCAGCTTTTCTCAACAGGACCCGGCTTCCACTCCCAACATAGAAATGTCATCCCC	3571
Db	3541	GCCAGCTTTTCTCAACAGGACCCGGCTTCCACTCCCAACATAGAAATGTCATCCCC	3600
QY	3572	AGATTGSCCATGTTTCAACCCCTGCGCTGCTCCCTCTTGGCTTCCACCCCAACCATCCAG	3631
Db	3601	AGATTGSCCATGTTTCAACCCCTGCGCTGCTCCCTCTTGGCTTCCACCCCAACCATCCAG	3660
QY	3632	GTGAGACCTTGAAAGGACCTGGAGCTCTGGAAATTTGAGTGAACCAAGGTGTGCC	3691
Db	3661	GTGAGACCTTGAAAGGACCTGGAGCTCTGGAAATTTGAGTGAACCAAGGTGTGCC	3720
QY	3692	CTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGTCAAAATTGGGGGGA	3751
Db	3721	CTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGTCAAAATTGGGGGGA	3780
QY	3752	GGTGTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGTGAAAAAATTTGAAAAA	3811
Db	3781	GGTGTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGTGAAAAAATTTGAAAAA	3840
QY	3812	AAAAAAAAAAAAA 3824	
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RESULT 8
US-09-432-503-4
; Sequence 4, Application US/09432503

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Db 1081 GCGCTCTCTCTACTCTCAGTCTCTGAGGCGCCAGCTGAGTGGCGCTCGAGGCTCGTGA 1140
QY 1148 GACCATCTTCTGAGGTTCCAGGCGCTGATGCGGAGGAGTCTCCCGGAGGTTGCGCGCT 1207
Db 1141 GACCATCTTCTGAGGTTCCAGGCGCTGATGCGGAGGAGTCTCCCGGAGGTTGCGCGCT 1200
QY 1208 GCGCCAGCGCTACTGCGAAATGCGGCGCTGTTTCTGAGCTGCTTGGGAAACCAAGCGCA 1267
Db 1201 GCGCCAGCGCTACTGCGAAATGCGGCGCTGTTTCTGAGCTGCTTGGGAAACCAAGCGCA 1260
QY 1268 GTGCCCCCTACGGGGTGTCTCTCAGAGCGACTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1327
Db 1261 GTGCCCCCTACGGGGTGTCTCTCAGAGCGACTGCGCGCTGCGAGCTGCGGTCAACCCAGC 1320
QY 1328 AGCGGCTGTCTGTGCGCGGAGAGAGCGCGCTCTGTGCGCGCGCGCGAGAGAGAGA 1387
Db 1321 AGCGGCTGTCTGTGCGCGGAGAGAGCGCGCTCTGTGCGCGCGCGCGAGAGAGAGA 1380
QY 1388 CACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447
Db 1381 CACAGACCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1448 CGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1507
Db 1441 CGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
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Db 1501 CAACGACCGCGCTTCTCTCAGGAAACCAAGTTCATCTCTGCGGAGAGCATGCCAA 1560
QY 1568 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1627
Db 1561 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1628 GAGCCAGAGGTTGGCTGTGTTCCGCGCGAGAGACCGTCTGCGTGAAGAGATCTGGC 1687
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QY 2372 GCTGTGCTACGCGGCAATGGAACAAGTGTGTTGCGGGGATTCGCGGGAACGCGTGC 2431
Db 2401 GCTGTGCTACGCGGCAATGGAACAAGTGTGTTGCGGGGATTCGCGGGAACGCGTGC 2460
QY 2432 TCCTGCGTTGCTGATGATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2491
Db 2461 TCCTGCGTTGCTGATGATTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2520
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QY 3032 GCGCTCTGCGCTCCGAGGCGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3091
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Db 3181 TGAGTCGGAAGCTCCCGGGGACGACCTGACTGCTGAGGCGCCGACGACCGGAC 3240
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QY 3392 TGTCGGCTGAAGGCTGAGTGTGTCGCTGAGGCTGAGGCTGAGGCTGAGGCTGCA 3451
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QY 3512 GCCAGCTTTCTCACCAGAGGCGCGCTTCCACTCCGACATAGGATAGTCCATCC 3571
Db 3541 GCCAGCTTTCTCACCAGAGGCGCGCTTCCACTCCGACATAGGATAGTCCATCC 3600
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Db 3841 AAAAAAAAAA 3853

RESULT 9

US-09-721-477-4
Sequence 4, Application US/09721477
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Linsner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: -
LOCATION: 1..3855
OTHER INFORMATION: /note= "nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"
FEATURE:
NAME/KEY: CDS
LOCATION: 56..2479
OTHER INFORMATION: /product= "delta-182 variant polypeptide"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-721-477-4
Query Match 98.5%; Score 3767.8; DB 31; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;
QY 8 GCAGGCTGCGTCTGCTGCGACAGTGGAAGCCCTGGCGCCCGCCGACCGCGATGCC 67
Db 1 GCAGGCTGCGTCTGCTGCGACAGTGGAAGCCCTGGCGCCCGCCGACCGCGATGCC 60
QY 68 GCGGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGACGACCTACCGGAGTGTCT 127
Db 61 GCGGCTCCCGCTGCGAGCCGCTGCGCTCCCTGCTGCGACGACCTACCGGAGTGTCT 120
QY 128 GCGGCTGCGACGTTCTGCGCGCGCTGCGGCGCCGACGAGGCTGCGGCTGCTGCA 187
Db 121 GCGGCTGCGACGTTCTGCGCGCGCTGCGGCGCCGACGAGGCTGCGGCTGCTGCA 180
QY 188 GGAACCGCGCGCTTCCGCGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCA 247
Db 181 GGAACCGCGCGCTTCCGCGCGCTGCTGCGGCGCTGCTGCTGCTGCTGCTGCTGCA 240

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Db	241	ACGCGCCCCC	CGCCCTTCTTCGCCAGGTGTCTGCTGAAGAAGCTGGTG	300
QY	308	CCGAGTGTCA	GAGGCTGTGCGAAGCGCGGCAGAAACGTGTGGCTTCGGCTTCG	367
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Db	841	GCGTGACCG	AGTAGCCGTGTTCTGTGTGTGTCACTGCGACACCCGCGAAGAGC	900
QY	908	CACCTCTTT	GAGGGTGCCTCTGTGGCACGCGCCACTCCACCATTCCGTGGGCGGCCA	967
Db	901	CACCTCTTT	GAGGGTGCCTCTGTGGCACGCGCCACTCCACCATTCCGTGGGCGGCCA	960
QY	968	GCAACACG	CGGGCCCCCATCCAATCGCGGCCACCAAGTCCCTGGGACAAGCCTTGTC	1027
Db	961	GCAACACG	CGGGCCCCCATCCAATCGCGGCCACCAAGTCCCTGGGACAAGCCTTGTC	1020
QY	1028	CCCGGTGTA	CGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTA	CGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAGCAGCTGCG	1080
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Db	1201	GCCCCAGCG	CTACTGGCAAATGCGCCCCCTGTCTTCTGAGGTGCTTGGGAACCAAGCGCA	1260
QY	1268	GTGCCCCTA	CGGGTGTCTCTCAAGCAGCACTGCCCCGTGCGAGCTGCGGTACCCCCAGC	1327
Db	1261	GTGCCCCTA	CGGGTGTCTCTCTCAAGCAGCACTGCCCCGTGCGAGCTGCGGTACCCCCAGC	1320
QY	1328	AGCCGGTGT	GTGCCCCGGAAGACCCCAAGGGCTCTGTGGCGGCCCCCCGAGGAGGAGGA	1387

Dp	1321	AGCCGGTGTCTGTGCCCCGGAGAGAGCCCAAGGGCTCTGTGGCGGCCCCCGAAGAGAGGA	1380
Qy	1388	CACAGACCCCGCTCGCTGTGTGACGTGTCCTCCAGCACAGACAGCCCTTGACGTGTA	1447
Dp	1381	CACAGACCCCGCTCGCTGTGTGACGTGTCCTCCAGCACAGACAGCCCTTGACGTGTA	1440
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RESULT 10
US-09-721-506-4
Sequence 4, Application US/09721506
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,506
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618

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1 FILING DATE: 01-OCT-1997
2 APPLICATION NUMBER: WO PCT/US97/17885
3 FILING DATE: 01-OCT-1997
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Apple, Randolph Ted
6 REGISTRATION NUMBER: 36,429
7 REFERENCE/DOCKET NUMBER: 015389-002610US
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: (415) 576-0200
10 TELEFAX: (415) 576-0300
11 INFORMATION FOR SEQ ID NO: 4:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 3855 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17 MOLECULE TYPE: cDNA
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20 LOCATION: 1..3855
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27 OTHER INFORMATION: /product="delta-182 variant
28 polypeptide"
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Db 2401 GCGTGTGCTACGCGGAGCATGAGAAACAAGCTGTTTGGCGGAGATTGCGGCGGAGCGGCTGC 2460
QY 2432 TCCGCTGTTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAAACCT 2491
Db 2461 TCCGCTGTTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAAACCT 2520
QY 2492 TCCTCAGAGACCTGTGTCGAGAGTGTCCCTGAGTATGAGTGTGTAACCTTGGGAGAA 2551
Db 2521 TCCTCAGAGACCTGTGTCGAGAGTGTCCCTGAGTATGAGTGTGTAACCTTGGGAGAA 2580
QY 2552 CAGTGTGAACTTCCCTGTAGAAAGACGAGGCGCTGGGTGGCAAGGCTTTTGTTCAGATGC 2611
Db 2581 CAGTGTGAACTTCCCTGTAGAAAGACGAGGCGCTGGGTGGCAAGGCTTTTGTTCAGATGC 2640
QY 2612 CGGCCCCAGGCTATTTCCCTGTGTCGCGGCTGTGCTGATACCCGAGACCTTGAAGGTGC 2671
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QY 2672 AGAGCGACTACTCCAGCTATGCGGAGACCTCCATCAGAGCCAGTCTCACTTCAACCGCG 2731
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QY 2912 AGCAAGTTTGAAGAACCCCAATTTTCTCTGCGGCTGATCTTGACACGCGCTCCCTCT 2971
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QY 2972 GCTACTCATCTCTGAAGACCAAGACGAGGATGTGCTGGGGGCGGAGGCGGCGGCGG 3031
Db 3001 GCTACTCATCTCTGAAGACCAAGACGAGGATGTGCTGGGGGCGGAGGCGGCGGCGG 3060
QY 3032 GCCCTGTGCTCTCCGAGGCGGCTGCAAGTGTGCTGTCACCAAGCATCTCTGCTCAAGCTGA 3091
Db 3061 GCCCTGTGCTCTCCGAGGCGGCTGCAAGTGTGCTGTCACCAAGCATCTCTGCTCAAGCTGA 3120
QY 3092 CTCGACACCGTGTCACTACGTCGCACTCTCTGCGGCTCACTCAGACAGCCAGACGAC 3151
Db 3121 CTCGACACCGTGTCACTACGTCGCACTCTCTGCGGCTCACTCAGACAGCCAGACGAC 3180
QY 3152 TGAGTGGAGAGCTCCCGGAGAGAGCGCTGACTGCTGAGAGGCGGAGCCAGCCAGCGGAC 3211
Db 3181 TGAGTGGAGAGCTCCCGGAGAGAGCGCTGACTGCTGAGAGGCGGAGCCAGCCAGCGGAC 3240
QY 3212 TGCCCTCAGACTTCAAGACCATCTCTGAGTGTGAGGCGGCGGAGAGGCGGAGGCGG 3271
Db 3241 TGCCCTCAGACTTCAAGACCATCTCTGAGTGTGAGGCGGCGGAGAGGCGGAGGCGG 3300
QY 3272 GCAGACACGAGCGGCTGTGACGCGGCGGCTTACGTCGAGAGGAGGAGGCGGAGGCGG 3331
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QY 3332 CACCCAGGCGGAGCGGCTGAGGAGTGTGAGGCGGCTGAGTGTGTTGGCGGAGGCTGCA 3391
Db 3361 CACCCAGGCGGAGCGGCTGAGGAGTGTGAGGCGGCTGAGTGTGTTGGCGGAGGCTGCA 3420
QY 3392 TGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCGGCTGAGGAGTGTGCGGAGGCTGCA 3451
Db 3421 TGTCCGCTGAAGGCTGAGTGTGCGGCTGAGGCGGCTGAGGAGTGTGCGGAGGCTGCA 3480
QY 3452 GTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGCGGCTGCGGCTGCAACCCAGG 3511
Db 3481 GTGTCCAGACACCTGCGGCTTCACTTCCCAAGGCTGCGGCTGCGGCTGCAACCCAGG 3540
QY 3512 GCCAGCTTTTCTCAGCAGAGGCGGCTTCCATCCCAATAGGATAGTCCATCC 3571
Db 3541 GCCAGCTTTTCTCAGCAGAGGCGGCTTCCATCCCAATAGGATAGTCCATCC 3600
QY 3572 AGATTCGCAATTTTCAACCCCTGCGGCTGCGGCTTCCATCCCAATAGGATAGTCCAG 3631
Db 3601 AGATTCGCAATTTTCAACCCCTGCGGCTGCGGCTTCCATCCCAATAGGATAGTCCAG 3660
QY 3632 GTGAGACCTTGAGAGAGCCTGGAGCTTGGAGATTGGAGTGACCAAGGTGTGC 3691
Db 3661 GTGAGACCTTGAGAGAGCCTGGAGCTTGGAGATTGGAGTGACCAAGGTGTGC 3720
QY 3692 CTGTACACAGGCGAGACCTGACCTGATGGGCGGCTTGTGGTCAAAATTTGGGAGGA 3751
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QY	1088	GCCCTCCTTCTACTCAGCTCTGTAGGCCCCAGCCCTGACTGGCGCTCGAGGCTCTGGA	1147
Db	1081	GCCCTCCTTCTACTCAGCTCTGTAGGCCCCAGCCCTGACTGGCGCTCGAGGCTCTGGA	1140
QY	1148	GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCCAGGTTGCCCGCT	1207
Db	1141	GACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCCAGGTTGCCCGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAGCTGCTTGGAAACCAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAGCTGCTTGGAAACCAGCGCA	1260
QY	1268	GTCGCCCTACGGGGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCACCCCAGC	1327
Db	1261	GTCGCCCTACGGGGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCACCCCAGC	1320
QY	1328	AGCCGCTGTCTGTGCCCGGAGAAAGCCCCAGGGCTCTGTGGCGCCCCCGAGGAGGAA	1387
Db	1321	AGCCGCTGTCTGTGCCCGGAGAAAGCCCCAGGGCTCTGTGGCGCCCCCGAGGAGGAA	1380
QY	1388	CACAGACCCCCGCTGCGCTGTGTGACGTGCTCCGCCAGCAAGACGCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCGCTGCGCTGTGTGACGTGCTCCGCCAGCAAGACGCCCTGGCAGGTGA	1440
QY	1448	CGGCTTCGTGCGGGCTGCTGCGCGCGCTGTGTGTCGCCCAAGGCTCTGGGGCTCCAGCA	1507
Db	1441	CGGCTTCGTGCGGGCTGCTGCGCGCGCTGTGTGTCGCCCAAGGCTCTGGGGCTCCAGCA	1500
QY	1508	CAACGAACGCCGCTTCTCTAGGAACAACCAAGAATTCATCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCCGCTTCTCTAGGAACAACCAAGAATTCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGAG	1627
Db	1561	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGCTTGGCTGCGAG	1620
QY	1628	GAGCCCCAGGGGTTGGCTGTGTTCGGCCGACAGACACCGTCTGCGTGAAGAGATCCTGCG	1687
Db	1621	GAGCCCCAGGGGTTGGCTGTGTTCGGCCGACAGACACCGTCTGCGTGAAGAGATCCTGCG	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCAACGAGAACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCAACGAGAACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAGCATTGGAATCAGACAGCACTTGAAGAAGGGGTGACGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAGCATTGGAATCAGACAGCACTTGAAGAAGGGGTGACGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCCCTGTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCCCTGTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGGCTGCGGCCGATTGTGAACATGGAATAAGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGGCTGCGGCCGATTGTGAACATGGAATAAGTCGTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAAAGAGAGGGCCGAGCGTCTCACTCGAGAGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGACAGAAAGAGAGGGCCGAGCGTCTCACTCGAGAGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCAACTACGAGCGGGCGCGGCGCCCCCGGCTCTGTGGGCGCTCTGTGTGGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGGCGCCCCCGGCTCTGTGGGCGCTCTGTGTGGG	2100

QY	2108	CCTGGACGATATCCACAGGGCCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGGACCC	2167
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QY	2168	GCCGCCCTGAGCTGTA-----CATCCCCCA	2191
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QY	2192	GGAACAGGCTCACGGAGGTCATCGCCAGCATTCATCAAACCCCAAGAACGTACTGCGGTGCG	2251
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QY	2252	TCGGTATGCCGTGGTGTCCAGAAAGGCCGCCCATGGGCACTCCGCAAGGCTTCAAGAGCA	2311
Db	2281	TCGGTATGCCGTGGTGTCCAGAAAGGCCGCCCATGGGCACTCCGCAAGGCTTCAAGAGCA	2340
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QY	2432	TCCTGCGTTGGTGTGATGATTTCTGTGTGTGACACCTCACTCAACCCACGGCAAAACCT	2491
Db	2461	TCCTGCGTTGGTGTGATGATTTCTGTGTGTGACACCTCACTCAACCCACGGCAAAACCT	2520
QY	2492	TCCTCAAGAACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCGGAGA	2551
Db	2521	TCCTCAAGAACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACCTTGCGGAGA	2580
QY	2552	CAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGACAGGCTTTGTTCAGATGC	2611
Db	2581	CAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGACAGGCTTTGTTCAGATGC	2640
QY	2612	CGGCCCAACGGCCTATTTCCCTGTGTGCGGCTGTGCTGATACCCCGAACCTTGAGAGGTGC	2671
Db	2641	CGGCCCAACGGCCTATTTCCCTGTGTGCGGCTGTGCTGATACCCCGAACCTTGAGAGGTGC	2700
QY	2672	AGAGCGACTACTCCAGCTATATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCG	2731
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QY	2732	GCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTG	2791
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QY	2852	AGATCCTCCTGCTGCGAGGGCGTACAGGTTTACGCGCATGTGTGCTGCAGCTCCCATTTTCATC	2911
Db	2881	AGATCCTCCTGCTGCGAGGGCGTACAGGTTTACGCGCATGTGTGCTGCAGCTCCCATTTTCATC	2940
QY	2912	AGCAAGTTTGAAGAAACCCCAACATTTTCTGCGCGTCACTCTGACACAGGCTTCCCTCT	2971
Db	2941	AGCAAGTTTGAAGAAACCCCAACATTTTCTGCGCGTCACTCTGACACAGGCTTCCCTCT	3000
QY	2972	GCTACTCCATCTGAAAGCCCAAGAACGCAAGGATGTGCTGGGGGGCCAAAGGGCGCGCGG	3031
Db	3001	GCTACTCCATCTGAAAGCCCAAGAACGCAAGGATGTGCTGGGGGGCCAAAGGGCGCGCGG	3060
QY	3032	GCCCTCTGGCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTCAAGCTGA	3091
Db	3061	GCCCTCTGGCCCTCCGAGGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTCAAGCTGA	3120
QY	3092	CTCGACACCGTGTCACTTACGTGCCACTCTCTGGGGGTCACTCAGGACAGCCCAAGCGCAGC	3151
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QY	3152	TGAGTCGAAGCTCCCGGGGACGACGCTGACTGCCCTTGAGAGCCGACGCCAACCTGGGCAC	3211

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QY 3392 TGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGGAGTGTCCAGCCAGGCTGA 3451
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Db 3481 GTGTCCAGCAGCAGCAGCTGCTCTTCACTTCCCAAGGCTGAGGCTGAGGCTGCA 3540
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QY 3752 GGTGCTGTGGAGTAATACTGATATATGAGTTTTCAGTTTGAATAAAAAAAAAAAAA 3811
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QY 3812 AAAAAAAAAAAAAA 3824
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RESULT 12
US-10-044-692-4

Sequence 4, Application US/10044692
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3855 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: 1.3855
LOCATION: 56..2479
OTHER INFORMATION: /note= "nucleic acid sequence with an open reading frame encoding a delta-182 variant polypeptide"
FEATURE:
NAME/KEY: CDS
LOCATION: 56..2479
OTHER INFORMATION: /product= "delta-182 variant polypeptide"
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-044-692-4
Query Match 98.5%; Score 3767.8; DB 43; Length 3855;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;
QY 8 GCAGCGCTGCGTCTGCTGCGCAGCGTGGAGAGCCCTGGGCCCCCGGCAACCCCGGATGCC 67
Db 1 GCAGCGCTGCGTCTGCTGCGCAGCGTGGAGAGCCCTGGGCCCCCGGCAACCCCGGATGCC 60
QY 68 GCGGCTCCCGGCTGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Db 61 GCGGCTCCCGGCTGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 128 GCGGCTGCGCAGTGTGCTGCGGCGGCTGCGGCGGCCCCCAGGGGCTGGGCTGTCAGCGCG 187
Db 121 GCGGCTGCGCAGTGTGCTGCGGCGGCTGCGGCGGCCCCCAGGGGCTGGGCTGTCAGCGCG 180
QY 188 GGACCCGGGCGGCTTTCGCGCGGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 247
Db 181 GGACCCGGGCGGCTTTCGCGCGGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 248 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 307
Db 241 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 308 CCGAGTCTTCAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
Db 301 CCGAGTCTTCAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360

Db	2521	TCCTCAGGACCCTGGTCCGAGGTGTCCTGAGTATGGCTGCGTGAACCTTGGCGAAGA	2580
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QY	2672	AGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCGCAGTCTCACTTCAACCGCG	2731
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QY	2732	GCTTCAGGCTGGAGGAACATGCGTCCAAACTCTTTGGGTCCTGGGCTGAAGTGC	2791
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QY	2912	AGCAAGTTTGAAGAACCACATTTTCTCTGCGGTCATCTCTGACACAGGCTTCCCTCT	2971
Db	2941	AGCAAGTTTGAAGAACCACATTTTCTCTGCGGTCATCTCTGACACAGGCTTCCCTCT	3000
QY	2972	GCTACTCCATCTCTGAAGAACCACAAAGACGACAGGATGTGCTGGGGGCCAAGGGCGCGCG	3031
Db	3001	GCTACTCCATCTCTGAAGAACCACAAAGACGACAGGATGTGCTGGGGGCCAAGGGCGCGCG	3060
QY	3032	GCCCTCTGCCCCCTCCGAGGCCGTGTCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3091
Db	3061	GCCCTCTGCCCCCTCCGAGGCCGTGTCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGA	3120
QY	3092	CTGCACACCGGTGTACCTACGTGCCACTCCTGGGGTCACTCAGACAGGCCAGACGACG	3151
Db	3121	CTGCACACCGGTGTACCTACGTGCCACTCCTGGGGTCACTCAGACAGGCCAGACGACG	3180
QY	3152	TGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCCGACGCCAACCCGGGAC	3211
Db	3181	TGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCCGACGCCAACCCGGGAC	3240
QY	3212	TGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCACAGCCAGGCCGAGA	3271
Db	3241	TGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCCGCCACAGCCAGGCCGAGA	3300
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Db	3301	GCAGACACCAAGCAGCCCTGTCAAGCCCGGCTCTACGTCCAGAGGAGGAGGGGGCGGCCA	3360
QY	3332	CACCCAGGCCCCGACCCGCTGGGAGTCTGAGGCGCTGAGTGAAGTGTGGCCGAGGCTTGA	3391
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QY	3392	TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGACGAGTGTCCAGGCCAAGGGCTGA	3451
Db	3421	TGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGACGAGTGTCCAGGCCAAGGGCTGA	3480
QY	3452	GTGTCCAGACACCTGCCGCTTCTCACTTCCCAACAGGCTGGCGCTCCACCCCAAGG	3511
Db	3481	GTGTCCAGACACCTGCCGCTTCTCACTTCCCAACAGGCTGGCGCTCCACCCCAAGG	3540
QY	3512	GCCAAGCTTTTCTCACCAGAGACCCGGCTTCCATCTCCCACATAGGAATAGTTCATCCCC	3571
Db	3541	GCCAAGCTTTTCTCACCAGAGACCCGGCTTCCATCTCCCACATAGGAATAGTTCATCCCC	3600
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QY	3752	GGTGCTGTGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTGAAAAAAAAAAAA	3811
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Db	3841	AAAAAAAAAAAAAAAA 3853	

RESULT 13
 : Sequence 4, Application US/10325810
 : GENERAL INFORMATION:
 : APPLICANT: Cech, Thomas R.
 : Lingner, Joachim
 : Nakamura, Toru
 : Chapman, Karen B.
 : Morin, Gregg B.
 : Harley, Calvin B.
 : Andrews, William H.
 : TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 : NUMBER OF SEQUENCES: 633
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, Eighth Floor
 : CITY: San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94111-3834
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent in Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/10/325,810
 : FILING DATE: 20-Dec-2002
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/09/402,181
 : FILING DATE: 29-Sep-1997
 : APPLICATION NUMBER: US 08/724,643
 : FILING DATE: 01-Oct-1996
 : APPLICATION NUMBER: US 08/844,419
 : FILING DATE: 18-Apr-1997
 : APPLICATION NUMBER: US 08/846,017
 : FILING DATE: 25-Apr-1997
 : APPLICATION NUMBER: US 08/851,843
 : FILING DATE: 06-May-1997
 : APPLICATION NUMBER: US 08/854,050
 : FILING DATE: 09-May-1997
 : APPLICATION NUMBER: US 08/911,312
 : FILING DATE: 14-Aug-1997
 : APPLICATION NUMBER: US 08/912,951
 : FILING DATE: 14-Aug-1997
 : APPLICATION NUMBER: US 08/915,503
 : FILING DATE: 14-Aug-1997
 : APPLICATION NUMBER: WO PCT/US97/17885
 : FILING DATE: 01-Oct-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Ausenhus, Scott L.
 : REGISTRATION NUMBER: 42,271
 : REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 3855 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY:

LOCATION: 1..3855

OTHER INFORMATION: /note= "nucleic acid sequence with an

open reading frame encoding a delta-182

variant polypeptide"

FEATURE:

NAME/KEY: CDS

LOCATION: 56..2479

OTHER INFORMATION: /product= "delta-182 variant

polypeptide"

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-325-810-4

Query Match

Best Local Similarity 98.5%; Score 3767.8; DB 49; Length 3855;

Matches 3815; Conservative 0; Mismatches 2; Indels 36; Gaps 1;

QY 8 GCAGCGCTGCTCTCTGCTGCGACGCTGGAGAGCCCTGCGCCCGGACACCCCGCGATGCC 67
Db 1 GCAGCGCTGCTCTCTGCTGCGACGCTGGAGAGCCCTGCGCCCGGACACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGAGCCGCTGCTCTGCTGCGAGCCACTACCGCGAGCTGCT 127
Db 61 GCGCGCTCCCGCTGCGAGCCGCTGCTCTGCTGCGAGCCACTACCGCGAGCTGCT 120
QY 128 GCGCGTGGCAGCTGCTGCGCGCGCTGGGCGCCAGGCGCTGGCGCTGCTGCGAGCGG 187
Db 121 GCGCGTGGCAGCTGCTGCGCGCGCTGGGCGCCAGGCGCTGGCGCTGCTGCGAGCGG 180
QY 188 GGACCCCGGCGCTTTCGCGCGCTGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
Db 181 GGACCCCGGCGCTTTCGCGCGCTGCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 248 ACGGCG 307
Db 241 ACGGCG 300
QY 308 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCGAGAGAGCTGCTGCTGCTGCTGCT 367
Db 301 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGAGAGAGCTGCTGCTGCTGCTGCTGCT 360
QY 368 GCTGCTGGAAGGCT 427
Db 361 GCTGCTGGAAGGCT 420
QY 428 CCGCT 487
Db 421 CCGCT 480
QY 488 CCGCGTGGGCGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Db 481 CCGCGTGGGCGAGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GGTCTCCAGCTGCGCTACAGAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGCTGCCAC 607
Db 541 GGTCTCCAGCTGCGCTACAGAGTGTGCGGGCGCGCGCTGTACAGCTGCGCGCTGCCAC 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGAACATAGCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727

Db 661 CTGAACATAGCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGCG 787
Db 721 GAGCG 780
QY 788 TGCCCTGAGCGCGAGCG 847
Db 781 TGCCCTGAGCGCGAGCG 840
QY 848 GCGTGACCGAGTGACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 907
Db 841 GCGTGACCGAGTGACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 908 CACCTCTTTGAGAGGTGCGCTGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
Db 901 CACCTCTTTGAGAGGTGCGCTGCTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 968 GCACCG 1027
Db 961 GCACCG 1020
QY 1028 CCGGCTGTACCG 1087
Db 1021 CCGGCTGTACCG 1080
QY 1088 GCGCT 1147
Db 1081 GCGCT 1140
QY 1148 GACCATCTTTCTGGGTTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1207
Db 1141 GACCATCTTTCTGGGTTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
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QY 1508 CAACGACCG 1567
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QY 1628 GAGCCAGGGGTGCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1687
Db 1621 GAGCCAGGGGTGCTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1680
QY 1688 CAAGTTCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTTA 1747
Db 1681 CAAGTTCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTTA 1740
QY 1748 TGTCAAGAGACCACTTTCAAAAGACAGGCTTTTCTTACCGGAAGAGTGTCTGAG 1807

GENERAL INFORMATION:

```

      APPLICANT: Hagen, Gustav
      APPLICANT: Siegmund, Hans-Ulrich
      APPLICANT: Weichel, Walter
      APPLICANT: Wick, Maresa
      APPLICANT: Zubov, Dmitry
      TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Therap
      TITLE OF INVENTION: Use
      FILE REFERENCE: Bayer 10,203
      CURRENT APPLICATION NUMBER: US/09/424,686F
      CURRENT FILING DATE: 1999-11-29
      PRIOR APPLICATION NUMBER: PCT/EP98/03468
      PRIOR FILING DATE: 1998-06-09
      NUMBER OF SEQ ID NOS: 32
      SOFTWARE: Microsoft Word
      SEQ ID NO 9
      LENGTH: 4006
      TYPE: DNA
      ORGANISM: Human
      FEATURE:
      NAME/KEY: CDS
      LOCATION: (1)..(4006)
      OTHER INFORMATION: Nucleotides 2184 to 2219 of SEQ ID NO. 1 have been deleted to pro
      OTHER INFORMATION: vide this sequence.
      JS-09-424-686F-9

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Query Match	95.0%;	Score 3632;	DB 20;	Length 4006;
Best Local Similarity	95.5%;	Pred. No. 0;		
Matches 3824;	Conservative	0;	Mismatches	0;
			Indels	182;
			Gaps	1;

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Db	61	CGATGCCCGCGCTCCCGCGCTGCCGAGCCGTGGGCTCCCTGCTGCGCAGCCACTACCGCG	120
QY	121	AGGTGCTGCCGCTGGCCACGTTCTGTGCGCGCGCTGGGGCCCCAGGCGCTGGCGGTGTGC	180
Db	121	AGGTGCTGCCGCTGGCCACGTTCTGTGCGCGCGCTGGGGCCCCAGGCGCTGGCGGTGTGC	180
QY	181	AGCGCGGGGACCCGCGGCTTTCGCGCGCTGTGGCCAGTGCTGTGTGCGTGCCCT	240
Db	181	AGCGCGGGGACCCGCGGCTTTCGCGCGCTGTGGCCAGTGCTGTGTGCGTGCCCT	240
QY	241	GGGACGACGCGCGCCCGCCCGCCCTCTTCGCCAGGTGTCTGCTGAAGAGC	300
Db	241	GGGACGACGCGCGCCCGCCCGCCCTCTTCGCCAGGTGTCTGCTGAAGAGC	300
QY	301	TGCTGACCCGAGTGTGTGACAGGCTGTGCGAGCGCGCGGAAGAACGTGTGACCTTGC	360
Db	301	TGCTGACCCGAGTGTGTGACAGGCTGTGCGAGCGCGCGGAAGAACGTGTGACCTTGC	360
QY	361	GCTTCGCGCTGTGACGCGGGCCCCCGGGGGCCCCGAGGCTTCAACCAACGAGCTGC	420
Db	361	GCTTCGCGCTGTGACGCGGGCCCCCGGGGGCCCCGAGGCTTCAACCAACGAGCTGC	420
QY	421	GCACTACCTGCCAACACGGTGACCGACGCACTGCCGGGGAGCGGGCGTGGGGGCTGC	480
Db	421	GCACTACCTGCCAACACGGTGACCGACGCACTGCCGGGGAGCGGGCGTGGGGGCTGC	480
QY	481	TGCTGCGCGCGCGTGGGCGACGAGTGTGTGTTCACTGCTGGCACGCTGCGCGCTTTG	540
Db	481	TGCTGCGCGCGCGTGGGCGACGAGTGTGTGTTCACTGCTGGCACGCTGCGCGCTTTG	540
QY	541	TGCTGAGTGGCTCCCAAGTGGCCTTACCAAGTGTGCGGGCGCGCGCTGTACCAAGTGGCG	600
Db	541	TGCTGAGTGGCTCCCAAGTGGCCTTACCAAGTGTGCGGGCGCGCGCTGTACCAAGTGGCG	600
QY	601	CTGCCACTCAGGCCCGCGCCCGCCACACACGCTAGTGAACCCCGAAGGCGTCTGGGATGCG	660
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QY	721	GTGCGAGGAGGGCGGGGGGCGAGTGCCAGCCGAAGTCTGCCGTGGCCCAAGAGCCCAAGC	780
Db	721	GTGCGAGGAGGGCGGGGGGCGAGTGCCAGCCGAAGTCTGCCGTGGCCCAAGAGCCCAAGC	780
QY	781	GTGCGGCTGCCCCCTGAGCCCGGAGCGGACGCCCGTTGGGCAAGGGGTCTGGGCCCACTCCG	840
Db	781	GTGCGGCTGCCCCCTGAGCCCGGAGCGGACGCCCGTTGGGCAAGGGGTCTGGGCCCACTCCG	840
QY	841	GCAAGACGCGGTGAGCCGAGTGACCGTGTTTCTGTGTGTCACTTCCAGACCCCGCG	900
Db	841	GCAAGACGCGGTGAGCCGAGTGACCGTGTTTCTGTGTGTCACTTCCAGACCCCGCG	900
QY	901	AAGAAGCCACTTTTGGAGGGGTGCGCTCTTGGACAAGCCACTCCACCAATCCGTG	960
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QY	1141	TCGTGAGACCATTTTCTGGGTTCCAGGCCCTGAGATGCCAGGACTCCCCGAGGTTGC	1200
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Db	1201	CCCGCCTGCCCAAGCGCTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTTGGAAAC	1260
QY	1261	ACGCGAGTGCCCTACGGGGTGCTCTCTCAAGACGACTGCCGCTGCGAGCTGCGTCA	1320
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Db	1321	CCCCAGAGCCGGTGTCTGTGCCCGGAGAGGCCCAAGGCTCTGTGCGGCCCGGAGG	1380
QY	1381	AGGAGGACACAGACCCCCGCTGCGCTGGTGACGTGCTCCGACGACAGAGCCCTGGC	1440
Db	1381	AGGAGGACACAGACCCCCGCTGCGCTGGTGACGTGCTCCGACGACAGAGCCCTGGC	1440
QY	1441	AGGTGTACGGCTTGTGCGGGGCTGCTGCGCGCGGCTGTGCCCCAGGCTCTGGGGCT	1500
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QY	1501	CCAGGACACACGACCGCGCTTCTCAAGAAACCAAGAATTATCTCCCTGGGGAAGC	1560
Db	1501	CCAGGACACACGACCGCGCTTCTCAAGAAACCAAGAATTATCTCCCTGGGGAAGC	1560
QY	1561	ATGCCAAGCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGGGACTGCCCTTGGC	1620
Db	1561	ATGCCAAGCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGGGACTGCCCTTGGC	1620
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QY	1681	TCCTGGCCAAATTCTTCACTGGCTGATGAGTGTACGTCTGAGCTGCTCAAGTCTT	1740
Db	1681	TCCTGGCCAAATTCTTCACTGGCTGATGAGTGTACGTCTGAGCTGCTCAAGTCTT	1740

QY 1741 TCTTTATGTACGAGACCAAGTCTTTCAAAAGACAGCTCTTTTCTACCGGAGAGTG 1800
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QY 1801 TCTGAGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGG 1860
Db 1801 TCTGAGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGG 1860
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Db 1861 AGCTGTGGAAGCAGAGTTCAGGACATCGGAAAGCCAGGCGCGCTGTGAGCTCCA 1920
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QY 2308 -----GCAAGTCTTACGTCAGTCCAGTCCAGGAGTCC 2338
Db 2461 TCATGTGCCACACAGCGCTGCGCATCAGGCGCAAGTCTTACGTCAGTCCAGGAGTCC 2520
QY 2339 CGCAGGCTCCATCTCTTCCACGCTGTCTGACGCTGTGTCACGCGCATGAGAGACA 2398
Db 2521 CGCAGGCTCCATCTCTTCCACGCTGTCTGACGCTGTGTCACGCGCATGAGAGACA 2580
QY 2399 AGCTGTTGCGGATTCGCGCGGAGCGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2458
Db 2581 AGCTGTTGCGGATTCGCGCGGAGCGGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
QY 2459 TGTGACACCTCACTCAACCAAGCAAAACCTTCTCAGAGACCTGCTCGAGGTGCC 2518
Db 2641 TGTGACACCTCACTCAACCAAGCAAAACCTTCTCAGAGACCTGCTCGAGGTGCC 2700
QY 2519 CTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2578
Db 2701 CTGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
QY 2579 AGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2638
Db 2761 AGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2820
QY 2639 GCCTGTCTGTGATACCGGAGCCCTGAGGTGAGAGCGACTACTCCAGCTATGCCCGGA 2698

Db 2821 GCCTGTCTGTGATACCGGAGCCCTGAGGTGAGAGCGACTACTCCAGCTATGCCCGGA 2880
QY 2699 CTTCCATCAGAGCCAGTCTCACTTCAACCGCGCTTCAAGGCTGGAGGACATGCGTC 2758
Db 2881 CTTCCATCAGAGCCAGTCTCACTTCAACCGCGCTTCAAGGCTGGAGGACATGCGTC 2940
QY 2759 GCAAACTCTTTGGGCTTTCGCGCTGAGGTGTCAGAGCTGTTCTGATTTGAGGTGA 2818
Db 2941 GCAAACTCTTTGGGCTTTCGCGCTGAGGTGTCAGAGCTGTTCTGATTTGAGGTGA 3000
QY 2819 ACAGCTCCAGACGCTGTCACCAACATCTACAAGATCTCTCTGCTGAGGCTACAGGT 2878
Db 3001 ACAGCTCCAGACGCTGTCACCAACATCTACAAGATCTCTCTGCTGAGGCTACAGGT 3060
QY 2879 TTCAAGCATGTGTGCTGAGCTCCCATTTTCATCAGCAAGTTTGAAGAACCCCATTTT 2938
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QY 2939 TCTGCGGCTCATCTTGAACAAGGCTCTCTGCTACTCTCATCTCTGAAAGCAAGAAC 2998
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QY 2999 CAGGATGTGCTGCGGCGCAAGGCGCGCGCGCGCGCTCTGCGCTCCGAGCGCTGAGT 3058
Db 3181 CAGGATGTGCTGCGGCGCAAGGCGCGCGCGCGCGCTCTGCGCTCCGAGCGCTGAGT 3240
QY 3059 GGTGTGCGCACCAAGCAATCTGCTCAAGCTGACTGACACCGTGTACCTACGTGCCAC 3118
Db 3241 GGTGTGCGCACCAAGCAATCTGCTCAAGCTGACTGACACCGTGTACCTACGTGCCAC 3300
QY 3119 TCTGGGCTCACTCAGACAGCCAGAGCGAGCTGAGTCCGAGCTCCCGGGAAGAGC 3178
Db 3301 TCTGGGCTCACTCAGACAGCCAGAGCGAGCTGAGTCCGAGCTCCCGGGAAGAGC 3360
QY 3179 TCACTGCCCTGAGGCGCGAGCCCAACCGGCACTGCCCTCAGACTTCAAGACCATCTG 3238
Db 3361 TCACTGCCCTGAGGCGCGAGCCCAACCGGCACTGCCCTCAGACTTCAAGACCATCTG 3420
QY 3239 ACTGATGGCCACCGGCCCAAGCCAGGCGCGAGAGAGACACCAAGGCGCTGTACGCG 3298
Db 3421 ACTGATGGCCACCGGCCCAAGCCAGGCGCGAGAGAGACACCAAGGCGCTGTACGCG 3480
QY 3299 GGTCTTACGTCCAGAGGAGGAGGCGCGGCCCAACCAAGGCGCGCTGTGAGGTCT 3358
Db 3481 GGTCTTACGTCCAGAGGAGGAGGCGCGGCCCAACCAAGGCGCGCTGTGAGGTCT 3540
QY 3359 GAGGCTGAGTGTGTTTGGCGGAGGCTGTGATGCTGCGGTGAAGGCTGAGTGTCCGC 3418
Db 3541 GAGGCTGAGTGTGTTTGGCGGAGGCTGTGATGCTGCGGTGAAGGCTGAGTGTCCGC 3600
QY 3419 TGAAGCTGAGCGAGTGTCCAGCCAGGCGCTGAGTGTCCAGACACCTGCGCTTCACT 3478
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QY 3539 CTTCCACTCCCAATAGGAATAGTCCATCCCAAGATTGCGCAATTGTTCAACCTGCGCC 3598
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QY 3599 TGCCTCTCTTGTCTTCAACCCCAAGCTGAGGTGAGAGCCCTGAGAGAGCCCTGGGA 3658
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Db 3841 GCTCTGGGAATTGAGTGAACCAAGGTGCTCTGTACACAGGCGAGAGCCCTGACCT 3900
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QY 1681 TCCTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGCTCTT 1740
Db 1681 TCCTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGCTCTT 1740
QY 1741 TCTTTTATGTCACGAGAGACCAGCTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGAGTG 1800
Db 1741 TCTTTTATGTCACGAGAGACCAGCTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGAGTG 1800
QY 1801 TCTGGAGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAGGAGTGACGTCGGG 1860
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QY 1861 AGCTGTGGAGAGCAGAGGTCAAGCAGCATCGGGAAGCCAGCCCGCTGCTGACGTCGA 1920
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QY 1921 GACTCCGCTTCATCCCAAGCTGACGGGCTGCGCGCATTTGTGAACATGACTACGTCG 1980
Db 1921 GACTCCGCTTCATCCCAAGCTGACGGGCTGCGCGCATTTGTGAACATGACTACGTCG 1980
QY 1981 TGGAGCCAGAAAGCTTCCGACAGAAAAGAGGCGCCAGCTCTCAGCTGAGGAGTGAAG 2040
Db 1981 TGGAGCCAGAAAGCTTCCGACAGAAAAGAGGCGCCAGCTCTCAGCTGAGGAGTGAAG 2040
QY 2041 CACTGTTCAGCGTGTCAACTACGAGCGGCGCGCGCGCGCGCTCTGAGGCGCTCTG 2100
Db 2041 CACTGTTCAGCGTGTCAACTACGAGCGGCGCGCGCGCGCGCTCTGAGGCGCTCTG 2100
QY 2101 TGCTGGGCTTGAGCATATCAAGAGGCTGCGCACTTCTGCTGCTGCGGCGGCCC 2160
Db 2101 TGCTGGGCTTGAGCATATCAAGAGGCTGCGCACTTCTGCTGCTGCGGCGGCCC 2160
QY 2161 AGGACCCGCGCTGAGCTGA-----CA 2184
Db 2161 AGGACCCGCGCTGAGCTGA-----CA 2184
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QY 2245 GCTGCGCTGCTGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2304
Db 2245 GCTGCGCTGCTGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2304
QY 2281 GCTGCGCTGCTGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2340
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QY 2305 AGA----- 2307
Db 2305 AGA----- 2307
QY 2341 AGAGCCACGCTCTCTACCTTGAACAGACCTCCAGCCGTAATGCGACAGTTGCTGCTCACC 2400
Db 2341 AGAGCCACGCTCTCTACCTTGAACAGACCTCCAGCCGTAATGCGACAGTTGCTGCTCACC 2400
QY 2308 ----- 2307
Db 2308 ----- 2307
QY 2401 TGCAAGAGACAGAGCCCGCTGAGGAGATGCCGTGCTATGAGCAGAGCTCTCTGTAATG 2460
Db 2401 TGCAAGAGACAGAGCCCGCTGAGGAGATGCCGTGCTATGAGCAGAGCTCTCTGTAATG 2460
QY 2308 ----- 2307
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QY 2461 AGGCCAGCAGTGAGCTCTTGAACGCTCTTCTACGCTTCAATGTCACCAAGCCGTGCGCA 2520
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QY 2308 -----GCAAGTCTACCTGCAAGTGCAGAGGAGTCCCGAGGCTCCATCTCTCCAGCG 2362
Db 2308 -----GCAAGTCTACCTGCAAGTGCAGAGGAGTCCCGAGGCTCCATCTCTCCAGCG 2362
QY 2521 TCAGGGGCAAGTCTACCTGCAAGTGCAGAGGAGTCCCGAGGCTCCATCTCTCCAGCG 2580
Db 2521 TCAGGGGCAAGTCTACCTGCAAGTGCAGAGGAGTCCCGAGGCTCCATCTCTCCAGCG 2580
QY 2363 TGCTCTGCAAGCTGTGCTACGCGCAGCATGAGAACAGCTGTTGCGGGGATTCGGCGGG 2422
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QY 2581 TGCTCTGCAAGCTGTGCTACGCGCAGCATGAGAACAGCTGTTGCGGGGATTCGGCGGG 2640
Db 2581 TGCTCTGCAAGCTGTGCTACGCGCAGCATGAGAACAGCTGTTGCGGGGATTCGGCGGG 2640
QY 2423 ACGGGCTGCTCTGCGCTTGGTGATGATTTCTTGTGTGACACCTCACTCACCACAG 2482
Db 2423 ACGGGCTGCTCTGCGCTTGGTGATGATTTCTTGTGTGACACCTCACTCACCACAG 2482
QY 2641 ACGGGCTGCTCTGCGCTTGGTGATGATTTCTTGTGTGACACCTCACTCACCACAG 2700
Db 2641 ACGGGCTGCTCTGCGCTTGGTGATGATTTCTTGTGTGACACCTCACTCACCACAG 2700
QY 2483 CGAAAAAAGCTTCTCTCAGAGACCTGCTGCGAGGAGTCCCTGAGTATGCTGCTGCTGTA 2542
Db 2483 CGAAAAAAGCTTCTCTCAGAGACCTGCTGCGAGGAGTCCCTGAGTATGCTGCTGCTGTA 2542
QY 2701 CGAAAAAAGCTTCTCTCAGAGACCTGCTGCGAGGAGTCCCTGAGTATGCTGCTGCTGTA 2760
Db 2701 CGAAAAAAGCTTCTCTCAGAGACCTGCTGCGAGGAGTCCCTGAGTATGCTGCTGCTGTA 2760

QY 2543 TGCCGAGACAGTGTGTAATTTCCCTGTAGAGACGAGGCGCTTGGGTGGACAGGCTTTTG 2602
Db 2543 TGCCGAGACAGTGTGTAATTTCCCTGTAGAGACGAGGCGCTTGGGTGGACAGGCTTTTG 2602
QY 2603 TTCAAGTGGCGGCGCCACCGGCTATTTCCCTGTGTGCGGCTGCTGCTGATACCCGAGCC 2662
Db 2603 TTCAAGTGGCGGCGCCACCGGCTATTTCCCTGTGTGCGGCTGCTGCTGATACCCGAGCC 2662
QY 2663 TGGAGGTGACAGAGCGCTACTTCCAGCTATGCCCCGAGCTTCCATCAGAGCCAGTTCACCT 2722
Db 2663 TGGAGGTGACAGAGCGCTACTTCCAGCTATGCCCCGAGCTTCCATCAGAGCCAGTTCACCT 2722
QY 2723 TCAACCGCGGCTTCAAGGCTGGGAGGAAACATGCGTGGCAACTTTTGGGGTCTTGGCGG 2782
Db 2723 TCAACCGCGGCTTCAAGGCTGGGAGGAAACATGCGTGGCAACTTTTGGGGTCTTGGCGG 2782
QY 2941 TCAACCGCGGCTTCAAGGCTGGGAGGAAACATGCGTGGCAACTTTTGGGGTCTTGGCGG 3000
Db 2941 TCAACCGCGGCTTCAAGGCTGGGAGGAAACATGCGTGGCAACTTTTGGGGTCTTGGCGG 3000
QY 2783 TGAAGTGTCAAGGCTGTTTCTGGAATTTGCAAGGTGAACAGCTTCCAGAGCGTGGCA 2842
Db 2783 TGAAGTGTCAAGGCTGTTTCTGGAATTTGCAAGGTGAACAGCTTCCAGAGCGTGGCA 2842
QY 3001 TGAAGTGTCAAGGCTGTTTCTGGAATTTGCAAGGTGAACAGCTTCCAGAGCGTGGCA 3060
Db 3001 TGAAGTGTCAAGGCTGTTTCTGGAATTTGCAAGGTGAACAGCTTCCAGAGCGTGGCA 3060
QY 2843 ACATCTACAGATCTCTGCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCC 2902
Db 2843 ACATCTACAGATCTCTGCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCC 2902
QY 3061 ACATCTACAGATCTCTGCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCC 3120
Db 3061 ACATCTACAGATCTCTGCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCC 3120
QY 2903 CATTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACACAGG 2962
Db 2903 CATTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACACAGG 2962
QY 3121 CATTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACACAGG 3180
Db 3121 CATTCATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTGACACAGG 3180
QY 2963 CTTCCCTCTGCTACTCTCACTCTGAAAGCCAGAAAGGAGGAGTGTGCTGGGCGCAAGG 3022
Db 2963 CTTCCCTCTGCTACTCTCACTCTGAAAGCCAGAAAGGAGGAGTGTGCTGGGCGCAAGG 3022
QY 3181 CTTCCCTCTGCTACTCTCACTCTGAAAGCCAGAAAGGAGGAGTGTGCTGGGCGCAAGG 3240
Db 3181 CTTCCCTCTGCTACTCTCACTCTGAAAGCCAGAAAGGAGGAGTGTGCTGGGCGCAAGG 3240
QY 3023 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGC 3082
Db 3023 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGC 3082
QY 3241 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGC 3300
Db 3241 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGC 3300
QY 3083 TCAAGCTGACTGACACCGGTGACACCTACGTGCGCACTCTGGGGTCACTCAGACAGCC 3142
Db 3083 TCAAGCTGACTGACACCGGTGACACCTACGTGCGCACTCTGGGGTCACTCAGACAGCC 3142
QY 3301 TCAAGCTGACTGACACCGGTGACACCTACGTGCGCACTCTGGGGTCACTCAGACAGCC 3360
Db 3301 TCAAGCTGACTGACACCGGTGACACCTACGTGCGCACTCTGGGGTCACTCAGACAGCC 3360
QY 3143 AGAGGCACTGAGTGGAGCTCCCGGAGCGAGCTGAGGCTGAGGCGCGGCGCAAGCC 3202
Db 3143 AGAGGCACTGAGTGGAGCTCCCGGAGCGAGCTGAGGCTGAGGCGCGGCGCAAGCC 3202
QY 3361 AGAGGCACTGAGTGGAGCTCCCGGAGCGAGCTGAGGCTGAGGCGCGGCGCAAGCC 3420
Db 3361 AGAGGCACTGAGTGGAGCTCCCGGAGCGAGCTGAGGCTGAGGCGCGGCGCAAGCC 3420
QY 3203 ACCCGGCACTGCGCTGAGCTTCAAGACCATCTGAGCTGAGGCGCGGCGCAAGCC 3262
Db 3203 ACCCGGCACTGCGCTGAGCTTCAAGACCATCTGAGCTGAGGCGCGGCGCAAGCC 3262
QY 3421 ACCCGGCACTGCGCTGAGCTTCAAGACCATCTGAGCTGAGGCGCGGCGCAAGCC 3480
Db 3421 ACCCGGCACTGCGCTGAGCTTCAAGACCATCTGAGCTGAGGCGCGGCGCAAGCC 3480
QY 3263 AGCGGAGAGACAGACACCAAGCAGCCCTGTCAAGCGCGGCTTACGTCAGGAGGAGG 3322
Db 3263 AGCGGAGAGAGACAGACACCAAGCAGCCCTGTCAAGCGCGGCTTACGTCAGGAGGAGG 3322
QY 3481 AGCGGAGAGAGACAGACACCAAGCAGCCCTGTCAAGCGCGGCTTACGTCAGGAGGAGG 3540
Db 3481 AGCGGAGAGAGACAGACACCAAGCAGCCCTGTCAAGCGCGGCTTACGTCAGGAGGAGG 3540
QY 3323 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3382
Db 3323 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3382
QY 3541 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3600
Db 3541 GCGCGCGCGGCGCTCTGCGCTCCGAGGCGGTGAGGCTGAGGCTGAGGCTGAGGCTGAGG 3600
QY 3383 AGGCTGCAATGTCCGCTGAAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCT 3442
Db 3383 AGGCTGCAATGTCCGCTGAAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCT 3442
QY 3601 AGGCTGCAATGTCCGCTGAAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
Db 3601 AGGCTGCAATGTCCGCTGAAAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCT 3660
QY 3443 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3502
Db 3443 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3502
QY 3661 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3720
Db 3661 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGAGGCTGAGGCTGAGGCT 3720
QY 3503 CACCCAGAGGCGCAGCTTTTCTCAACAGAGAGCGGCTTCCACTCCCAATAGGAATAG 3562
Db 3503 CACCCAGAGGCGCAGCTTTTCTCAACAGAGAGCGGCTTCCACTCCCAATAGGAATAG 3562
QY 3721 CACCCAGAGGCGCAGCTTTTCTCAACAGAGAGCGGCTTCCACTCCCAATAGGAATAG 3780
Db 3721 CACCCAGAGGCGCAGCTTTTCTCAACAGAGAGCGGCTTCCACTCCCAATAGGAATAG 3780
QY 3563 TCCATCCCAAGATTCGCAATTTTCAACCCCTGCGCTGCGCTCTTGGCTTCCACCCCG 3622
Db 3563 TCCATCCCAAGATTCGCAATTTTCAACCCCTGCGCTGCGCTCTTGGCTTCCACCCCG 3622
QY 3781 TCCATCCCAAGATTCGCAATTTTCAACCCCTGCGCTGCGCTCTTGGCTTCCACCCCG 3840
Db 3781 TCCATCCCAAGATTCGCAATTTTCAACCCCTGCGCTGCGCTCTTGGCTTCCACCCCG 3840
QY 3623 ACCATCCAGGTGAGAGCCCTGAGAGGAGCCCTGGGAGCTCTGGGAATTTGAGTGAACCA 3682
Db 3623 ACCATCCAGGTGAGAGCCCTGAGAGGAGCCCTGGGAGCTCTGGGAATTTGAGTGAACCA 3682

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Db 3841 ACCATCCAGGTGAGAGACCCCTGAGAGAGACCCCTGGAGCTCTGGGAATTGGAGTGACCAA 3900
QY 3683 AGGTGTGCCCTGTACACAGGCGAGAGACCCCTGACCTGATGGGGGTCCCTGTGGGTCAA 3742
Db 3901 AGGTGTGCCCTGTACACAGGCGAGAGACCCCTGACCTGATGGGGGTCCCTGTGGGTCAA 3960
QY 3743 TTGGGGGAGGTGTGTGGGAGTAATACTGAATATATGAGTTTTCAGTTTGAATA 3802
Db 3961 TTGGGGGAGGTGTGTGGGAGTAATACTGAATATATGAGTTTTCAGTTTGAATA 4020
QY 3803 AAAAAAAAAAAAAAAAAAAAAA 3824
Db 4021 AAAAAAAAAAAAAAAAAAAAAA 4042
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Search completed: March 1, 2004, 22:57:45
Job time : 7781.54 secs

[illegible]

DB 301 CCGCCGCCGACCTCGGCCCCCGGCCCGC-TCTCCGCGCTCCGGGTGCCCGCCCGCC 359

QY 168 TGGCGGCTGTGTCAGACCGCGGGACCGCGGCTTCCGCGGCTGTGTGAGCCAGTGCTG 227
DB 126 TCGCGGCTCGACACCGCTCGCGCGCGCGCGCTGCTCGCGCGCGCGCGCGCGCGCG 185
QY 228 GTGTGCGCTGCGCTGAGACGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 287
DB 186 CGCGGGGACG 245
QY 288 TGCCTGAAGAGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 347
DB 246 CCG 305
QY 348 GTGTGCGCTTGTGCG 407
DB 306 TGTTCGCGGCTGC-GCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 364
QY 408 ACCACGAGCGGTGCG 467
DB 365 CTGCGCGCTGTGCG 424
QY 468 GCGTGGGCGCTGTGCG 527
DB 425 CCTGCGCGTGCAGCG 484
QY 528 TGGCGGCTTGT 567
DB 485 TCGCGCTCGCTGAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 524

RESULT 5

US-10-767-471-10913/c
; Sequence 10913, Application US/10767471

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10913
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(40000)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-767-471-10913

Query Match 1.5%; Score 56.8; DB 6; Length 40000;
Best Local Similarity 48.2%; Pred. No. 0.0046;
Matches 160; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

QY 1 GTTTCAGGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
DB 24768 GTGCG 24709
QY 61 CGATGCG 120
DB 24708 CGGTCTGAGAGCG 24649
QY 121 AGGTGCTGCG 180
DB 24648 GCG 24589
QY 181 AGCGCGGAGACCG 240
DB 24588 CCTTACCTCG 24529
QY 241 GGGACGACG 300

DB 24528 CGCGGAGCTTGTCCG 24469
QY 301 TGTGAGCGCGAGTGTGTCAGAGCGCTGTGCGAG 332
DB 24468 CGCGGAGCTTGTGCG 24437

RESULT 6

US-10-767-701-4866
; Sequence 4866, Application US/10767701

; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4866
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS92278_1
US-10-767-701-4866

Query Match 1.4%; Score 54.6; DB 6; Length 666;
Best Local Similarity 46.8%; Pred. No. 0.0029;
Matches 240; Conservative 0; Mismatches 269; Indels 4; Gaps 2;

QY 228 GTGTGCGTGGCTGCG 287
DB 38 GCGCGCGCTGACAGCTTCCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 97
QY 288 TGCCTGAAGAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 347
DB 98 GCG 157
QY 348 GTGTGCGCTTGTGCG 407
DB 158 GCG 217
QY 408 ACCACGAGCGGTGCG 467
DB 218 TCCCTCG 274
QY 468 GCGTGGGCGCTGTGCG 527
DB 275 CCGCGCGCGCTTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 334
QY 528 TGGCGGCTTGT 587
DB 335 GTGCGCGCGCTGCTACAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
QY 588 TACAGCTCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 647
DB 395 TCG 453
QY 648 CGTCTGGAGTGCAGACG 707
DB 454 CCG 513
QY 708 CTGCGAGCG 740
DB 514 CCGCGCGCTCGCGAGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546

RESULT 7

US-10-767-701-4186
; Sequence 4186, Application US/10767701
; GENERAL INFORMATION:

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4186
LENGTH: 584
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS73536_1
US-10-767-701-4186

Query Match 1.4%; Score 54.2; DB 6; Length 584;
Best Local Similarity 45.7%; Pred. No. 0.0033;
Matches 188; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

QY 20 CCTGCTGCGACAGTGGAGAACCCCTGAGCCCGCCGACCCCGGATGCGCGCTCCCGG 79
DB 144 CCCCCCGCGCCCGCCACCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 203
QY 80 CTGCGGAGCGGTGCGCTCCCTGCTGCGAGCACTACCGGAGGTGCTGCGCTGCGCAC 139
DB 204 CCG 263
QY 140 GTTGTGCGCGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 199
DB 264 GCG 323
QY 200 TTTCGCGCGCGGTGCG 259
DB 324 CG 383
QY 260 CG 319
DB 384 GCTCCCG 443
QY 320 GAGGCTGTGCGAGCGCGCGCGCGCGAGAGAGTGTGCGCTTCCGCTTCCGCTGAGCG 379
DB 444 CCGCGAGGCGGTCACTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 503
QY 380 GGGCG 430
DB 504 CGACCG 554

RESULT 8
US-10-767-701-2473/c

Sequence 2473, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 2473
LENGTH: 570
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(570)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41826_1

US-10-767-701-2473

Query Match 1.4%; Score 53.4; DB 6; Length 570;
Best Local Similarity 52.9%; Pred. No. 0.0049;
Matches 137; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 574 GCGGCG 633
DB 260 GCGGCG 201
QY 634 GTG-GACCCCGAGAGCGGTGAGTCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 692
DB 200 GTGCG 141
QY 693 GGGGTCCCTGCG 752
DB 140 GGGGCG 81
QY 753 AGTCTGCG 812
DB 80 CCG 21
QY 813 GTTGGCAGGCGGTCTCTGGG 831
DB 20 CCGGCGCGCGCGCGCGCGCGCG 2

RESULT 9

US-10-767-701-4466
Sequence 4466, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4466
LENGTH: 580
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS80039_1
US-10-767-701-4466

Query Match 1.4%; Score 53.4; DB 6; Length 580;
Best Local Similarity 52.3%; Pred. No. 0.005;
Matches 147; Conservative 0; Mismatches 126; Indels 8; Gaps 1;

QY 12 CGGTGCTGCTGCTGCGACGTGGAGAACCCCTGAGCCCGCGCGCGCGCGCGCGCGCG 71
DB 125 CG 184
QY 72 GCTCCCG 131
DB 185 CG 244
QY 132 CTGCGCAGTTCGTGCG 191
DB 245 GGGGCG 304
QY 192 CCGGCG 251
DB 305 CTGCTCTCT-----GCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 356
QY 252 CCG 292
DB 357 CTCCCG 397

RESULT 10

US-10-767-701-9739
; Sequence 9739, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9739
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS33367_1
US-10-767-701-9739

Query Match

1.4%; Score 53.4; DB 6; Length 1092;
Best Local Similarity 45.0%; Pred. No. 0.0063;
Matches 201; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 39 GCCTGGCCCCGGCCACCCCGCATGCGCGGCTCCCGCTGCGGAGCGGTGCGTCC 98
DB 177 GGGCTGGCGCGCGCGCGCTCCACCCCTCCCGCGCGCGCGCTCCCGCTCCCGCC 236
QY 99 CTGCTGGCGAGCCACTACCGGAGGTGCTGCGGCTGGCCACGTTCTGCGCGCGCTGGGG 158
DB 237 CGCCCCCGCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 296
QY 159 CCCCCAGGCTGGCGCGCTGGTGCAGCGCGCGGAGCCCGCGCGCTTCCCGCGCGCTGGCC 218
DB 297 CGCC 356
QY 219 CAGTGCCTGTGTGCTGCTGCGCTGGGAGCGCAGCGCGCGCGCGCGCGCGCGCTTCCGC 278
DB 357 CGCTCCC 416
QY 279 CAGGTGCTCTGCTGCTGAGGAGCTGTGGCGCGAGTGTGCAGAGGCTGTGCGAGCGCGGC 338
DB 417 CCGCC 476
QY 339 GCGAAGACGTGCTGCTGCGCTTGGGCTTGGCGCTGTGAGCGCGCGCGCGCGCGCGCGCC 398
DB 477 GTCTGTCTCTCCACGTGCTC 536
QY 399 GAGGCTCTCACCACCGAGCTGCGAGCTACTGCGCCACACAGGTGAGCGACGCACTGCGG 458
DB 537 CCGGTGCG 596
QY 459 GGGAGCGGGCGGTGGGCTGTGCTG 485
DB 597 GGGCG 623

RESULT 11

US-10-767-701-30024
; Sequence 30024, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30024
; LENGTH: 522

;; TYPE: DNA
;; ORGANISM: Sorghum bicolor
;; FEATURE:
;; OTHER INFORMATION: Clone ID: 9848339
US-10-767-701-30024

Query Match 1.4%; Score 53.2; DB 6; Length 522;
Best Local Similarity 49.4%; Pred. No. 0.0053;
Matches 167; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

QY 122 GGTGCTCCCGCTGGCCACGTTCTGTGCGCGCGCTGGGAGCCCAAGGCTGGCGGCTGTGCA 181
DB 56 GAGCGCGGTGCTGGCGCGCTGGCGCGCGCTGATGGCGGAGGCGGGGTGACGCGCG 115
QY 182 GCGCGGGGACCGCGCG--GCTTCCCGCGCGCTGTGAGCCCAAGTGCCTGTGTGCGTGC 238
DB 116 GCGCGCGCGCACGCTGTCTCCCTACGCGCGCGCAGCTGGGCGCGCGCGCTGGCGCGCC 175
QY 239 CTGGGACGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCCGCGAGGTGCTGCTGAAGA 298
DB 176 GCTGTGCTGGCG 235
QY 299 GCTGTGCGCGCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCTT 358
DB 236 CATGCTTACCGCGTGCCTGG 295
QY 359 CGGCTTGGCGCTGTGAGAGCTTACACACGCGT 418
DB 296 CGACCTCGT 355
QY 419 GCGGAGTACTGCGTGC 456
DB 356 GCTGTGAGCTCTCCCGACCTTGTGATGACGAGCGCG 393

RESULT 12

US-10-767-701-8805
; Sequence 8805, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8805
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56975_1
US-10-767-701-8805

Query Match 1.4%; Score 53.2; DB 6; Length 667;
Best Local Similarity 45.0%; Pred. No. 0.0058;
Matches 199; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

QY 126 CTGCGCGCTGGCCACGTTCTGTGCGCGCGCTGGGAGCCCAAGGCTGGCGGCTGTGCAAGCGC 185
DB 23 CTCTCTGTATGCGCGCATGTGCG 82
QY 186 GGGGACCGCGCGCTTTCG 245
DB 83 CACCAACCGCGCTCTCCACTCCACTCCACTCCACTCCACTCCACTCCACTCCACTCCACTCCACTCC 142
QY 246 GACGT 305
DB 143 GCGTGGCGCTCCCGT 202
QY 306 GCGGAGTGTGAGAGGCTGTGCGAGCGT 365

Db 5608 GCGCCGCGTCTTCCCTCGGACGCTG---CCGCTGCCGCTTTGGCCTCTTCCGCCAGGGGAC 5552

QY 608 TCAGGC--CCGGCCCCCGGCACACGCTAGTGAGACCCCGAAGCGCTCTGGATGCCAACGG 665

Db 5551 GCAGGCGGGCGGCTCTCTCGGCCAGCTCGCGGAACGGCGGCGCTCGGCGCTCCAGCCTCT 5492

QY 666 GCCTGGAACCATAGCGTCAGGAGAGCGCGGGTCCCGCTGGGCTGCC 712

Db 5491 GCTTGACTTCTCGCTGGTGGAGCGCGACTCCTCCTCAGCGCTTYGCC 5445

RESULT 15

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US-10-767-471/603/C
; Sequence 603, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 11409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-603

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Query Match	1.4%	Score 52;	DB 6;	Length 11409;
Best Local Similarity	44.2%;	Pred. No. 0.031;		
Matches 184;	Conservative	6;	Mismatches 226;	Indels 0;
				Gaps 0;

QY	17	CGTCCTGCTGCGCAGCTGGGAAAGCCCTGAGCCCCCGGCCACCCCCCGGATGCGCGCGCTCC	76
Db	1943	CCTCCTCCAGCAGCTGCCGCTGCTGCTCCCCCTGCTCCGCTCTGGGCCCGACCGGATCA	1884
QY	77	CCGTCGCCGAGCCGCTGGGCTCCCTGCTGCGCAGCCACTACCGCAGGTGTCGCCGCTGGC	136
Db	1883	ACTCCTGCTCCGCGGCGCAGGCGCTGCTGCGCGGTGCTTCGCCAGCTGCGCGCTGTCT	1824
QY	137	CACGTTGTCGCGCGCGCTGGGGCCCCCAGAGGCTGGCGGCTGCTGTCAGCGCGGGACCCGGC	196
Db	1823	CCAGCTCTGTTCAGCCAGCTCCCGCTRCCGACGCGCTGCTCTCCGCTTGGCGGCGC	1764
QY	197	GCGTTCCGCGCGCTGCTGAGCCAGTGCCTGTGTGCTGCCCTGGAGCAGCGGCGCC	256
Db	1763	GCGGCGCTGCGCGCTCGGCTCTCTCTCTGCTTTCAGCCTCGGCTGCGCCAGGCTCT	1704
QY	257	CCCCGCGCCCCCTCTTCCGCCAGGTGTCCTGCTGAAGAGCTGTGCGCCGAGTGT	316
Db	1703	TCTGCTGCRSACACTCTCCGCTGCAGCCGACGCCGTAGCGCTCGTTGGCCTTAGCT	1644
QY	317	GCAGAGCTGTGCGAAGCGCGCGGCGAAGAACGTGTGCGCTTCGGCTTCGCGCTGTGA	376
Db	1643	GCCAGCGCTCCAGCTSCCGCTCTGCTCTCTCRGCGCGCGCTCGGCTCRGCTGTGCT	1584
QY	377	CGGGGCCCCGCGGGGCCCCCGAGGCTTACCAACCAAGCTGCGCAGCTACTTGC	432
Db	1583	GTGCGCGCGCTCAGCTCTCTCCCGCAGCTGTGCCACAGCCACAGTGTCTCTCTGC	1528

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Search completed: March 1, 2004, 23:56:46
Job time : 58.1579 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 17:50:03 ; Search time 6059.79 Seconds

(without alignments)
18844.394 Million cell updates/sec

Title: US-09-424-686F-10

Perfect score: 3824

Sequence: 1 gtttcagcagcgcgtgcgtc.....aaaaaaaaaaaaaaaa 3824

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_estbda: *
2: em_estbnu: *
3: em_estlin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_hic: *
9: gb_est1: *
10: gb_est2: *
11: gb_hic: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1255.4	32.8	1826	29 AY407349	AY407349 Homo sapi
2	980	25.6	1584	29 AY407350	AY407350 Pan trogl
3	628.2	16.4	1835	29 AY407351	AY407351 Mus muscu
4	465.4	12.2	468	10 AW270031	AW270031 xv57e03.x

5	445	11.6	492	12 BM824748	BM824748 K-EST0096
6	441.6	11.5	925	12 BM453198	BM453198 AGENCOURT
7	419	11.0	851	12 BG917907	BG917907 602820830
8	416	10.9	416	10 AW276315	AW276315 xrl0b12.x
9	385.8	10.1	389	9 AA281296	AA281296 zt08g02.r
10	379.6	9.9	851	13 BU702370	BU702370 UI-M-F10-
11	346.2	9.1	688	14 CF531121	CF531121 UI-M-FY0-
12	340.4	8.9	649	14 CF531069	CF531069 UI-M-FY0-
13	322	8.4	599	10 BB618671	BB618671 BB618671
14	317.8	8.3	664	13 BQ258274	BQ258274 NISC_Kp11
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16	290.8	7.6	614	10 BB651920	BB651920 BB651920
17	284.4	7.4	315	9 AA748707	AA748707 ny02e05.s
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19	249.6	6.5	409	9 AA311750	AA311750 EST182469
20	248.8	6.5	679	10 BE396606	BE396606 601289077
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22	243.2	6.4	649	10 BE514070	BE514070 601316575
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25	208.6	5.5	779	10 BE268183	BE268183 601125261
26	203.8	5.3	336	13 BY775178	BY775178 BY775178
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28	200.6	5.2	338	13 BY784804	BY784804 BY784804
29	192.2	5.0	326	13 BY149368	BY149368 BY149368
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33	160.4	4.2	775	12 BI388013	BI388013 BFL26_002
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35	150.4	3.9	668	14 CA380121	CA380121 659344 NC
36	148	3.9	148	9 AI824948	AI824948 wb04c01.x
37	132	3.5	641	28 AZ972318	AZ972318 2M0246F07
38	128.8	3.4	875	13 BU122597	BU122597 603148441
39	123.8	3.2	813	12 BG198331	BG198331 RST17589
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41	114.8	3.0	739	13 BX315053	BX315053 BX315053
42	113.4	3.0	568	13 BX521269	BX521269 BX521269
43	113.2	3.0	732	13 BX889962	BX889962 BX889962
44	111.8	2.9	534	10 AW318894	AW318894 un09a02.Y
45	107.4	2.8	366	10 BF511837	BF511837 UI-H-B14-

ALIGNMENTS

RESULT 1
AY407349
LOCUS
DEFINITION
Homo sapiens TERT gene, VIRUTAL TRANSCRIPT, partial sequence.
ACCESSION
AY407349
VERSION
AY407349.1 GI:39763320
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1826)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 1826)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering

them based on alignment.

FEATURES

Location/Qualifiers

1.1826

/organism="Homo sapiens"

/mol_type="genomic DNA"

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/gene="TERT"

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gene

ORIGIN

Query Match 32.8%; Score 1255.4; DB 29; Length 1826;

Best Local Similarity 82.6%; Pred. No. 8e-145;

Matches 1509; Conservative 0; Mismatches 99; Indels 218; Gaps 2;

1636 GGGTTGCTGTCTCCGGCCGACAGACCGTCTGCTGAGGAGATCCTGGCCAGTTCC 1695
1 GGGTTGCTGTCTCCGGCCGACAGACCGTCTGCTGAGGAGATCCTGGCCAGTTCC 60
1696 TGCACCTGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCTTTCTTATGTCAGG 1755
61 TGCACCTGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCTTTCTTATGTCAGG 120
1756 AGACCACGTTTCAAAAGACAGGCTTTTCTTACCGGAAGAGTGTCTGAGCAAGTTGC 1815
121 AGACCACGTTTCAAAAGACAGGCTTTTCTTACCGGAAGAGTGTCTGAGCAAGTTGC 180
1816 AAAGCATTTGATCAGACAGCAGCTTGAAGAGGCTGACGCTGCGGAGAGTGTCTGAGCAAG 1875
181 AAAGCATTTGATCAGACAGCAGCTTGAAGAGGCTGACGCTGCGGAGAGTGTCTGAGCAAG 240
1876 AGGTACAGGAGCATTCGGGAAGCCAGGCCCCCTGCTGACGTCAGACTCCGCTTCAATCC 1935
241 AGGTACAGGAGCATTCGGGAAGCCAGGCCCCCTGCTGACGTCAGACTCCGCTTCAATCC 300
1936 CCAAGCTGACGGGCTGCGGCGGATTTGTGAACATGAGTACGTCGTGGAGCCAGAACGT 1995
301 CCAAGCTGACGGGCTGCGGCGGATTTGTGAACATGAGTACGTCGTGGAGCCAGAACGT 360
1996 TCCGACAGAAAAGAGGGCCGAGCGCTTCACTCGAGGGTGAAGGCACTGTTCAAGCTGC 2055
361 TCCGACAGAAAAGAGGGCCGAGCGCTTCACTCGAGGGTGAAGGCACTGTTCAAGCTGC 420
2056 TCAACTACGAGCGGGCGCGGCGGCTCTGCGGCGCTCTGTGCTGGGCGCTGACG 2115
421 TCAACTACGAGCGGGCGCGGCGGCTCTGCGGCGCTCTGTGCTGGGCGCTGACG 480
2116 ATATCCACAGGGCTGCGCAGCTTCTGCTGCTGCTGCGGCGCAGGACCCGCGCTG 2175
481 ATATCCACAGGGCTGCGCAGCTTCTGCTGCTGCTGCGGCGCAGGACCCGCGCTG 540
2176 AGCTGTACATCCCCCAGACAGGCTCAGGAGGTGATCGCCAGCA----- 2220
541 AGCTGTACTTGTCAAGNN 600
2221 ----- 2220
601 NNN 660
2221 ----- 2220
661 NNN 720
2221 ----- 2220
721 CCTTGACAGACCTCAAGCCGTACATGCGAGAGTTGCTGCTCACTGACAGAGACCAAGCC 780
2248 TCGCTCGGTATGCGGTGTC----- 2267
781 CGCTGAGGAGTGCCTGCTCATCGACAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840

2268 -----CAGAGGCCGCCCATGGGACAGTCCGCAAGGCTTCAAGAGCAAGTCT 2317
841 NNN 900
2318 ACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTGACGCTGT 2377
901 ACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTGACGCTGT 960
2378 GCTACGCGCAGATGAGAACAGAGTGTTCGCGGGATTCCGGCGGAGACGGGCTGCTCTGC 2437
961 GCTACGCGCAGATGAGAACAGAGTGTTCGCGGGATTCCGGCGGAGACGGGCTGCTCTGC 1020
2438 GTTGGTGAATGATTTCTTGTGTGACACCTCACCCTCACCCACGCGAAACCTTCTCTCA 2497
1021 GTTGGTGAATGATTTCTTGTGTGACACCTCACCCTCACCCACGCGAAACCTTCTCTCA 1080
2498 GGACCTGTGTCGAGGAGTGTCCCTGAGTATGCTGCGTGTGAACTTCCGGAAGACAGTGG 2557
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2738 AGGCTGGAGAAACATGCGTGCAGAACTTTGGGGCTTTGGGGCTGGAAGTGCACAGCC 2797
1321 AGGCTGGAGAAACATGCGTGCAGAACTTTGGGGCTTTGGGGCTGGAAGTGCACAGCC 1380
2798 TGTTCGTGAATTTGACAGGTGAACAGCTCCAGACGCTGTGACACCAATCTACAGATCC 2857
1381 TGTTCGTGAATTTGACAGGTGAACAGCTCCAGACGCTGTGACACCAATCTACAGATCC 1440
2858 TCCTGCTGACGCGTACAGAGTTTCAAGCATGTGTGCTGACGCTCCATTTCATCAGCAAG 2917
1441 TCCTGCTGACGCGTACAGAGTTTCAAGCATGTGTGCTGACGCTCCATTTCATCAGCAAG 1500
2918 TTTGGAAGAACCCACATTTTCTGCGGCTGATCTGTGACACGAGCTCCCTCTGCTACT 2977
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2978 CCATCTGAAAGCCAAAGACGAGGATGTGCTGAGGCGCAAGGGCGCGCGGCGCTC 3037
1561 CCATCTGAAAGCCAAAGACGAGGATGTGCTGAGGCGCAAGGGCGCGCGGCGCTC 1620
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1681 ACCGTGTACCTACGTGCCACTCTGCGGCTCACTCAGACAGCCAGACGAGCTGAGTC 1740
3158 GGAAGCTCCCGGGGAGCAGCGCTGACTCCCTGAGGCGCGCAGCCAAACCCGCACTGCCCC 3217
1741 GGAAGCTCCCGGGGAGCAGCGCTGACTCCCTGAGGCGCGCAGCCAAACCCGCACTGCCCC 1800
3218 CAGACTTCAAGACCATCTGACTGA 3243
1801 CAGACTTCAAGACCATCTGACTGA 1826

RESULT 2
AY407350
LOCUS AY407350 1584 bp DNA linear GSS 15-DEC-2003

DEFINITION	Pan troglodytes TERT gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION	AY407350
VERSION	AY407350.1 GI:39763321
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.U., Adams,M.D. and Cargill,M.
TITLE	Interferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL	Science 302 (5652), 1960-1963 (2003)
PUBMED	14671302
REFERENCE	2 (bases 1 to 1584)
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.U., Adams,M.D. and Cargill,M.
TITLE	Direct Submission
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES	Location/Qualifiers
source	1..1584
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	/mol_type="genomic DNA"
	/db_xref="taxon:9598"
	<1..>1584
	/gene="TERT"
ORIGIN	/locus_tag="HCM2861"
Query Match	25.6%; Score 980; DB 29; Length 1584;
Best Local Similarity	78.2%; Pred. No. 5e-111;
Matches 1239; Conservative	0; Mismatches 127; Indels 218; Gaps 2;
QY	1636 GGGTTGGCTGTGTTCCGGCCGACAGACACCGTGTGCGTAGAGAGATCCTGGCCAAAGTTC 1695
DB	1 GGGTTGGCTGTGTTCCGGCCGACAGACACCGTGTGCGTAGAGAGATCCTGGCCAAAGTTC 60
QY	1696 TGCACCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTATATGACGG 1755
DB	61 TGCACCTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTATATGACGG 120
QY	1756 AGACCACGTTTCAAAAGAACACAGGCTCTTTTCTACCGGAAGTGTCTGAGCAAGTTGC 1815
DB	121 AGACCACGTTTCAAAAGAACACAGGCTCTTTTCTACCGGAAGTGTCTGAGCAAGTTGC 180
QY	1816 AAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTCCGAAGCAG 1875
DB	181 AAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTGTCCGAAGCAG 240
QY	1876 AGGTACGACGATCGGGAAAGCCAGGCCGCCCTGTGACGTCCAGACTCCGGCTTATCC 1935
DB	241 AGGTACGACGATCGGGAAAGCCAGGCCGCCCTGTGACGTCCAGACTCCGGCTTATCC 300
QY	1936 CCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGAGCCAGAACGT 1995
DB	301 CCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTCGTGGGAGCCAGAACGT 360
QY	1996 TCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTACGGGTGC 2055
DB	361 TCCGACAGAAAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAGGCACTGTTACGGGTGC 420
QY	2056 TCAACTACGAGCGGGCGCGCGCCCGCGGCTCTCTGGCGGCTCTGTGCTGGGCTTGAACG 2115
DB	421 TCANNACGAGCGGGCGCGCGCCCGCGGCTCTCTGGCGGCTCTGTGCTGGGCTTGAACG 480

QY	2116	ATATCCACAGGCGCTGGCGCACCTTCGTGCTCGCTGTGCGGGCCCAAGACCCGCCCTG	2173
Db	481	ATATCCACAGGCGCTGGCGCACCTTCGTGCTCGCTGTGCGGGCCCAAGACCCGCCCTG	540
QY	2176	AGCTGTACATCCCCCAGGACAGGCTCACGGAGGTCAATGCCAGCATCATCAA-----	2228
Db	541	AGCTGTACTTTGTCAAGNN	600
QY	2229	-----	2228
Db	601	NN	660
QY	2229	-----	2228
Db	661	NN	720
QY	2229	-----	2228
Db	721	CCTTGACAGACCTCCAGCCGTACATGCCAGATTGCTGCTCACCTGCAGAGACCAAGCC	780
QY	2248	TGCGTCGTATGCGCTGCTC-----	2267
Db	781	CAGTGGAGGATGCCGTTCATCATCGAGCAGNNNNNNNNNNNNNNNNNNNNNNNNNNNN	840
QY	2268	-----CAGAGGCCGCCCATGCGCAGCTCCGCAAGCCTTCAAGAGCAAGTCTT	2317
Db	841	NN	900
QY	2318	ACGTCCAGTGCAGGGGATCCCGCAGGCTCCATCCTCTCCACGCTGCTGACGCTGT	2377
Db	901	ACGTCCAGTGCAGGGGATCCCGCAGGCTCCATCCTCTCCACGCTGCTGACGCTGT	960
QY	2378	GCTACGGCGACATGAGAAACAAGCTGTTTGGCGGATTCGGCGGAGACGGGCTGCTCTGC	2437
Db	961	GCTACGGCGACATGAGAAACAAGCTGTTTGGCGGATTCGGCGGAGACGGGCTGCTCTGC	1020
QY	2438	GTTTGGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGCGAAACCTTCTCA	2497
Db	1021	GTTTGGTGATGATTTCTTGTGTGTGACACCTCACCTCACCCACGCGAAACCTTCTCA	1080
QY	2498	GGAACCTGTCGCGAGGTGTCCTGAGTATGGCTGCTGCTGTAACCTGCGGAAGACAGTGG	2557
Db	1081	NGAACCTGTCGCGAGGTGTCCTGAGTATGGCTGCTGCTGTAACCTGCGGAAGACAGTGG	1140
QY	2558	TGAACCTCCCTGTAGAAAGACGAGGCCCTGGGTGCGACGGCTTTGTTAGATGCCGCC	2617
Db	1141	TGAACCTCCCTGTAGAAAGATGAGCCCTGGGTGCGACGGCTTTGTTAGATGCCGCC	1200
QY	2618	ACGGCTATTCCTGCTGCTGCGGCTGCTGCTGATACCCGGACCTGAGGTGACAGCG	2677
Db	1201	ACGGCTATTCCTGCTGCTGCGGCTGCTGCTGATACCCGGACCTGAGGTGACAGCG	1260
QY	2678	ACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGCTTCA	2737
Db	1261	ACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGCTTCA	1320
QY	2738	AGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGTGAAGTTCACAGCC	2797
Db	1321	AGGCTGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGGCGTGAAGTTCACAGCC	1380
QY	2798	TGTTCTGATTTGACGTGAACAGACCTCCAGACGGTGTGCAACCAACATCTAACAGATCC	2857
Db	1381	TGTTCTGATTTGACGTGAACAGACCTCCAGACGGTGTGCAACCAACATCTAACAGATCC	1440
QY	2858	TCCTGCTGACGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCCATTTTATCAGCAAG	2917
Db	1441	TCCTGCTGACGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCCATTTTATCAGCAAG	1500
QY	2918	TTTGAAGAACCCACATTTTTTCTGCGGCTCATCTTGACACGGCCTCCCTCTGCTACT	2977
Db	1501	TTTGAAGAACCCACATTTTTTCTGCGGCTCATCTTGACACGGCCTCCCTCTGCTACT	1560

[illegible]

RESULT 3
AY407351

LOCUS	AY407351	1835 bp	DNA	linear	GSS 15-DEC-2003
DEFINITION	Mus musculus TERT gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				

ORIGIN

Query Match	16.4%;	Score 628.2;	DB 29;	Length 1835;
Best Local Similarity	61.5%;	Pred. No. 6.9e-68;		
Matches 1128; Conservative	0;	Mismatches 480;	Indels 227;	Gaps 4;

QY	1636	GGGTGGCTGTGTTCCGGCCGACAGACACCGCTGCGCTAGAGAGATCCTGGCCAAAGTTCC	1693
Db	1	GGAAGGACCGTGTCGCCCTGCAGAGACCGCTGTGAGGAGAGGATCCTGGCTACGTTCC	60
QY	1696	TGCACCTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGCTTTCTTTATGTACGG	1755
Db	61	TGTTCTGGCTGATGAGACATACGTGTACAGCTGCTTAGGTCAATCTTTACATCACAG	120
QY	1756	AGACCACGTTTCAAAAGAACAGAGCTCTTTTCTACCCGGAAGTGTCTGAGCAAGTTGC	1815
Db	121	AGAGCACATTCAGAGAACAGAGCTCTTCTTCTACCGTAAGAGTGTGTGAGCAAGCTGC	180
QY	1816	AAAGCATTTGAATCAGACAGCACTTGAAGAGGTCAGCTGCGGAGCTGTCGAAGCAG	1875
Db	181	AGAGCATTTGAGTCAGGCAACACCTTGAGAGAGTGGGCTACGGGAGCTGTCAACAAGAG	240
QY	1876	AGGTCAGGCAGCATCGGGAAGCCAGGCCGCCCTGTGAAGTCCAGACTCCGCTTCATCC	1935
Db	241	AGGTCAGGCATCACCAAGACACCTGGCTAGCCATGCCCATCTGCAGACTGCGCTTCATCC	300
QY	1936	CCAAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGAATACGTCTGTGGAGCCAGAACGT	1995
Db	301	CCAAAGCCCAACGGGCTGCGGCCCATTTGTGAACATGAGTTATAGCATGGGTACCAAGCTT	360

QY	1996	TCCGAG-AGAAAAGAGGGCCGAGCGCTCAACCTCGAGGGTGAAGGCACTGTTCAAGCTG	2054
Db	361	TGGGAGAAAGAGGAGGGCCAGCATTTCAACCCAGCGTCTAAGACTCTCTCAGCATG	420
QY	2055	CTCAACTACGAGCGGGCGGGCGCCCGGCTCTGGGGCGCTCTGTGCTGGGCTGGAC	2114
Db	421	CTCACTATGAGCGGACAAACATCTCTCACTTATGGGGTCTTCTGTACTGGGTATGAAT	480
QY	2115	GATATCCACAGGGGCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGAACCCGCGCT	2174
Db	481	GACATCTACAGGACCTGGCGGGCTTTGTGCTGCGTGTGCGTCTTGACACAGACACC	540
QY	2175	GAGCTGTACATCCCCCAGGACAGGCTCACGGAGGTATCGCCAGCATCATCAACCCAG	2234
Db	541	AGGATGTACTTTGTTAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	600
QY	2235	AACACGTACTGCGTGCCTCGGTATGCGGTGTCAGAAG-----	2273
Db	601	NN	660
QY	2274	-----	2273
Db	661	NN	720
QY	2274	-----GCCGCCATGGGACGTCCGCAAGGCT-----	2301
Db	721	ACCCTCTGACCTCCAGCCATACATGGGCCAGTTCCTTAAGCATCTGCAGATTCAAT	780
QY	2302	-----	2301
Db	781	GCCAGTCACTGAGGAATCCGTTGTATCATGACAGCAGNNNNNNNNNNNNNNNNNNNN	840
QY	2302	-----TCAGAAGGC	2310
Db	841	NN	900
QY	2311	AAGTCCCTACGTCAGTCCAGGGGATCCCGCAGGCTCCATCCTCTCACGCTGCTGC	2370
Db	901	MMGTGTATACGACGTGCCAGGCGATCCCCCAGGGCTCCAGCCTATCACCTGCTGCG	960
QY	2371	AGCCTGTGCTACGGCGCATGAGAAACAAGCTTTGCGGGATTCGCGGGAACGGGCTG	2430
Db	961	AGTGTGTTCGAGAGCATGAGAAACAAGCTTTGCTGAGGTGACGCGGATGGGTTG	1020
QY	2431	CTCCTGCGTTGGTGGATGATTTCTGTTGGTGACACCTCACCTCACCCACGCAAAAAC	2490
Db	1021	CTTTACGTTTGTGATGACTTCTGTTGGTGACGCTCACCTTGACCAAGCAAAAAC	1080
QY	2491	TTCCTCAGACCTCGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAATTCGCGAAG	2550
Db	1081	TTCCTCAGACCTCGTCCGAGGTGTCCTGAGTATGGCTGCGTGGTGAATTCGCGAAG	1140
QY	2551	ACAGTGTGAATTCCTCTGTAGAGACGAGGCCCTGGGTGGCACGGCTTTGTTCAATG	2610
Db	1141	ACAGTGTGAATTCCTCTGTAGAGACGAGGCCCTGGGTGGTGACCTCCATCAAGACTG	1200
QY	2611	CCGGCCCAACGGCTATTCCTCTGTGCGGCTGCTGCTGATACCCGGAACCTGGAAGTG	2670
Db	1201	CCTGCTCACTGCTGTTTCCTCTGTGCGGCTGCTGCTGATACCCGGAACCTGGAAGTG	1260
QY	2671	CAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAAGAGCCAGTCTCACTTCAACCGC	2730
Db	1261	TTCTGTGACTACTCAGGTTATGCCAGAGCTCAATTAAAGCAGGCTCACCTTCCAGAGT	1320
QY	2731	GGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	2790
Db	1321	GTCTTCAAGGCTGGGAGGAACATGCGGAGCAAGCTCCTGTCCGCTCTTGCGGTTGAAGTG	1380
QY	2791	CACAGCCTGTTCTGGATTGCAAGGTGAACAGCCTCCAGACGCGTGTGACCAACATCTAC	2850
Db	1381	CACGCTATTTCTAGACTTGCAAGGTGAACAGCCTCCAGACAGTCTGCAATATATATAC	1440

QY 2851 AAGATCCTCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCCATTTCAT 2910
Db 1441 AAGATCTTCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCCATTTCAT 1500
QY 2911 CAGCAAGTTTGAAGAACCCACATTTTCTGCGCTCATCTGTGACACGCGCTCCCTC 2970
Db 1501 CAGCGTTTGAAGAACCCACATTTTCTGCGCTCATCTGTGACACGCGCTCCCTC 1560
QY 2971 TGCTACTCCATCTGAAAGCCAGAGGAGGATGTGCTGG--GGGCCAAGGCGCGC 3028
Db 1561 TGCTATGCTATCTGAAAGGTCAGAGATCCAGATCCCGCCAGAGATGACACTAAAGGCT 1620
QY 3029 CCGGCCCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTTCTGCTCAAGC 3088
Db 1621 CTGGCTCTCTTCTCTGAGGCGGCACATGTGCTGTACAGGCTTCTGCTCAAGC 1680
QY 3089 TGAATCGACACCGGTGACCTACGTGCTGCTGGGTCTGCTGAGACAGAGCCAGAGCG 3148
Db 1681 TGCTGCTCATTTCTGATCTCAATATGTCTCTGGGACCTCTGAGACAGCCCAAAAC 1740
QY 3149 AGCTGAGTGGAGAGTCCCGGGGAGCAGCGCTGACTGCGCTGAGGCGGAGCCAGCCCG 3208
Db 1741 TGCTGTGCGGAGCTCCAGAGGCGGACATGACCATCTTAAGCTGCAAGCTGACCCAG 1800
QY 3209 CACTGCCCTCAGACTTCAAGACCATCTGAGCTGA 3243
Db 1801 CCTAAGACAGACTTTTCAAGACCATTTTGAAGCTAA 1835

RESULT 4
AM270031/c 468 bp mRNA linear EST 03-JAN-2000
LOCUS xv57e03.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2817244 3',
DEFINITION mRNA sequence.

ACCESSION AM270031
VERSION AM270031.1 GI:6657061

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 468)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov

REFERENCE Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
www-bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 416.

FEATURES

source 1..468
Location/Qualifiers
1..468
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2817244"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu28"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies."

ORIGIN

Query Match 12.2%; Score 465.4; DB 10; Length 468;

Best Local Similarity 99.6%; Pred. No. 9.5e-48;
Matches 466; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3332 CACCCAGGCGCCGACCGCTGGAGTCTGAGCGCTGAGTGTGCGGAGGCGCTGCA 3391
Db 468 CACCCAGGCGCCGACCGCTGGAGTCTGAGCGCTGAGTGTGCGGAGGCGCTGCA 409
QY 3392 TGTCGGCTGAAGGCTGAGTGTGCGGCTGAGCGCTGAGCGAGTGTCCAGCCAAAGGCTGA 3451
Db 408 TGTCGGCTGAAGGCTGAGTGTGCGGCTGAGCGCTGAGCGAGTGTCCAGCCAAAGGCTGA 349
QY 3452 GTGTCAGACACCTGCGCTCTTCACTTCCCAAGGCTGAGCGCTGAGCGCTGAGCGCTGAG 3511
Db 348 GTGTCAGACACCTGCGCTCTTCACTTCCCAAGGCTGAGCGCTGAGCGCTGAGCGCTGAG 289
QY 3512 GCCAGCTTTTCTGACAGAGAGCGCGCTTCCACTCCCAATAGATAGTCCATCCCC 3571
Db 288 GCCAGCTTTTCTGACAGAGAGCGCGCTTCCACTCCCAATAGATAGTCCATCCCC 229
QY 3572 AGATTGCGCATTTTCAACCCCTGCGCTCTTCTGCTTCAACCCCAACCATCCAG 3631
Db 228 AGATTGCGCATTTTCAACCCCTGCGCTCTTCTGCTTCAACCCCAACCATCCAG 169
QY 3632 GTGAGAGCCCTGAGAGAGAGCCCTGGAGCTCTGGAATTGAGTGAACCAAGGTGTGCC 3691
Db 168 GTGAGAGCCCTGAGAGAGAGCCCTGGAGCTCTGGAATTGAGTGAACCAAGGTGTGCC 109
QY 3692 CTGTACACAGGCGGAGAGCCCTGACCTGATGGGGGTCCCTGTGGTCAATTGGGGGGA 3751
Db 108 CTGTACACAGGCGGAGAGCCCTGACCTGATGGGGGTCCCTGTGGTCAATTGGGGGGA 49
QY 3752 CGTGTGTGGGAGTAAATATCTGATATATGAGTTTTCAGTTTGA 3799
Db 48 CGTGTGTGGGAGTAAATATCTGATATATGAGTTTTCAGTTTGA 1

RESULT 5

BM824748 492 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0096335 S22SN16n1 Homo sapiens cDNA clone S22SN16n1-99-E07

DEFINITION 5', mRNA sequence.
ACCESSION BM824748
VERSION BM824748.1 GI:19181161

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 492)

AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 99 row: E column: 07
High quality sequence stop: 492.

FEATURES

source 1..492
Location/Qualifiers
1..492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SN16n1-99-E07"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"

ORIGIN

/lab_host="DH10B"
/clone_lib="S22SNU16n1"
/note="Organ: Stomach; Vector: pT73-Pac; Site 1: EcoRI;
Site 2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research, 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

Query Match 11.6%; Score 445; DB 12; Length 492;
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 GTGAATTCCTCTGTAGAAGACGAGGCGCTTGGTGGACCGCTTTTGTTCAGATGCCGCC 2616
DB 1 GTGAATTCCTCTGTAGAAGACGAGGCGCTTGGTGGACCGCTTTTGTTCAGATGCCGCC 60
QY 2617 CACGGCTATTCCTCTGTGGCGGCTGTGTGATACCCCGACCTGGAGGTGACAGC 2676
DB 61 CACGGCTATTCCTCTGTGGCGGCTGTGTGATACCCCGACCTGGAGGTGACAGC 120
QY 2677 GACTACTCCAGTATGCCCCGACCTCATCAGAGCCAGTCTCACTTCAACCGCGCTTC 2736
DB 121 GACTACTCCAGTATGCCCCGACCTCATCAGAGCCAGTCTCACTTCAACCGCGCTTC 180
QY 2737 AAGGCTGGAGAACATGCGTCCAACTCTTGGGGTCTTGGCGGCTGAAGTGTACAGC 2796
DB 181 AAGGCTGGAGAACATGCGTCCAACTCTTGGGGTCTTGGCGGCTGAAGTGTACAGC 240
QY 2797 CTGTTCTGATTTGACAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTACAGATC 2856
DB 241 CTGTTCTGATTTGACAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTACAGATC 300
QY 2857 CTCCTGTCAGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCCATTTTCATGACAA 2916
DB 301 CTCCTGTCAGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCCATTTTCATGACAA 360
QY 2917 GTTGAAGAACCCCAATTTTCTGCGGCTCATCTGTGACAGGCTCCCTCTGTAC 2976
DB 361 GTTGAAGAACCCCAATTTTCTGCGGCTCATCTGTGACAGGCTCCCTCTGTAC 420
QY 2977 TCCATCTGAAGCAAGACGAG 3001
DB 421 TCCATCTGAAGCAAGACGAG 445

RESULT 6
BM453198 925 bp mRNA linear EST 05-FEB-2002
LOCUS AGENCOURT_6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840
DEFINITION 5', mRNA sequence.

ACCESSION BM453198
VERSION BM453198.1 GI:18502238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 925)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM1208 row: p column: 01
High quality sequence stop: 646.
Location/Qualifiers
1. 925

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5529840"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN

Query Match 11.5%; Score 441.6; DB 12; Length 925;
Best Local Similarity 95.7%; Pred. No. 6.5e-45;
Matches 465; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

QY 2280 CATGGGACGTCGCCAAGCGCTTCAAGAGCAAGTCTTACGTTCCAGTCCAGGGGATCCC 2339
DB 344 CATGGGACGTCGCCAAGCGCTTCAAGAGCAAGTCTTACGTTCCAGTCCAGGGGATCCC 403
QY 2340 GCAGGGCTCATCTCTCTCCACCGCTGTCTGACGCTGTGTACGCGACATGAGAGACA 2399
DB 404 GCAGGGCTCATCTCTCTCCACCGCTGTCTGACGCTGTGTACGCGACATGAGAGACA 463
QY 2400 GCTGTTGGGGGATTCGGCGGAGCGGCTGCTCTGCTGCTTGTGATGATTTCTTGT 2459
DB 464 GCTGTTGGGGGATTCGGCGGAGCGGCTGCTCTGCTGCTTGTGATGATTTCTTGT 523
QY 2460 GGTGACACCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 2519
DB 524 GGTGACACCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 583
QY 2520 TGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2579
DB 584 TGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 643
QY 2580 GGCCCTGGTGGACAGCGCTTTTGTTCAGATGCGGCGCCAGGCTATTTCCCTGTGCG 2639
DB 644 GGCCCTGGTGGACAGCGCTTTTGTTCAGATGCGGCGCCAGGCTATTTCCCTGTGCG 703
QY 2640 CCTGCTGTGATACCCGAGACCTTGAAGGTGACAGGCACTACTCCAGCTATGCCGAC 2699
DB 704 CCTGCTGTGATACCCGAGACCTTGAAGGTGACAGGCACTACTCCAGCTATGCCGAC 763
QY 2700 CTCCATGAGACGAGTCTCACTTCAACCGCGGCTTCAA--GGCTGGAGGAACATGCGT 2757
DB 764 CTCCATGAGACGAGTCTCACTTCAACCGCGGCTTCAAAGGCTGGAGGAACATGCGT 823
QY 2758 CGCAAA 2763
DB 824 CGCAAA 829

RESULT 7
BG917907 851 bp mRNA linear EST 05-JUN-2001
LOCUS BG917907
DEFINITION 602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
mRNA sequence.
ACCESSION BG917907
VERSION BG917907.1 GI:14298383
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: L1M10903 row: k column: 08
High quality sequence stop: 753.
Location/Qualifiers

FEATURES

source

1. 851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4949887"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam6"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match 11.0%; Score 419; DB 12; Length 851;
Best Local Similarity 71.9%; Pred. No. 4e-42;
Matches 579; Conservative 0; Mismatches 215; Indels 11; Gaps 2;
QY 2440 TTGGTGAATGTTCTTGTGTGACACCTCACTCAACCGGAAACCTTCTCAGG 2499
DB 38 TTGTGTGATGATCTTCTGTAGTGACCTCACTTGACCAAGCAAAACCTTCTCAGC 97
QY 2500 ACCCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGTGAATTGCGAAGACAGTGTG 2559
DB 98 ACCCTGTCATGGCGTCTCTGAGTATGGGTGATGATTAACCTTGAGAAAGACAGTGTG 157
QY 2560 AACTTCCCTGTAGAAGACGAGGCGCTGGGTGGACAGCGCTTTGTTCAGATGCGGCCAC 2619
DB 158 AACTTCCCTGTAGAAGACGAGGCGCTGGGTGGACAGCGCTTTGTTCAGATGCGGCCAC 217
QY 2620 GGCTATTCCTGCTGTGCGGCTGCTGTGATACCGGACCTTGAGGTGACAGCGAC 2679
DB 218 TGCTGTTCCTGCTGTGCTGTGCTGTGACACTCACTCTGAGGTGTCTGTGAC 277
QY 2680 TACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACTTCAACCGCGCTCAAG 2739
DB 278 TACTCAGGTATGCCAGACCTCAATTAAGACGAGCCTCACTTCCAGAGTGTCTCAAA 337
QY 2740 GCTGGAGGACATGCGTCAAACTTTGGGCTTTGGCGCTGAAGTGTCAAGCCTG 2799
DB 338 GCTGGAGGACATGCGGAAACAGCTCTGTGCTTGGCGTTGAAGTGTCAAGCCTG 397
QY 2800 TTTCTGATTTGACAGGTGAACAGCTCCAGACGCTGTGACCAACATCTACAGATCCTC 2859
DB 398 TTTCTGATTTGACAGGTGAACAGCTCCAGACGCTGTGACCAACATCTACAGATCCTC 457
QY 2860 CTGCTGACGGCGTACAGGTTCACGATGTGTGCTGACAGTCCCATTTCAATCAGCAAGT 2919
DB 458 CTGCTGACGGCGTACAGGTTCACGATGTGTGATTCAGCTTCCCTTGACCAAGCGTGT 517
QY 2920 TGAAGAAGACCCACATTTTCTGCGCGCTCATCTGTGACAGCGCCTCCCTCTGCTACTCC 2979
DB 518 AGGAAGACCTCACTTTCTTGGGCATCATCTCCAGCAAGCATCCTGCTGTATGCT 577
QY 2980 ATCCTGAAGCCAGAACGAGGATGTGCTGGGGCCAGGGCGCGCGCCCTCTG 3039

DB 578 ATCCTGAAGTCAAGATCCAGGATGACACTAAAGCCTCTGGCTC-----CTT 627
QY 3040 CCTCCGAGCGCGTCACTGGCTGTGCCACCAAGCATTCCT-GCTCAAGCTGACTGACA 3098
DB 628 TCCTCCTGAAGCCGACATTTGGCTCTGTACCAAGCGCTTCTGGCTCAAGCTGCTCA 687
QY 3099 CCGTTCACCTCACTGCGCACTCTGCGGTCACTCAGACAGAGCCAGACGCTGAGTCC 3158
DB 688 TTCTGTATCTCAATATGTCTCTGGAACCTCTGAGGACAGCCCAAAACCGCTGTGCC 747
QY 3159 GAAGTCCCGGGGACGACGCTGACTGCGCTGAGAGCGCCGACGCCAACCAGCTGCCCTC 3218
DB 748 GAAGCTCGAGAGCGGACCAATGATCATCTTACAGCTGACGTGACCCAGACCTAAGAC 807
QY 3219 AGACTTCAAGACCATCTGACTGA 3243
DB 808 AGACTTCAAGACCATTTGGACTAA 832

RESULT 8
AM276315/c 416 bp mRNA linear EST 03-JAN-2000
LOCUS xr10b12.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2759711 3',
DEFINITION mRNA sequence.
ACCESSION AM276315 GI:6663345
VERSION AM276315.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 416)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 413.
Location/Qualifiers

FEATURES

source

1. 416
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2759711"
/tissue_type="two pooled squamous cell carcinomas"
/lab_host="DH10B"
/clone_lib="NCI CGAP Lu28"
/note="Organ: lung; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies."

ORIGIN

Query Match 10.9%; Score 416; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1e-41;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3383 AGGCTGATGTCGCGTGAAGCTGAGTGTCCGGCTGAGGCTTGAAGAGTGTCCAGCC 3442
DB 416 AGGCTGATGTCGCGTGAAGCTGAGTGTCCGGCTGAGGCTTGAAGAGTGTCCAGCC 357
QY 3443 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGCGCTGCTC 3502
DB 356 AAGGCTGAGTGTCCAGACACCTGCGCTTCACTTCCCAAGGCTGCGCTGCTC 297

QY 3503 CACCCAGGGCCAGCTTTTCTCAGCAGAGAGCCGCTTCCACTCCCATAGAGATAG 3562
DB 296 CACCCAGGGCCAGCTTTTCTCAGCAGAGAGCCGCTTCCACTCCCATAGAGATAG 237
QY 3563 TCCATCCCGAGATTGCGCATTTGTCACTCCCTGCGCTTCCCTTGTGCTTCCACCCCC 3622
DB 236 TCCATCCCGAGATTGCGCATTTGTCACTCCCTGCGCTTCCCTTGTGCTTCCACCCCC 177
QY 3623 ACCATCCAGGTGAGAGACCCCTGAGAGACCCCTGGAGCTTGGCAATTGTGAGTACCAA 3682
DB 176 ACCATCCAGGTGAGAGACCCCTGAGAGACCCCTGGAGCTTGGCAATTGTGAGTACCAA 117
QY 3683 AGGTGTGCTGTACACAGGCGAGAGACCCCTGACCTGATGGGGGTCCCTGTGGGTCAA 3742
DB 116 AGGTGTGCTGTACACAGGCGAGAGACCCCTGACCTGATGGGGGTCCCTGTGGGTCAA 57
QY 3743 TTGGGGGAGGTGCTGTGGAGTAAATACTGATATATGAGTTTTCAGTTTGA 3798
DB 56 TTGGGGGAGGTGCTGTGGAGTAAATACTGATATATGAGTTTTCAGTTTGA 1

RESULT 9
AA281296 389 bp mRNA linear EST 14-AUG-1997
LOCUS zt08902.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
DEFINITION mRNA sequence.
ACCESSION AA281296
VERSION AA281296.1 GI:1924194
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 389)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 2187 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 385.

FEATURES
source
1.389
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:712562"
/tissue_type="germlinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germlinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTACCAATCTGAGTGGAGGCGCGCTCATTTTCTTTTCTTTT-3'
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bernaldo."

ORIGIN

Query Match 10.1%; Score 385.8; DB 9; Length 389;
Best Local Similarity 99.5%; Pred. No. 5.8e-38;
Matches 387; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1686 GCCAAGTTCCTGCACTGGCTGATGATGTGTACCTGCTGAGCTGCTAGGTCTTTCTTT 1745
DB 1 GCCAAGTTCCTGCACTGGCTGATGATGTGTGTACCTGCTGAGCTGCTAGGTCTTTCTTT 60
QY 1746 TATGTACGAGAGACCAAGCTTTCAAAAGACAGAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1805
DB 61 TATGTACGAGAGACCAAGCTTTCAAAAGACAGAGGCTCTTTTCTACCGGAAGAGTGTCTGG 120
QY 1806 AGCAAGTTGCAAAAGCATTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTG 1865
DB 121 AGCAAGTTGCAAAAGCATTGGAAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGCTG 180
QY 1866 TCGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCGCCCTGCTGACCTCAGACTC 1925
DB 181 TCGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCGCCCTGCTGACCTCAGACTC 240
QY 1926 CGCTTCATCCCAAGCCTGACGCGGCTGCGGCGCATTTGTGAACATGACTACGTCTGGGA 1985
DB 241 CGCTTCATCCCAAGCCTGACGCGGCTGCGGCGCATTTGTGAACATGACTACGTCTGGGA 300
QY 1986 GCCAAGCTTCCGAGAGAAAGAGGCGGCGGCTCTCACTCGAGGGGTGAAGGCACTG 2045
DB 301 GCCAAGCTTCCGAGAGAAAGAGGCGGCGGCTCTCACTCGAGGGGTGAAGGCACTG 360
QY 2046 TTCAGCGTGTCTCAACTACGAGCGGCGCGG 2074
DB 361 TTCAGCGTGTCTCAACTACGAGCGGCGCGG 389

RESULT 10
BU702370 851 bp mRNA linear EST 15-JUL-2003
LOCUS BU702370
DEFINITION UI-M-F10-byx-f-12-0-UI.r1 NIH BMAP_F10 Mus musculus cDNA clone
IMAGE:6400523 5', mRNA sequence.
ACCESSION BU702370
VERSION BU702370.1 GI:23627105
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 851)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov

FEATURES
source
1.851
Location/Qualifiers
Seq primer: pYX-5.

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6400523"
/tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH BMAP_F10"
/note="Organ: Brain; Vector: pYX-Abs; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bernaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose

Db 483 TGCATGATGCTACTGTGAGCCGAGTGGCGGACGACTGCTGTCTACTGCTGGCACA 542
QY 527 CTGCGCGCTCTTGTGTGCTGCTGCCAGCTGCGCCTTACCAGGTGTGCGGCGCGCT 586
Db 543 CTGTGCTCTTTATCTCTGTGTCGCCCCCAGCTGTGCTTACCAAGGAGATGGCCANGAGC 602
QY 587 GTACCACTGCGCGCTGCCACTCAGGCCCCCGCCGACACAGCTAGTGAC 639
Db 603 GTCTAACCCCTCATCTCTACTCAGCANCCTCCAGCTTACTTACTGAGGCGC 655

RESULT 12
CF531069

LOCUS 649 bp mRNA linear EST 12-SEP-2003
DEFINITION UI-M-FYO-cgp-c-19-0-UI.r1 NIH_BMAP_FYO Mus musculus cDNA clone
IMAGE:30355746 5', mRNA sequence.
ACCESSION CF531069 GI:34583033
VERSION CF531069
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 649)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: PYX-5.
FEATURES
Source 1. 649
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FYO"
/note="Organ: Brain; Vector: PYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares. Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 8.9%; Score 340.4; DB 14; Length 649;
Best Local Similarity 77.3%; Pred. No. 1.9e-32;
Matches 413; Conservative 0; Mismatches 121; Indels 0; Gaps 0;
QY 47 CCGGACACCCCGGATGCGCGGCTCCCGCTGCCGAGCCGTGGCTCCCTGCTGCG 106
|||||

Db 26 CCGGCGCTTGAGCACAATGACCCGCGCTCCTGTTGCCCGCGGTGCGCTCTCTGCG 85
QY 107 CAGCCACTACCGGAGGTGCTGCCGCTGGCCACGTTGTCGGCGCCTGGGGCCCAAGG 166
Db 86 CAGCCGATACCGGAGGTGCTGCCGCTGGCCACGTTGTCGGCGCCTGGGGCCCAAGG 145
QY 167 CTGCGCGCTGCTGTCAGCGCGCGGAGACCCGCGGCTTCCGCGCGCTGTCAGTGCC 226
Db 146 CAGCGGCTTGTGCAACCCCGGAGACCCGAGATCTACCGCACTTGTGTCGCAATGCT 205
QY 227 GGTGTGCGTGGCTGGGAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 286
Db 206 AGTGTGATGCACTGGGGCTCAGCGCTCCACCTGCGGACCTTCTTCCACGAGTGT 265
QY 287 CTGCTGAAGAGAGCTGTGGCGCGCGAGTGTGTCAGAGCTGTGCGAGCGCGCGAGAA 346
Db 266 ATCCCTGAAGAGAGCTGTGGCGCGAGGTGTGTCAGAGACTGTGCGAGCGCAAGAGAA 325
QY 347 CGTGTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 406
Db 326 CGTGTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 385
QY 407 CACCACAGCGGTGCGCAGCTAAGTCCCAACAGCGTGAACGACGCTGCGGAGAGCGG 466
Db 386 CACTAGTAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 445
QY 467 GCGGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
Db 446 TGCATGATGCTACTGTGAGCCGAGTGGGCGAGCACTGTGTCTACTGCTGGCACA 505
QY 527 CTGCGCGCTCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 580
Db 506 CTGTGCTCTTTATCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559

RESULT 13
BB618671

LOCUS 599 bp mRNA linear EST 26-OCT-2001
DEFINITION BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus
cDNA clone 5730412M20 5', mRNA sequence.
BB618671
BB618671.1 GI:16458173

ACCESSION BB618671
VERSION BB618671
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 599)
AUTHORS Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Komno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

TITLE BB618671
JOURNAL
COMMENT

Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.

FEATURES

Source

Location/Qualifiers

1. 599
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="5730412M20"
/sex="mixed"
/dev_stage="8 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 8 days embryo"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',
GAGAGAGAGAGATCCAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rct = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGATCTCGAGTAAATTAATATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI."

ORIGIN

Query Match 8.4%; Score 322; DB 10; Length 599;
Best Local Similarity 74.9%; Pred. No. 3.5e-30;
Matches 403; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 9 CAGCGCTGCTCTGTCGCGACGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCG 68
DB 61 CACCCCTGCATCTTGTTCCCGCAGCTGGAGAGGCCCATCCGGCTTGAGCACATGACC 120
QY 69 CGCGTCCCGCTGCGAGCCGTGGCTCTCTGCTGCGAGCCACTACCGCGAGGTCTG 128
DB 121 CGCGCTCTGCTGTCGCCCGCGGTGGCTCTCTGCTGCGAGCCGATACCGGAGGTGG 180
QY 129 CGCGTGGCAGCTTGTGCGCGCGCTGGGGCCCGAGGGTGGCGGCTGTGACGCGGG 188
DB 181 CCGCTGGCACTTTGTGCGCGCGCTGGGGCCCGAGGGCAAGCGGCTTGTGCAACCCGG 240
QY 189 GACCCGCGGCTTTCCGCGCGCTGGTGGCCAGTGGCTGTGCGTGGCTGGGAGCGA 248
DB 241 GACCCGAGATCTACCGCACTTTGTTGCCCAATGCTTAGTGTGATGACATGGGGCTCA 300
QY 249 CGCGCGCGCGCGCGCGCGCGCTCTCCGCGAGGTGCTGCTGAAGAGCTGTGGCC 308
DB 301 CAGCTTCCACCTGCGGACCTTCTTCCACGAGGTGCTATCCCTGAAGAGCTGTGGCC 360
QY 309 CGAGTGTGACAGAGGCTGTGCGAGCGCGCGGCGAGAAAGCTGTGCTTGGCTTGGCC 368

DB 361 AGGTTGTGACAGAGACTTGGCAGCGCAACGAGAAAGTGTGCTTGGCTTGGAG 420
QY 369 CTGCTGACGCGGCG 428
DB 421 CTGCTTAACGAGCGCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 429 CTGCGCAACACGCTGACCGACGCACTGCGGGGAGCGCGCGCGCGCGCGCGCGCG 488
DB 481 TTGCCCAACACTGTTATTGAGACCCCTGCTGTGATGTCATGATGCTGTGAGC 540
QY 489 CGCGTGGCGGACGACGCTGCTGTTACCTGCTGCGACCGCTGCGCGCTTGTGCTGG 546
DB 541 CGAGTGGCGGACGACGCTGCTGTTACCTGCTGCGACACTGTGCTTATTCTTCTGG 598

RESULT 14

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

664 bp mRNA linear EST 06-MAY-2002
IMAGE:5409222, mRNA sequence.
BQ258274
BQ258274.1 GI:20459030
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 664)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
cDNA Library Preparation: J. Baker (Stanford University)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
MGI:1845958
Plate: LLAMA12043 row: N column: 7
Seq primer: Sp6 primer.
Location/Qualifiers
1. 664
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:5409222"
/tissue_type="embryo, late gastrula"
/dev_stage="embryo, 7.5 dpc"
/lab_host="XLI-Blue"
/clone_lib="Baker mouse embryo e7.5"
/note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA made by oligo-dT priming. Directionally cloned into SalI/NotI sites using the following 5' adaptor:
5'-TCGACCCACGCGTCCG-3'. Size-selected for average insert size 1.8-1.9 kb. Library constructed by J. Baker (Stanford University)."

FEATURES

Source

Query Match 8.3%; Score 317.8; DB 13; Length 664;
Best Local Similarity 68.3%; Pred. No. 1.1e-29;
Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;

ORIGIN

QY 1115 GCCCAGCTGACTGGCGCTTGGAGAGGCTGTGAGACCATTTCTGGTTCAGGCGCTG 1174
DB 9 GCTTACTTGAATGGGGCGAGAGACTGTGAGATCATCTTCTGGGCTCAAGCCTAG 68
QY 1175 GATGCCAGGAGCTCCCGCAGGTTGCCCGCGCTGCCCGCAGCGCTACTGCAATGCGGC 1234

Db 69 GACATCAGACCACTCTGCAGAGACACACCGCTATCGCGTGCATATGGCAGATGGCGCC 128
QY 1235 CCTGTTCTGAGCTGCTGGGAACACGCGGAGTGGCCCTACGGGGTGTCTCAAGAC 1294
Db 129 CCTGTTCCAAACAGCTGCTGGTGAACCATGAGAGTGCACATATGTCAAGATCTCAGGTC 188
QY 1295 GCACTGCCCCGCTGCGAGCTGCGGTCAACCCGAGCAGCCGCTGTCTGCCCCGGAGAACCC 1354
Db 189 ACATTGACAGTTTCAACAGCAACCAACAGGTGACAGATGCT----- 232
QY 1355 CCAGGCTCTGTGGCGGCCCCCGAGAGAGAGACACAGACCCCGCTGCTGTGAGCT 1414
Db 233 -----TGAACACAGCCCGACCGCATGATTT 263
QY 1415 GCTCCGCGCAGACAGACGCCCTGGCAGGTGTACGGCTTGTGCGGCTGCTGCGCCG 1474
Db 264 GCTCCGCGCTGACAGAGTCCCTGGCAGGTATATGTTTCTTGGGCTGTCTGTGCA 323
QY 1475 GCTGTGCCCCCAGGCTCTGGGGCTCCAGGACCAACGACCGCTTCTCAGGAACAC 1534
Db 324 GGTGTGTCTGTAGTCTCTGGGGTACAGGACCAATGAGCGCCCTTCTTAAGACTT 383
QY 1535 CAAGAAGTTCATCTCCCTGGGGAAGCATGCCAAGCTCTGCTGCAGAGAGCTGACGTGAA 1594
Db 384 AAAGAAGTTCATCTCTGCGGGAATATCGGCAAGCTATCATCTGCAGGAAGTATGTGAA 443
QY 1595 GATGAGCGTGGCGGAGTCCGCTTGGCTGCGGAGAGAGCCAGGGGTTGGCTGTGTCGCGC 1654
Db 444 GATGAAGTAGAGATGCTCCACTGCTCCGAGAGAGCCAGGGAGAGACCGTGTCCCGC 503
QY 1655 CGCAGAGACCGCTGCTGCGTGAAGAGATCTGCGCCCAAGTCTCTGCACTGCTGATGATGT 1714
Db 504 TGCAGAGACCGCTGAGGAGAGAGATCTGCGCTACGTTCTGCTGCTGATGAGAC 563
QY 1715 GTACGCTGCTGAGCTGCTCAGGCTCTTCTTTATGTACAGGAGACACGTTTCAAAAGAA 1774
Db 564 ATACGTGTACAGCTGCTTAGTCAATCTTTTACATCACAGAGAGACATTCAGAGAA 623
QY 1775 CAGGCTCTTTTCTACCGGAAGAGTGTGAGCAAGTGC 1815
Db 624 CAGGCTCTTCTTCTACCGTAAGAGTGTGAGCAAGCTGC 664

RESULT 15
AA811084/c 340 bp mRNA linear EST 19-FEB-1998
LOCUS AA811084
DEFINITION oa85c05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1319048 3',
mRNA sequence.
ACCESSION AA811084
VERSION AA811084.1 GI:2880695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 340)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Straudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
www-bio.lnlnl.gov/bdrp/image/image.html
Insert Length: 2249 Std Error: 0.00

FEATURES
source
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 331.
Location/Qualifiers
1.340
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1319048"
/issue_type="germlinal center B cell"
/lab_host="DH10B"
/clone_1ib="NCI CGAP GCB1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germlinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Straudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGAGCGCGCTCAATTTTCTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 8.3%; Score 316.4; DB 9; Length 340;
Best Local Similarity 99.1%; Pred. No. 2e-29;
Matches 339; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 3474 TCACTTCCCAAGAGCTGGCGCTCGGCTCCACCCAGGCGCAGCTTTCTCACCAGAG 3533
Db 340 TCACTTCCCAAGAG-TGGCGCTCGGCTCCACCCAGGCGCAGCTTTCTCACCAGAG 282
QY 3534 CCGGCTTCCACTCCCAACATAGAAATAGTCCATCCCAAGATGCGCATTTGTACCCCT 3593
Db 281 CCGGCTTCCACTCCCAACATAGAAATAGTCCATCCCAAGATGCGCATTTGTACCCCT 222
QY 3594 CGCCCTGCTCTTCTTGCCTTCCACCCCAACCATCCAGGTGAGAACCTGAGAAAGACC 3653
Db 221 CGCCCTGCTCTTCTTGCCTTCCACCCCAACCATCCAGGTGAGAACCTGAGAAAGACC 162
QY 3654 TGGAGCTCTGGGAATTTGAGGTGACCAAGGTGTGCCCTGTACACAGGCGAGACCTG 3713
Db 161 TGGAGCTCTGGGAATTTGAGGTGACCAAGGTGTGCCCTGTACACAGGCGAGACCTG 102
QY 3714 CACCTGATGGGGTCCCTGTGGTCAATTTGGGGGAGGTGCTGTGGAGTAAATACT 3773
Db 101 CACCTGATGGGGT-CCTGTGGTCAATTTGGGGGAGGTGCTGTGGAGTAAATACT 43
QY 3774 GAATATATAGATTTTTCAGTTTGAATAAAAAAAAAAAAAAAAAAAAAA 3815
Db 42 GAATATATAGATTTTTCAGTTTGAATAAAAAAAAAAAAAAAAAAAAAA 1

Search completed: March 1, 2004, 03:42:16
Job time : 6069.54 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 19:44:23 ; Search time 10073.5 Seconds
(without alignments)
17262.293 Million cell updates/sec

Title: US-09-424-686F-12
Perfect score: 4012
Sequence: 1 gtttcagcagcgctgcgctc.....aaaaaaaaaaaaaaaaaaaa 4012

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBml:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: gb_vl:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3333.6	83.1	4042	AX001446	AX001446 Sequence
2	3333.6	83.1	4042	AX003121	AX003121 Sequence
3	3333.6	83.1	4042	BD136185	BD136185 Human tel
4	3320.2	82.8	4037	E36819	E36819 Human telom
5	3320.2	82.8	4037	AR390496	AR390496 Sequence
6	3320.2	82.8	4037	AR393110	AR393110 Sequence
7	3320.2	82.8	4037	AR810378	AR810378 Sequence
8	3320.2	82.8	4037	BD011070	BD011070 Human tel
9	3307	82.4	4070	AX391846	AX391846 Sequence
10	3306.6	82.4	4015	AR104587	AR104587 Sequence
11	3306.6	82.4	4015	AR175848	AR175848 Sequence
12	3306.6	82.4	4015	E36793	E36793 Human telom
13	3306.6	82.4	4015	AR182221	AR182221 Sequence
14	3306.6	82.4	4015	AR224455	AR224455 Sequence
15	3306.6	82.4	4015	AR226390	AR226390 Sequence
16	3306.6	82.4	4015	AR243328	AR243328 Sequence
17	3306.6	82.4	4015	AR263555	AR263555 Sequence
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VERSION AX001446.1 GI:7241612
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ORGANISM unidentified
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AUTHORS Wick, M. and Hagen, G.
TITLE HUMAN CATALYTIC TELOMERASE SUB-UNIT AND ITS DIAGNOSTIC AND
THERAPEUTIC USE
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ORIGIN

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AUTHORS
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DEFINITION Human telomerase catalytic subunit, diagnostic and therapeutic utilization thereof and structure and function of chromosome end.
ACCESSION BD136185
VERSION BD136185.1 GI:23231130
KEYWORDS JP 2002508662-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 4042)
AUTHORS Hagen,G., Siegmund,H.U., Weichel,W., Wick,M. and Zubo,D.
TITLE Human telomerase catalytic subunit, diagnostic and therapeutic utilization thereof and structure and function of chromosome end
JOURNAL Patent: JP 2002508662-A 1 19-MAR-2002;
BAYER AG
COMMENT OS Unidentified
PN JP 2002508662-A/1
PD 19-MAR-2002
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PI DMITRY ZUBOV
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PC A61K31/70
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CC Topology: linear;
CC Human telomerase catalytic subunit, diagnostic and therapeutic utilization
CC thereof and structure and function of chromosome end FH Key
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ORIGIN

Query Match 83.1%; Score 3333.6; DB 6; Length 4042;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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 14-AUG-1997 US 08/912.951,14-AUG-1997 US 08/915.503 PI THOMAS
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 MORIN,
 PI CALVIN B HAREI, WILLIAM H ANDREWS
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ORIGIN

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Query Match	82.8%;	Score 3320.2;	DB 6;	Length 4037;
Best Local Similarity	90.0%;	Pred. No. 0;		
Matches 3638; Conservative	3;	Mismatches 356;	Indels 46;	Gaps 6;

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Db	1	GCAGCGCTGCCTCTCTGCTGCGCACGTGGGAAGCCCTTGCCCCGGGCCACCCCTCGCATGCC	60
QY	68	GCGCGCTCCCCCGCTGCCGAGCCGTGCGCTTCCCTGCTGTGCGCAGCCACTTACCGCGAGTGCT	127
Db	61	GCGCGCTCCCCCGCTGCCGAGCCGTGCGCTTCCCTGCTGTGCGCAGCCACTTACCGCGAGTGCT	120
QY	128	GCCGCTGGCCACGTTCTGTGCGGCGCCTGGGGCCCCCAGGGCTGGCGGCTGTGTGACGCGG	187
Db	121	GCCGCTGGCCACGTTCTGTGCGGCGCCTGGGGCCCCCAGGGCTGGCGGCTGTGTGACGCGG	180
QY	188	GGACCCCGCGCGCTTCCGCGCGCTGTGGCCAGTGCTGTGTGTGCTGCTGGGACGC	247
Db	181	GGACCCCGCGCGCTTCCGCGCGCTGTGGCCAGTGCTGTGTGTGCTGCTGGGACGC	240
QY	248	ACGCGCGCCCCCGCGCGCCCCCTCTCCGTCAGGTGTCTGCTGAAGAGCTGTGGC	307
Db	241	ACGCGCGCCCCCGCGCGCCCCCTCTCCGTCAGGTGTCTGCTGAAGAGCTGTGGC	300
QY	308	CCGAGTGTGACAGAGGTGTGCGAGCGCGCGCGGAAGAACGTGTGCGCTTCGGCTTCGC	367
Db	301	CCGAGTGTGACAGAGGTGTGCGAGCGCGCGCGGAAGAACGTGTGCGCTTCGGCTTCGC	360
QY	368	GCTGTGACCGGGCCCCCGGGGGCCCCCGAGGCTTCACCAACAAGCTGCGCAGCTA	427
Db	361	GCTGTGACCGGGCCCCCGGGGGCCCCCGAGGCTTCACCAACAAGCTGCGCAGCTA	420
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QY	488	CCGCGTGGGCGACGACGTGTGTTACCTGTGCAAGCTGCGCGCTTCTTGTGCTGT	547
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QY	548	GGCTCCCAAGTGCCTACCAAGTGTGGGGCGCGCTGTACCAAGCTGCGCGCTGCCAC	607
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QY	908	CACCTCTTTGGAGGGTGCCTCTCTGAGCAGCGCCACTCCCAACCCATCCGTGGGCCGCCA	967
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QY	968	GCACCAAGCGGGCCCCCATCCATCCATGCGGCCAACCAAGTCCCTTGGGACACGCTTGTTC	1027

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VERSION	AR390496.1	GI:40112420	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
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AUTHORS      Morin,G.B. and Andrews,W.H.
TITLE        Promoter for telomerase reverse transcriptase
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Db	1	GCAGCGCTGCGTCTGTGCGCAGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCC	60
QY	68	GCAGCGTCCCCGCTGCGGAGCCGTCGCTCCCTGTGCGCAACCACTACCGCGAGTGCT	127
Db	61	GCAGCGTCCCCGCTGCGGAGCCGTCGCTCCCTGTGCGCAACCACTACCGCGAGTGCT	120
QY	128	GCCGCTGACCACGTTGTCGCGCGCCTTGGGGCCCCCAAGGAGTGGCGGCTGTGCAAGCGG	187
Db	121	GCCGCTGACCACGTTGTCGCGCGCCTTGGGGCCCCCAAGGAGTGGCGGCTGTGCAAGCGG	180
QY	188	GGACCCCGCGGCTTTCGCGCGCTGGTGGCCCAAGTCCTGCTGTGCGTGCCTGGGACGC	247
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Db	601	TCAAGCCCCGCCCCCGCACACGCTAGTGACCCCGAAGGCGTGTGAGTGGAAACGGGC	660
QY	668	CTGGAACCATAGCGTCAAGGAGGCCGGGTCCTCCCTTGGGCTTGCCAGCCCCGGGTGCCAG	727
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AR393110 4037 bp mRNA linear PAT 18-DEC-2003
LOCUS AR393110
DEFINITION Sequence 343 from patent US 6617110.
ACCESSION AR393110
VERSION AR393110.1 GI:40118392

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4037)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
TITLE Harley,C.B. and Andrews,W.H.
JOURNAL Cells immortalized with telomerase reverse transcriptase for use in
FEATURES drug screening
source Location/Qualifiers
1. 4037
/organism="unknown"
/mol_type="mrna"

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Best Local Similarity 90.0%; Pred. No. 0;
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Db 1 GCAGCGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 68 GCGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 127
Db 61 GCGGCTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
QY 128 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 187
Db 121 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
QY 188 GGAACCGGCGGCTTCCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
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QY 248 ACGG 307
Db 241 ACGG 300
QY 308 CCGAGTGTGAGAGAGGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 367
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QY 368 GCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
Db 361 GCTGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
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Db 421 CTTGCCCAACACGCTGACCGACACTGCGGGGAGCGGGGCGTGGGGCTGCTGCTGCG 480
QY 488 CCGGCTGGGCGACGAGCTGTGCTTCACTGCTGCAACGCTGCGCGCTCTTGTGTGCT 547
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QY	968	GCACCAAGCGGGCCCCCATCCACATCGCGGGCCACCAAGTCCCTGGGACACGCTGTCC	1027
Db	961	GCACCAAGCGGGCCCCCATCCACATCGCGGGCCACCAAGTCCCTGGGACACGCTGTCC	1020
QY	1028	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGGACAAGAGCAGTGGC	1087
Db	1021	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGGACAAGAGCAGTGGC	1080
QY	1088	GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAGGCTCGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCGCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACACGCGCA	1260
QY	1268	GTCGCCCTACGGGGTGCTCTCAAGACGCACTGCCGCTGAGCTGCGTCAACCCAGC	1327
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QY	1328	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCGAGGGCTGTGGCGGCCCCCGAGGAGGAGA	1387
Db	1321	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCGAGGGCTGTGGCGGCCCCCGAGGAGGAGA	1380
QY	1388	CACAGACCCCCGCTGCGCTGGTGACGCTGCTCCGACAGCAAGCAAGCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCGCTGCGCTGGTGACGCTGCTCCGACAGCAAGCAAGCCCTGGCAGGTGA	1440
QY	1448	CGGCTTGTGCGGGCGCTGCTGCGCCGCGCTGCTGTCGCCCCAGGCTCTGGGGCTCAAGCA	1507
Db	1441	CGGCTTGTGCGGGCGCTGCTGCGCCGCGCTGCTGTCGCCCCAGGCTCTGGGGCTCAAGCA	1500
QY	1508	CAACGAACGCGGCTTCTCTAGAGAAACACCAAGAATTCACTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGGCTTCTCTAGAGAAACACCAAGAATTCACTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGGAAGCATGCCAG	1627
Db	1561	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGGGAAGCATGCCAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCGGGCGCAGAGCACCGTCTGCTGAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTTCGGGCGCAGAGCACCGTCTGCTGAGAGATCTGGC	1680
QY	1688	CAAGTCTCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTTTCTTTTA	1747
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QY	1748	TGTCACGGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1807
Db	1741	TGTCACGGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1800
QY	1808	CAAGTTCATAAGCATTTGAATCAGACGCACTTGAAGGGGTGAGCTGCGGAGCTGTC	1867
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QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGAATACTCGTGGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGAATACTCGTGGGAGC	1980
QY	1988	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAAGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTCGAAGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGGCCCTCTGTGCTGGG	2107
Db	2041	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGGGCCCTCTGTGCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCCTGGCGCACCTTGTGCTGCTGCTGCGGGCCAGAACCC	2167
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QY	2168	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCAATCCCCA	2227
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCAATCCCCA	2220
QY	2228	GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTACTCGTGGC	2287
Db	2221	GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAACACGTACTCGTGGC	2280
QY	2288	TCCGTATGCCGTGTGTCAGAAAGCCGCCATGGGCACTCCGCAAGGCTTCAAGAGCCA	2347
Db	2281	TCCGTATGCCGTGTGTCAGAAAGCCGCCATGGGCACTCCGCAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTTACTCTTGACACACTCCAGCCGTACATGCGACAGTTGCTGCTCACTGTCAGGA	2407
Db	2341	CGTCTTACTCTTGACACACTCCAGCCGTACATGCGACAGTTGCTGCTCACTGTCAGGA	2400
QY	2408	GACCAGCCCCGCTGAGGGAATGCCGTGTCATTCGACAGACAGCTCCTCCCTGAATGAGGCCAG	2467
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QY	2528	CAAGTCTTACGTCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGTCTG	2587
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QY	2588	CAGCCTGTGCTACGCGGACATGAGAACCAAGCTGTTTGGGGGATTGCGGGAAGGGCT	2647
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QY	2948	CGGCTTCAAGGCTGGGAGGAACATGCGTGGCAAACTCTTTGGGGTCTTGGCGGTGAAGTG	3007
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QY	3068	CAAGATCCTCCTGCTGCAAGCGCTACAGGTTTCAACGCAATGTGTCTGCAGACTCCCATTTTCA	3127
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QY 428 CCTGCCCAACACGGGTGACCGGACGCACTGCGGGGAGCGGGGCGTGGGGCTGTGCTGC 487
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DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011070
VERSION BD011070.1 GI:18639443
KEYWORDS JP 2001081042-A/27.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 4037)
AUTHORS Sechi,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Mori,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit
JOURNAL Patent: JP 2001081042-A 27 27-MAR-2001;
GERON CORP, UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 2001081042-A/27
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643,18-APR-1997 US 08/844419 PR
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09-MAY-1997 US 08/854050,14-AUG-1997 US 08/911312 PR
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DB 1081 GCGCT 1140
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1
AUTHORS Jones, C.J., Kipling, D.G., Wilkinson, G., Mosharry, B.D. and
Skinner, J.W.
TITLE Cell lines, their preparation and use
JOURNAL Patent: WO 021655-A 1 28-FEB-2002;
University of Wales College of Medicine (GB)
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Query Match 82.4%; Score 3307; DB 6; Length 4070;
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TITLE Telomerase
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ORGANISM Unknown.
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AUTHORS Cech, T.R. and Nakamura, T.
TITLE Telomerase
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Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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Db 1 GCAGCGCTGCTCTGCTGCGACAGTGGAGCCCTGGCCCCCGCCACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGAGCGCGCTGCGCTCCCTGCTGCGACCGCACTACCGGAGTGT 127
Db 61 GCGCGCTCCCGCTGCGAGCGCGCTGCGCTCCCTGCTGCGACCGCACTACCGGAGTGT 120
QY 128 GCGCGTGGCCAGTTCGTCGCGCGCGCTGGGGCCCCAGGGCTGGCGGCTGTGCAAGCGCG 187
Db 121 GCGCGTGGCCAGTTCGTCGCGCGCGCTGGGGCCCCAGGGCTGGCGGCTGTGCAAGCGCG 180
QY 188 GGAACCGCGCGCTTCGCGCGCGCTGTGTGCGCCAGTGTGTGTGTGCGTGGAGCGC 247
Db 181 GGAACCGCGCGCTTCGCGCGCGCTGTGTGCGCCAGTGTGTGTGTGCGTGGAGCGC 240
QY 248 ACCGCGCGCGCGCGCGCGCGCTCTCTTCCGCGCAAGTGTCTGCTGAAGAGCTGTGCG 307
Db 241 ACCGCGCGCGCGCGCGCGCGCTCTCTTCCGCGCAAGTGTCTGCTGAAGAGCTGTGCG 300
QY 308 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCGCAAGAACGTGTGCGCTTCGCGTTCGC 367
Db 301 CCGAGTGTGCAAGAGCTGTGCGAGCGCGCGCGCGCAAGAACGTGTGCGCTTCGCGTTCGC 360
QY 368 GCTGTGAGACGGGGCG 427
Db 361 GCTGTGAGACGGGGCG 420
QY 428 CCTGCCCAACACAGGTGACCGACGCACTGCGGGGGAAGCGGGCGGTGGGGGCTGTGCTGCG 487
Db 421 CCTGCCCAACACAGGTGACCGACGCACTGCGGGGGAAGCGGGCGGTGGGGGCTGTGCTGCG 480
QY 488 CCGCGTGGGCGCAAGCTGTGCTTCACTGCTGCGACGCTGCGCGCTCTTGTGTGCTGCT 547
Db 481 CCGCGTGGGCGCAAGCTGTGCTTCACTGCTGCGACGCTGCGCGCTCTTGTGTGCTGCT 540
QY 548 GCGTCCCAAGCTGCGCTTACAGGTGTGCGGGCGCGCGCGCTGTACAGCTGCGCGCTGCGAC 607
Db 541 GCGTCCCAAGCTGCGCTTACAGGTGTGCGGGCGCGCGCGCTGTACAGCTGCGCGCTGCGAC 600
QY 608 TCAGGCG 667

Db 601 TCAGGCG 660
QY 668 CTGGAACCATAGCGCTCAGGAGAGCGGGGTCCCTCTGGGCTGCGAGCGCGCGGTGCGAG 727
Db 661 CTGGAACCATAGCGCTCAGGAGAGCGGGGTCCCTCTGGGCTGCGAGCGCGCGGTGCGAG 720
QY 728 GAGGCGCGGGGCGAGTGCAGCGCGCAAGTCTGCGCTTGGCCCAAGAGGGCGCGGTGCGCG 787
Db 721 GAGGCGCGGGGCGAGTGCAGCGCGCAAGTCTGCGCTTGGCCCAAGAGGGCGCGGTGCGCG 780
QY 788 TGCCCTGAGCGCGAGCGGACCGCGCTTGGGCAAGGGGTCTGGGCCACCGCGGAGGAG 847
Db 781 TGCCCTGAGCGCGAGCGGACCGCGCTTGGGCAAGGGGTCTGGGCCACCGCGGAGGAG 840
QY 848 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
Db 841 GCGTGAACCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACTCTTTGAGGGGTGCGCTCTCTGCGACGCGCGCACTCCACCCATCCGTGGCGCGCA 967
Db 901 CACTCTTTGAGGGGTGCGCTCTCTGCGACGCGCGCACTCCACCCATCCGTGGCGCGCA 960
QY 968 GCACCAAGCGGGCG 1027
Db 961 GCACCAAGCGGGCG 1020
QY 1028 CCGGCTGACGCGCGAGCAAGCACTTCTCTACTCTCAGGCGCAAGAGCAAGTGGC 1087
Db 1021 CCGGCTGACGCGCGAGCAAGCACTTCTCTACTCTCAGGCGCAAGAGCAAGTGGC 1080
QY 1088 GCGCTCTCTCTACTCTCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1147
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Db 1141 GACCATTTTCTGGGTTCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1208 GCGCCAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1267
Db 1201 GCGCCAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1260
QY 1268 GTGCCCTTACGGGGGTCTCTCTCAAGCGCACTCCCGCTGCGAGCTGCGGTCAACCCAGC 1327
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QY 1328 AGCGGTGTCTGTGCG 1387
Db 1321 AGCGGTGTCTGTGCG 1380
QY 1388 CACAGACCGCGCTGCGCTGTGCAAGTCTCCGCGCAAGCAAGCGCGCGCGCGCGCGCG 1447
Db 1381 CACAGACCGCGCTGCGCTGTGCAAGTCTCCGCGCAAGCAAGCGCGCGCGCGCGCGCG 1440
QY 1448 CCGCTTGTGCGGGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1507
Db 1441 CCGCTTGTGCGGGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
QY 1508 CAACGAACCGCGCTTCTCTCAAGAACCAAGAAATTCTCTCTGGGGAAGCATGCGCAA 1567
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QY 1628 GAGCCCAAGGGGTGCGTGTGTTCGGCGCGCGAGAGCAACCGTGTGCGTGAAGAGATCTGCGC 1687
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QY 1688 CAAGTCTCTGCACTGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1747
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Db	1741	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTAACCGGAAGATGTCTGGAG	1800
QY	1808	CAAGTTGCCAAAGCATTGGAATCAGACAGCACTTGAAAGAGGTGCAGCTGCGGAGCTGTCTC	1867
Db	1801	CAAGTTGCCAAAGCATTGGAATCAGACAGCACTTGAAAGAGGTGCAGCTGCGGAGCTGTCTC	1860
QY	1868	GGAAAGCAGAGGTTCAGGCAGCATCGGGAAGCCAGGCCCCGCCCTCTGACGTCCAGACTCCG	1927
Db	1861	GGAAAGCAGAGGTTCAGGCAGCATCGGGAAGCCAGGCCCCGCCCTCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGACTACGTCTGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGACTACGTCTGTGGAGC	1980
QY	1988	CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCGCTCACTTCGAGGGTGAAGGCACGTCTT	2047
Db	1981	CAGAACGTTCCGCAGAGAAAGAGGGCCGAGCGCTCACTTCGAGGGTGAAGGCACGTCTT	2040
QY	2048	CAGCGTGTCAACTACGAGCGGGCGCGGCCCGGCTCTGTGGGCGCTCTGTGTGGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGGCCCGGCTCTGTGGGCGCTCTGTGTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCTTGCGCACCTTCGTGTGCTGCTGTGCGGCGCCAGAGACC	2167
Db	2101	CCTGACGATATCCACAGGGCTTGCGCACCTTCGTGTGCTGCTGTGCGGCGCCAGAGACC	2160
QY	2168	GCCGCTGAGCTGTACTTTGTTCAGGTGATGTGACGGGCGCTACGACACCATCCCCA	2227
Db	2161	GCCGCTGAGCTGTACTTTGTTCAGGTGATGTGACGGGCGCTACGACACCATCCCCA	2220
QY	2228	GGACAGGCTCACGGAAGTCAATCGCCAGCATCATCAAAOCCAGAACACGTACTGCGTGG	2287
Db	2221	GGACAGGCTCACGGAAGTCAATCGCCAGCATCATCAAAOCCAGAACACGTACTGCGTGG	2280
QY	2288	TCGGTATGCCGTGTCCAGAAAGCCGCCCATGCGGCACTCCGCAAGGCTTCAAGAGCCA	2347
Db	2281	TCGGTATGCCGTGTCCAGAAAGCCGCCCATGCGGCACTCCGCAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCACAGTTCTGTGGCTCACTTCAGAGA	2407
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCCACAGTTCTGTGGCTCACTTCAGAGA	2400
QY	2408	GACCAGCCCGCTGAGGGATGCCGTCTCATTCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2467
Db	2401	GACCAGCCCGCTGAGGGATGCCGTCTCATTCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2468	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCAACACGCCGTGCCCATCAGGGG	2527
Db	2461	CAGTGGCCTCTTCGACGCTTCTCTACGCTTCATGTGCCAACACGCCGTGCCCATCAGGGG	2520
QY	2528	CAAGTCTCTACGTCAGATGCCAGGGGATCCCGCAGGGCTCCATCTCTCCAAGCTGTCTG	2587
Db	2521	CAAGTCTCTACGTCAGATGCCAGGGGATCCCGCAGGGCTCCATCTCTCCAAGCTGTCTG	2580
QY	2588	CAGCCTGTGCTACGGGCAATGGAAGAACAGCTGTTTGGGGGATTCGGCGGGGACGGGCT	2647
Db	2581	CAGCCTGTGCTACGGGCAATGGAAGAACAGCTGTTTGGGGGATTCGGCGGGGACGGGCT	2640
QY	2648	GCTCCTGCGTTTGGTGAATGATTTCTTGTGTGTGACACTCACTCAOCCACGCGAAGAAC	2707
Db	2641	GCTCCTGCGTTTGGTGAATGATTTCTTGTGTGTGACACTCACTCAOCCACGCGAAGAAC	2700
QY	2708	CTTCCTCAGGACCCCTGTCCGAGGTGTCCCTGAGATGGCTGCGTGTGAACCTTGGCGGAA	2767
Db	2701	CTTCCTCAGGACCCCTGTCCGAGGTGTCCCTGAGATGGCTGCGTGTGAACCTTGGCGGAA	2760
QY	2768	GACAGTGTGAATTCCTCTGTAGAAAGCAGGCGCTGGGTGGCACGGCTTTTGTTCAGAT	2827
Db	2761	GACAGTGTGAATTCCTCTGTAGAAAGCAGGCGCTGGGTGGCACGGCTTTTGTTCAGAT	2820

QY	2828	GCCGGCCACGGCTAATTCCTGCTGGTGGCGGCTGCTGCTGATACCCGGACCTTGAGGT	2887
Db	2821	GCCGGCCACGGCTAATTCCTGCTGGTGGCGGCTGCTGCTGATACCCGGACCTTGAGGT	2880
QY	2888	GCAGAGCGACTACTCCAGCTATATGCCCGGACCTTCATCAGAGCCAGTCTCACTTCAACCG	2947
Db	2881	GCAGAGCGACTACTCCAGCTATATGCCCGGACCTTCATCAGAGCCAGTCTCACTTCAACCG	2940
QY	2948	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAACTCTTTGGGGCTTGCGGCTGAAGTG	3007
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAACTCTTTGGGGCTTGCGGCTGAAGTG	3000
QY	3008	TCACAGCCTGTTTCTGGAATTTGCAAGTGAACAGCCTCCAGACGGTGTGCACCAATCTA	3067
Db	3001	TCACAGCCTGTTTCTGGAATTTGCAAGTGAACAGCCTCCAGACGGTGTGCACCAATCTA	3060
QY	3068	CAAGATCCTCCTGCTGACAGGCGTACAGGTTTCAAGCATGTGTGTGCAGCTCCATTCA	3127
Db	3061	CAAGATCCTCCTGCTGACAGGCGTACAGGTTTCAAGCATGTGTGTGCAGCTCCATTCA	3120
QY	3128	TCAGCAAGTTTGAAGAACCCCAATTTTCTGGCGCTCATCTGTGACACGGCCTCCCT	3187
Db	3121	TCAGCAAGTTTGAAGAACCCCAATTTTCTGGCGCTCATCTGTGACACGGCCTCCCT	3180
QY	3188	CTGCTACTCCATCCTTGAAGCCAGAACCGCAGTAATGT-----GCAGTGCCTGG	3237
Db	3181	CTGCTACTCCATCCTTGAAGCCAGAACCGCAGTAATGTGCCTGGGGGCCAAGGGCGCCGC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTATGTGTGACGAGACTGAATGAATCTG	3297
Db	3241	CGGCCCTCTGCCCTCCGAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
QY	3298	GGCTTAGGAAGTCTTAACCCCTTTCCGATCAGGAAGTGTTTAACCAACCACTGTGAG	3357
Db	3301	GACTCGACACCGTGTCACCTACGTGCCACTCTGGGGTCACTCAGGACAGCCAGACGCA	3360
QY	3358	GCTGCTGTGCCCGCCTCTGCTGGGGTGAAGCAGACCACTGATGAAGGACAGAGCTG	3417
Db	3361	GCTGAGTCGAAGTCCCGGGGACGACGCTGACTGCTCGTAGAGCCGACGCCAACCCGGC	3420
QY	3418	TCTGGAGCTGCCATCCTTCCCACTTGCTCT-----GCCTG	3454
Db	3421	ACTGCCCTCAGATTCAAGACCATCTTGACTGATGACCACCCGCCACAGCCAGGCCGA	3480
QY	3455	GGGAAGCGCTGGGGGCGCTGCTCTCTCTGTTTGCCCATGTGGATTGGGGGCGCTG	3514
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QY	3575	CTTGTGCAAAACCAAGGCCAAG-----GCCTTAGAGAGGACGACGCCAGGCTAACCCAC	3629
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3630	CCCTCTCAGAGCAGAGGCGCGGCTATACCAACGACAGAGCCCCCGCGCTCTGCTTC	3689
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QY	3690	CCAGTCACCGTCTCTGCGCCTTGACACTTTGTCCAGCATCAGGGAAGTTTCTGATCCGT	3749
Db	3720	AGGGCCAGCTTTTCTCTACCAAGAGCGCGCTTCCACTCCCACATAGGAATAGTCCATC	3779
QY	3750	CTGAATTTCAAGCCATGTGGAACCTGCGGCTCTGAGCTTAACAGCTTCTACTTCTGTTTC	3809
Db	3780	CCCAAGATTCGCCATTGTTCAACCCCT-----CGCCCTGCGCTTCTTGGCTTCCACCCC	3832
QY	3810	TTTCTGTGTTGTGAGAGACCCCTGAGAAAGACCCCTGGGAGCTCTGGGAATTTGAGTGACCA	3869
Db	3833	CACCATTCAGGTGGAAGACCCCTGAGAAAGACCCCTGGGAGCTCTGGGAATTTGAGTGACCA	3892
QY	3870	AAGGTGCGCTGTACACAGGCGAGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAA	3929

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LOCUS Human telomerase catalytic subunit promoter.
DEFINITION E36793
ACCESSION E36793
VERSION E36793.1 GI:13022756
KEYWORDS JP 1999253177-A/1.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 4015)
AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
Calvin,B.H. and William,H.A.
TITLE Human telomerase catalytic subunit promoter
JOURNAL Patent: JP 1999253177-A 1 21-SEP-1999;
COMMENT JERON CORP,UNIVERSITY TECHNOLOGY CORP
OS Unclassified
PN JP 1999253177-A/1
PD 21-SEP-1999
PR 15-OCT-1998 JP 1998320169
PR 01-OCT-1996 US 08/724,643, 18-APR-1997 US 08/844,419, PR
25-APR-1997 US 08/846,017, 06-MAY-1997 US 08/851,843, PR
09-MAY-1997 US 08/854,050, 14-AUG-1997 US 08/911,312, PR
14-AUG-1997 US 08/912,951, 14-AUG-1997 US 08/915,503 PI THOMAS
R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
MORIN,
PI CALVIN B HAREI, WILLIAM H ANDREWS
PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
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PC (C12N1/21,C12R1:19),(C12N9/12,C12R1:19),(C12N9/12,C12R1:84),
PC (C12N9/12,C12R1:91),C12N15/00,A61K37/64,C12N5/00 CC
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CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 56..3454.
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ORIGIN
Query Match 82.4%; Score 3306.6; DB 6; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;
QY 8 GCAGCGCTGCTGCTGCTGCGCAGTGGGAGAGCCCTGCGCCCGGACACCCCGCGATGCC 67
Db 1 GCAGCGCTGCTGCTGCTGCGCAGTGGGAGAGCCCTGCGCCCGGACACCCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 127
Db 61 GCGCGCTCCCGCTGCGCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCT 120
QY 128 GCGCGTGGCCAGTTCGTGCGCGCTGCGCGCCCGGAGGCTGGCGGTGTCAGCGCG 187
Db 121 GCGCGTGGCCAGTTCGTGCGCGCTGCGCGCCCGGAGGCTGGCGGTGTCAGCGCG 180

QY 188 GAAACCCGGCGCTTTCGCGCGCTGTGCGCCCACTGCTGTGTGCTGCTGCGGAGCG 247
Db 181 GAAACCCGGCGCTTTCGCGCGCTGTGCGCCCACTGCTGTGTGCTGCTGCGGAGCG 240
QY 248 ACGGCG 307
Db 241 ACGGCG 300
QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGACGTGTGCTGCGCTTCCG 367
Db 301 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGACGTGTGCTGCGCTTCCG 360
QY 368 GCTGCTGAGAGGCG 427
Db 361 GCTGCTGAGAGGCG 420
QY 428 CCTGCCCAACACAGGTGACCGACGCACTGCGGGGAGAGCGGCGGTGGGGCTGCTGCG 487
Db 421 CCTGCCCAACACAGGTGACCGACGCACTGCGGGGAGAGCGGCGGTGGGGCTGCTGCG 480
QY 488 CCGCGTGGCGGACGAGCTGTGTTCACTGCTGCGACGCTGCGCGCTTTGTGCTGCT 547
Db 481 CCGCGTGGCGGACGAGCTGTGTTCACTGCTGCGACGCTGCGCGCTTTGTGCTGCT 540
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Db 541 GCGTCCAGCTGCGCTTACAGAGTGTGCGGGCGCGCGCTGTACAGCTCGCGCTGCCAC 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGAACCATATAGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
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QY 728 GAGGCG 787
Db 721 GAGGCG 780
QY 788 TGCGCCCTGAGCGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 781 TGCGCCCTGAGCGCGGAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
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QY 908 CACCTCTTTGAGAGGCTGCGCTTCTGTGCAACGCGCACTTCCACCATCCGTGGCGCG 967
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Db 961 GCACACAGCG 1020
QY 1028 CCGGTTGACGCGGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1087
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Db 1081 GCGCT 1140
QY 1148 GACCATCTTCTGTTCCAGGCGCTGATGCGAGGACTCCCGCAGATTGCGCGCGCT 1207
Db 1141 GACCATCTTCTGTTCCAGGCGCTGATGCGAGGACTCCCGCAGATTGCGCGCGCT 1200
QY 1208 GCGGCGCGCTACTGCGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Db 1201 GCGGCGCGCTACTGCGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260

QY 1268 GTGCCCCCTACGGGGTCTCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCACCCCAGC 1327
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QY 1448 CGGCTTGTGCGGGGCTGCTGCTGCGCGGCTGTGCCCCAGGCTCTGGGCTCCAGGA 1507
Db 1441 CGGCTTGTGCGGGGCTGCTGCTGCGCGGCTGTGCCCCAGGCTCTGGGCTCCAGGA 1500
QY 1508 CAACGAACGCGCTTCTCTCAGGAACACCAAGAAATTCTCTCTGGGGAAGCATGCCAA 1567
Db 1501 CAACGAACGCGCTTCTCTCAGGAACACCAAGAAATTCTCTCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGAGAGAGCTGACGTGAGAGATGAGCGTGGGAGCTGCGCTTGGCTGCCAG 1627
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Db 1621 GAGCCAGAGGGTGGCTGTGTTCCGGCGCAGAGACACCGCTGTGAGAGATCTGGC 1680
QY 1688 CAAGTCTCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTA 1747
Db 1681 CAAGTCTCTGCACTGGCTGATGATGTGTGTACGTGCTGAGCTGCTCAGGTCTTTCTTTA 1740
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Db 1741 TGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTAACCGGAAGAGTGTCTGAG 1800
QY 1808 CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCACTGCGGAGCTGTC 1867
Db 1801 CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCACTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCGCTGTGACGTCCAGACTCCG 1927
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AUTHORS    Morin,G.B.
TITLE       Human telomerase catalytic subunit variants
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ORIGIN

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D	b	121	GCCGCTGGCCACGTTCTGTGCGCGCCTTGGGGCCCCAGGGCTGGCGCTGTGACGCGG	180
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D	b	181	GGACCCGGCGGCTTTCGCGCGCTGGTGGCCAGTGCCTGTGTGCGTGGCCCTGGAGCGC	240
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Q	y	368	GCTGTGAGCGGGGGCCCCGCGGGGGCCCCCGAGGCTTCAACCACGCTGCGCAGCTA	427
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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Gaeta, F.C.A.
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for the treatment of cancer
JOURNAL Patent: US 6440735-A 1 27-AUG-2002;
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VERSION	AR226390.1	GI:27264905		
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SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 4015)			
TITLE	Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B., Harley,C.B. and Andrews,W.H.			
JOURNAL	Antisense compositions for detecting and inhibiting telomerase reverse transcriptase			
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Source	Location/Qualifiers			
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	Matches 3618;	Conservative	0;	Mismatches 359;	Indels 46; Gaps 5
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 17:46:48 ; Search time 945.857 Seconds
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9:	geneseqn2003cs:*
10:	geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3333.6	83.1	4042	2	AAV72117 Human cat
2	3318.6	82.7	4037	2	AAV22428 Human tel
3	3311.4	82.5	4023	2	AAV60320 Human tel
4	3307	82.4	4070	6	ABL53711 Human tel
5	3306.6	82.4	4015	2	AAZ00724 Human tel
6	3306.6	82.4	4015	2	AAZ20279 Human tel
7	3306.6	82.4	4015	2	AAZ30154 Human tel
8	3306.6	82.4	4015	4	AAH45901 Human hTE
9	3306.6	82.4	4015	6	AAD46821 Human tel
10	3306.6	82.4	4015	6	ABA97534 Cancer ce
11	3306.6	82.4	4015	7	ACC58039 Human tel
12	3306.6	82.4	4015	7	ACC57552 Human tel
13	3306.6	82.4	4015	7	ABZ22474 Human tel
14	3306.6	82.4	4015	7	ACC44482 Human tel
15	3305	82.4	4015	7	AAC08150 Human tel
16	3305	82.4	4015	2	ABZ18391 Group III
17	3304.6	82.4	4027	2	AAH89424 Human EST
18	3304.6	82.4	4027	3	AAA29388 hEST2, a
19	3304.6	82.4	4027	9	ADC47060 Human TER
20	3304.6	82.4	4027	9	ADC40481 Human tel
21	3252.4	81.1	3964	2	AAH18254 Human tel
22	3237.2	80.7	3955	2	AAV22379 Human tel
23	3216.6	80.2	3798	2	AAV27876 Human tel

24	3163.6	78.9	3918	2	AAH18269	AAH18269 Telomerases
25	3163.6	78.9	3918	2	AAH18278	AAH18278 Telomerases
26	3161.4	78.8	3396	4	AAH48235	AAH48235 Heart mus
27	3161.4	78.8	3396	4	AAH49601	AAH49601 Human cod
28	3161.4	78.8	3396	4	AAH44366	AAH44366 Human tel
29	3161.4	78.8	3399	6	ABV78144	ABV78144 Human tel
30	3161.4	78.8	3399	6	ABZ35720	ABZ35720 Human elo
31	3161.4	78.8	3399	6	ABX09963	ABX09963 Human tel
32	3161.4	78.8	3399	6	ABL91685	ABL91685 Human pol
33	3159.8	78.8	3203	2	AAH18268	AAH18268 Altered C
34	3158.4	78.7	3453	7	ABZ76217	ABZ76217 Human TER
35	3158.4	78.7	13766	6	AAD46790	AAD46790 pGRN145 P
36	3158.2	78.7	3396	2	AAH18266	AAH18266 Telomerases
37	3146.4	78.4	8742	6	AAD46793	AAD46793 pWGB5a pl
38	3079.4	76.8	3167	2	AAH18271	AAH18271 Altered C
39	3079.4	76.8	3167	2	AAH18280	AAH18280 Altered C
40	3044.2	75.9	3500	2	AAH18275	AAH18275 Telomerases
41	3031.4	75.6	3323	2	AAH18277	AAH18277 Altered C
42	3029.2	75.5	3543	7	ABZ69628	ABZ69628 Plasmid C
43	2952.6	73.6	3855	2	AAV22382	AAV22382 Human tel
44	2889.2	72.0	7797	2	AAH18350	AAH18350 Telomerases
45	2843	70.9	3069	2	AAH18276	AAH18276 Truncated

ALIGNMENTS

RESULT 1	AAV72117	standard; cDNA; 4042 BP.
ID	AAV72117	
XX	AAV72117;	
AC		
XX		
DT	24-MAY-1999	(first entry)
XX		
DE	Human catalytic telomerase sub-unit cDNA.	
XX		
KW	Human; catalytic telomerase subunit; therapy; diagnosis; hTC; assay;	
KW	modulator; treatment; inhibit; cellular disorder; death; defect; cancer;	
KW	ageing; antisense; neoplastic cell; telomerase-related condition;	
KW	tumour cell; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	63..3461
FT		/*tag= a
FT		/product= "catalytic telomerase subunit"
XX		
PN	W09859040-A2.	
XX		
PD	30-DEC-1998.	
XX		
PF	09-JUN-1998;	98WO-EP003468.
XX		
PR	20-JUN-1997;	97DE-01026329.
PR	26-MAR-1998;	98DE-01013274.
PR	14-APR-1998;	98DE-01016496.
XX		
PA	(FARB) BAYER AG.	
XX		
PI	Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;	
XX		
DR	WPI; 1999-081276/07.	
DR	P-PSDB; AAW90251.	
XX		
PT	New catalytically active subunit of human telomerase - used in the	
PT	modulation of telomerase activity, particularly for treating cancer and	
PT	ageing.	
XX		
PS	Claim 4; Fig 1; 76pp; German.	
XX		
CC	This sequence encodes a novel human catalytic telomerase sub-unit (hTC).	

CC The encoded protein can be used in screening assays to identify
CC modulators of telomerase and to treat or inhibit cellular disorders,
CC death, defects and/or other pathological processes involving telomerase,
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense
CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (i)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit

XX Sequence 4042 BP; 684 A; 1364 C; 1277 G; 717 T; 0 U; 0 Other;

Query Match 83.1%; Score 3333.6; DB 2; Length 4042;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 1 GTTTCAGGACGCGTCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCGCCACCCCG 60
Db 1 GTTTCAGGACGCGTCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCGCCACCCCG 60
QY 61 CGATGCCGCGCTCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGACGCCACTACCGCG 120
Db 61 CGATGCCGCGCTCTCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGACGCCACTACCGCG 120
QY 121 AGGTGCTGCGCTGCGACCGTTCTGCGCGCGCTGGGGCCCGACGGCTGGCGCTGTGC 180
Db 121 AGGTGCTGCGCTGCGACCGTTCTGCGCGCGCTGGGGCCCGACGGCTGGCGCTGTGC 180
QY 181 AGCGCGGGGACCGCGCGCTTCCGCGCGCTGGGCCAGTGCCTGTGCTGCTGCT 240
Db 181 AGCGCGGGGACCGCGCGCTTCCGCGCGCTGGGCCAGTGCCTGTGCTGCTGCTGCT 240
QY 241 GGGACGACG 300
Db 241 GGGACGACG 300
QY 301 TGGTGGCGCGAGTGTGACAGAGCGTGTGCGAGCGCGCGCGAGAGACGTGCTGCGCTTCG 360
Db 301 TGGTGGCGCGAGTGTGACAGAGCGTGTGCGAGCGCGCGCGAGAGACGTGCTGCGCTTCG 360
QY 361 GCTTGGCGCTGTGAGACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 361 GCTTGGCGCTGTGAGACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 421 GCAGCTACCTGCGCAACACGCGTACCGACGCACTGCGGGGAGCGGGCGTGGGGCGTGC 480
Db 421 GCAGCTACCTGCGCAACACGCGTACCGACGCACTGCGGGGAGCGGGCGTGGGGCGTGC 480
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Db 481 TGCTGCGCGCGCTGCGCGACGAGCGTGTGCTTCACTGTGCGACGCTGCGCGCTTTTG 540
QY 541 TGCTGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 541 TGCTGCTGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 601 CTGCGCACTACG 660
Db 601 CTGCGCACTACG 660
QY 661 AACGGGCTGGAACATAGCGTCAAGGAGCGCGCGGTCCCGCTGGGCTGCGACCGCGCG 720
Db 661 AACGGGCTGGAACATAGCGTCAAGGAGCGCGCGGTCCCGCTGGGCTGCGACCGCGCG 720
QY 721 GTGCGAGAGCG 780
Db 721 GTGCGAGAGCG 780

QY 781 GTGGCGCTGCCCTGAGCCCGAGCGGACCGCCCTTGGGACGGGTCTGGCCACCCCG 840
Db 781 GTGGCGCTGCCCTGAGCCCGAGCGGACCGCCCTTGGGACGGGTCTGGCCACCCCG 840
QY 841 GCAGAGCGGTGACCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 841 GCAGAGCGGTGACCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 AAGAAGCCACTCTTTGAGGGGTGCGCTCTGTGACGCGCGCACTCCCAACCATCCGTGG 960
Db 901 AAGAAGCCACTCTTTGAGGGGTGCGCTCTGTGACGCGCGCACTCCCAACCATCCGTGG 960
QY 961 GCCCGCAGCACACCG 1020
Db 961 GCCCGCAGCACACCG 1020
QY 1021 CTTGCCCCCGGTGACCGCGGAGACCGACCACTTCTCTACTCTCTAGCGGACAGAGAGC 1080
Db 1021 CTTGCCCCCGGTGACCGCGGAGACCGACCACTTCTCTACTCTCTAGCGGACAGAGAGC 1080
QY 1081 AGCTGCGCGCTCTCTCTCTACTACTGAGGCGCCAGCCTGACTGCGCTCGAGAGC 1140
Db 1081 AGCTGCGCGCTCTCTCTCTACTACTGAGGCGCCAGCCTGACTGCGCTCGAGAGC 1140
QY 1141 TCGTGAGACCACTTTTCTGCGTCCAGCGCCCTGATGCCAGGACTCCCGCAGGTTGC 1200
Db 1141 TCGTGAGACCACTTTTCTGCGTCCAGCGCCCTGATGCCAGGACTCCCGCAGGTTGC 1200
QY 1201 CCGCGCTGCCCGACCGCTACTGCGAATGCGCGCCCTGTTTCTGAGACTGCTTGGGAAC 1260
Db 1201 CCGCGCTGCCCGACCGCTACTGCGAATGCGCGCCCTGTTTCTGAGACTGCTTGGGAAC 1260
QY 1261 ACGCGAGTGCCTCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA 1320
Db 1261 ACGCGAGTGCCTCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCA 1320
QY 1321 CCCCAGCAGCGCGGTGTGTGCGCGCGGAGAACCCCAAGGCTGTGTGGCGCCCGAGG 1380
Db 1321 CCCCAGCAGCGCGGTGTGTGCGCGCGGAGAACCCCAAGGCTGTGTGGCGCCCGAGG 1380
QY 1381 AGGAGACACAGACCCCGCTGCTGTGAGAGACGCTGCTCCGCGACAGACAGCCCTGCG 1440
Db 1381 AGGAGACACAGACCCCGCTGCTGTGAGAGACGCTGCTCCGCGACAGACAGCCCTGCG 1440
QY 1441 AGGTGACGCTTGTGTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1500
Db 1441 AGGTGACGCTTGTGTGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1500
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Db 1681 TCGTGGCAAGTCTCTGCACTGGCTGATGATGTGTGATCGTGAAGTCTGCTGAGTCTT 1740
QY 1741 TCTTTATGTACGAGAGACCACTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTG 1800
Db 1741 TCTTTATGTACGAGAGACCACTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTG 1800
QY 1801 TCTGAGCAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGG 1860
Db 1801 TCTGAGCAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGG 1860
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QY 1921 GACTCCGCTTATCCCAAGCCTGACGGGTCGGCCGATTGTGAACATGACTACGTG 1980
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QY 1981 TGGAGCCAGAACGTTCCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAG 2040
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Db 2041 CACTGTTACGCTGTCACTACGAGCGGGCGGGCGCCCGCTCTGGGGCGCTCTG 2100
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QY 2761 TCGGAGAGACAGTGTGAATTCCTGTGAGAACAGAGGCGCTGGTGGCAGCGCTTGG 2820
Db 2761 TCGGAGAGACAGTGTGAATTCCTGTGAGAACAGAGGCGCTGGTGGCAGCGCTTGG 2820
QY 2821 TTCAAGATGCGGCGCCAGGCTATTCCTGTGCTGGCGCTGTGCTGTGATACCCGAGCC 2880
Db 2821 TTCAAGATGCGGCGCCAGGCTATTCCTGTGCTGGCGCTGTGCTGTGATACCCGAGCC 2880
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Db 3241 GCGCGCGCGCTGCTGCTGCTGAGGCGGTGAGTGTGACACAGCATTCCTGC 3300
QY 3291 GAATCTGGGCTTAGAAGTCTTACCCCTTTTCCATCAGGAAGTGTGTTAACCAACA 3350
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Db 3683 CTGCTTCCAGTACCGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3742
QY 3720 CCAACCCAGGCGCACTTTCTTCTACAGAGAGCCCGCTTCCACTCCCAATAGGAATA 3779
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Db 3743 GATCCGTGTGAATTCAGGCAATGTCGACCTGCGGTCTGAGCTTAAACAGCTTCTACT 3802
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Db 3803 TCTGTTCTTCTGTTGTGAGAGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3862
QY 3833 CCAACCCACCAATTCAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3892
Db 3833 CCAACCCACCAATTCAGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3892
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QY 3983 TTGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4012
Db 3983 TTGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4012
QY 4013 TTGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4042
Db 4013 TTGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4042
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Sequence 4037 BP; 682 A; 1362 C; 1275 G; 714 T; 0 U; 4 Other;

Query Match	82.7%;	Score 3318.6;	DB 2;	Length 4037;
Best Local Similarity	90.0%;	Pred. No. 0;		
Matches 3637; Conservative	3;	Mismatches 357;	Indels 46;	Gaps 6;

QY	8	GCAGCGCTGCGTCTCTGCTGCGCACAGTGGGAAAGCCCTGACCCCGGCCATGACC	67
Db	1	GCAGCGCTGCGTCTCTGCTGCGCACAGTGGGAAAGCCCTGACCCCGGCCATGACC	60
QY	68	GGCGGCTCCCCGCTGCGCGAGCCCGTGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT	127
Db	61	GGCGGCTCCCCGCTGCGCGAGCCCGTGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCT	120
QY	128	GCCGCTGACCAAGCTTCGTGCGCGCCCTGGGGCCCCAGAGGCTGGCGGCTGGTGCAGCGCGG	187
Db	121	GCCGCTGACCAAGCTTCGTGCGCGCCCTGGGGCCCCAGAGGCTGGCGGCTGGTGCAGCGCGG	180
QY	188	GGACCCGGCGGCTTTCGCGCGCGCTGCTGGCCCAAGTGCCTGGTGTGCGTGCCTGGGACGC	247
Db	181	GGACCCGGCGGCTTTCGCGCGCGCTGCTGGCCCAAGTGCCTGGTGTGCGTGCCTGGGACGC	240
QY	248	ACGCGCGCCCGCCCGCGCGCCCGCTCCTTCCGCCAGGTGCTGCTGTAAGAGAGCTGTGGC	307
Db	241	ACGCGCGCCCGCCCGCGCGCCCGCTCCTTCCGCCAGGTGCTGCTGTAAGAGAGCTGTGGC	300
QY	308	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACTGTCTGGCCCTTGGCTTGC	367
Db	301	CCGAGTGTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACTGTCTGGCCCTTGGCTTGC	360
QY	368	GCTGCTGACGGGGCCCGCGGGGGCCCCCGAGGCTTCAACCAACAGCGTGCAGCTA	427
Db	361	GCTGCTGACGGGGCCCGCGGGGGCCCCCGAGGCTTCAACCAACAGCGTGCAGCTA	420
QY	428	CCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGTCTGCTCG	487
Db	421	CCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGTCTGCTCG	480
QY	488	CCGCGTGGCGCAGCAGTGTGTTTACCTGCTGACGCTGCGCGCTCTTTGTGCTGCT	547
Db	481	CCGCGTGGCGCAGCAGTGTGTTTACCTGCTGACGCTGCGCGCTCTTTGTGCTGCT	540
QY	548	GGCTCCCAAGCTGCGCCTACCAAGTGTGCGGGCCCGCTGTACCAAGCTCGCGCTGCCAC	607
Db	541	GGCTCCCAAGCTGCGCCTACCAAGTGTGCGGGCCCGCTGTACCAAGCTCGCGCTGCCAC	600
QY	608	TCAGGCCCGGCCCGCCCAACAGCTAGTGAACCCCGAAGGCGCTGGGATGCCAACGGGC	667
Db	601	TCAGGCCCGGCCCGCCCAACAGCTAGTGAACCCCGAAGGCGCTGGGATGCCAACGGGC	660
QY	668	CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCCAG	727
Db	661	CTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCCAG	720
QY	728	GAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCGCTTGCCCAAGAGGCCCAAGCGTGGCGC	787
Db	721	GAGGCGCGGGGGCAGTGCCAGCCGAAGTCTGCGCTTGCCCAAGAGGCCCAAGCGTGGCGC	780
QY	788	TGCCCTTGAGCCGGAAGCGGACGCCCTTGGGGCAGGGGTCTGGGCCCAACCCGGGCAAGAC	847
Db	781	TGCCCTTGAGCCGGAAGCGGACGCCCTTGGGGCAGGGGTCTGGGCCCAACCCGGGCAAGAC	840
QY	848	GGGTGACCGAGTGAACCGTGGTTTCTGTGTGTGTCAACCTGCCAGAACCCGCCGAAGAAC	907
Db	841	GGGTGACCGAGTGAACCGTGGTTTCTGTGTGTGTCAACCTGCCAGAACCCGCCGAAGAAC	900
QY	908	CACCTCTTTGAGGGGTGCGCTCTTGCGACCGCGCCACTCCACCCCATCCGTGGGCGGCCA	967
Db	901	CACCTCTTTGAGGGGTGCGCTCTTGCGACCGCGCCACTCCACCCCATCCGTGGGCGGCCA	960
QY	968	GCACCAACGCGGGCCCCCATCCACATCGCGGCCAACAGTCCCTGGGACACGCGCTGTGCC	1027
Db	961	GCACCAACGCGGGCCCCCATCCACATCGCGGCCAACAGTCCCTGGGACACGCGCTGTGCC	1020

QY	1028	CCGGGTGTACGCCGCGAGACCAAGCACTTCTCTACTCTCAAGCCGACAAGAGCAGCTGCG	1087
Db	1021	CCGGGTGTACGCCGCGAGACCAAGCACTTCTCTACTCTCAAGCCGACAAGAGCAGCTGCG	1080
QY	1088	GCCCTCTTCTCTACTCAGCTCTCTGAGGCCAGCCGTGACTGAGCGCTCGGAGCTCGTGA	1147
Db	1081	GCCCTCTTCTCTACTCAGCTCTCTGAGGCCAGCCGTGACTGAGCGCTCGGAGCTCGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCCCTGAGTGCCAGGACTCCCCAGGTTGCCCGCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCCCTGAGTGCCAGGACTCCCCAGGTTGCCCGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAGCTGTTGGGAACCAACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAGCTGTTGGGAACCAACGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCAACCCAGC	1327
Db	1261	GTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTCAACCCAGC	1320
QY	1328	AGCGGTGTCTGTGCCCCGGGGAAGCCCCAGGGCTCTGTGGCGCCCCCGAGGAGGA	1387
Db	1321	AGCGGTGTCTGTGCCCCGGGGAAGCCCCAGGGCTCTGTGGCGCCCCCGAGGAGGA	1380
QY	1388	CACAGACCCCCGCTCGCTGTGTGACGTGCTCCGCGACAGACAGACCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCCGCTCGCTGTGTGACGTGCTCCGCGACAGACAGACCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTGTGTGCGGCGCTGCGCCGCGCTGCTGTGCCCCAGGCGCTCTGGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGTGCGGCGCTGCGCCGCGCTGCTGTGCCCCAGGCGCTCTGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCTTCTCTGAGGAACACCAAGAATTCACTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCTTCTCTGAGGAACACCAAGAATTCACTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGAGAGCTGACGTGAAGATGAGCGTGGCGGACTGCGCTTGGCTGGCGAG	1627
Db	1561	GCTCTCGCTGCAGAGAGCTGACGTGAAGATGAGCGTGGCGGACTGCGCTTGGCTGGCGAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTCTCCGGCCGACAGACACCGTCTGCGTGAAGAAATCCTGGC	1687
Db	1621	GAGCCCAAGGGGTTGGCTGTCTCCGGCCGACAGACACCGTCTGCGTGAAGAAATCCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTGAGCTGCTCAGGTCCTTTCTTTTA	1740
QY	1748	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCCGCGAGTGTCTGGAG	1800
QY	1808	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGGTGAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGGTGAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGSAGCATCGGGAAGCCAGGCCCGCTGTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGSAGCATCGGGAAGCCAGGCCCGCTGTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTCGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTCGTGGAGC	1980
QY	1988	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCTGTGCTGGG	2107
Db	2041	CAGCGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCTGTGCTGGG	2100

QY	2108	CCTGACGATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAGGACC	2167
Db	2101	CCTGACGATATCCACAGGGCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAGGACC	2160
QY	2168	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGCTACGACACCATCCCCA	2227
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGCTACGACACCATCCCCA	2220
QY	2228	GGACAGGCTCACGGAGTCATCGCCAGCATCATAAACCCAGAACACGTACTGCGTGG	2287
Db	2221	GGACAGGCTCACGGAGTCATCGCCAGCATCATAAACCCAGAACACGTACTGCGTGG	2280
QY	2288	TCGGATGCCGTGTGTCAGAGGCCGCCCATGGCAAGTCGCCAAGGCTTCAAGAGCCA	2347
Db	2281	TCGGATGCCGTGTGTCAGAGGCCGCCCATGGCAAGTCGCCAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGTTGCTCACCTGAGGA	2407
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGTTGCTCACCTGAGGA	2400
QY	2408	GACCAGCCCGCTGAGGGAATGCCGTGTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG	2467
Db	2401	GACCAGCCCGCTGAGGGAATGCCGTGTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2468	CAGTGGCTCTTCGACGTCTTCCTACGCTTCATGTGCCAACACGCCGTGCGCATCAGGGG	2527
Db	2461	CAGTGGCTCTTCGACGTCTTCCTACGCTTCATGTGCCAACACGCCGTGCGCATCAGGGG	2520
QY	2528	CAAGTCTACGTCCAGTGCACAGGGGATCCCGCAGAGGCTCCATCCTCCACAGCTGCTCTG	2587
Db	2521	CAAGTCTACGTCCAGTGCACAGGGGATCCCGCAGAGGCTCCATCCTCCACAGCTGCTCTG	2580
QY	2588	CAGCCTGTGCTACGGCGCATGGAACAACAGCTGTTTGGGGGATTGCGCGGAGCGGCT	2647
Db	2581	CAGCCTGTGCTACGGCGCATGGAACAACAGCTGTTTGGGGGATTGCGCGGAGCGGCT	2640
QY	2648	GCTCCTGCGTTTGGTGAATGATTTCTGTGTTGTGACACTCACTCAACCCAGCGAAAAAC	2707
Db	2641	GCTCCTGCGTTTGGTGAATGATTTCTGTGTTGTGACACTCACTCAACCCAGCGAAAAAC	2700
QY	2708	CTTCCTCAGGACCCCTGTCGAGGTGTCCTCGAATAGCTGCGTGTGAACCTTCCGAA	2767
Db	2701	CTTCCTCAGGACCCCTGTCGAGGTGTCCTCGAATAGCTGCGTGTGAACCTTCCGAA	2760
QY	2768	GACAGTGTGAACCTCCCTGTAGAAGACGAGCCCTGGGTGGCAAGCTTTTGTTCAGAT	2827
Db	2761	GACAGTGTGAACCTCCCTGTAGAAGACGAGCCCTGGGTGGCAAGCTTTTGTTCAGAT	2820
QY	2828	GCCGCCCCACGGCCTAATCCCCCTGATGCGGCTGCTGTGATACCCGGAACCTGAGGT	2887
Db	2821	GCCGCCCCACGGCCTAATCCCCCTGATGCGGCTGCTGTGATACCCGGAACCTGAGGT	2880
QY	2888	GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTGTCAACCTCAACCG	2947
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTGTCAACCTCAACCG	2940
QY	2948	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGCTTTGGCGCTGAAGTG	3007
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGCTTTGGCGCTGAAGTG	3000
QY	3008	TCACAGCCTGTTCCTGGAATTTGCAAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	3067
Db	3001	TCACAGCCTGTTCCTGGAATTTGCAAGGTGAACAGCCTCCAGACGGTGTGACCAACATCTA	3060
QY	3068	CAAGATCCTCCTGCTGCAAGGCGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA	3127
Db	3061	CAAGATCCTCCTGCTGCAAGGCGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA	3120
QY	3128	TCAGCAAGTTTGAAGAAGAACCCCAATTTTCTGCGCGTCATCTTCGACACGGCCTCCCT	3187
Db	3121	TCAGCAAGTTTGAAGAAGAACCCCAATTTTCTGCGCGTCATCTTCGACACGGCCTCCCT	3180
QY	3188	CTGCTACTGCATCCTGAAAGCCAGAACGCAAGTATGT-----GCAGGTGCTGTG	3237

Db 3181 CTGCTACTCCATCTGAAGCCAGAGGAGATGTCGCTGGGGCCCAAGGGCCCGC 3240
QY 3238 CCTCAGTGCAGAGTGCCTGCTGCTGTGTAGTGTGTCAGAGACTGATGATCTG 3297
Db 3241 CGGCCCTCTGCCCTCCGAGGCGCTGAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
QY 3298 GGCTTAGAAGTTCTTACCCCTTTTCGACACAGAAAGTGTGTTAACCAACCACTGTGAG 3357
Db 3301 GACTCGACACCGGTGACCTAGCTGACCTCTGGGTCACTGAGACAGCCAGACGCA 3360
QY 3358 GCTGCTGCCCCCTCTCTGCTGGGTGAGAGACACCTGATGGAAGGACAGAGCTG 3417
Db 3361 GCTGAGTCGGAAGCTCCCGGGGACGACGCTGAGCTGCCCTGAGGGCCGACCAACCCGCG 3420
QY 3418 TCTGGAGCTGCCATCCTTCCACCTGCTCT-----GCTG 3454
Db 3421 ACTGCCCTCAGACTCAAGACCATCTGAGCTGATGGCCACCCGCCACAGCCAGGCCGA 3480
QY 3455 GGAAGCGCTGGGGGCTGTCTCTCTCTGTTTGGCCCATGTTGGATTGGGGGCTG 3514
Db 3481 GAGCAGACACAGACGCTCTGTCACGCGGCTCTACGTCACGAGGAGGAGGGCGGCG 3540
QY 3515 GCCTCTCTGTTGCTCTGTGTGGATGGCTGTCTCCCGTCCATGGCACTTAGGGCC 3574
Db 3541 CACACCCAGCGCCGACCGCTGGAGTCTGAGCCCTGAGTGTGTTGGCCGAGGCTG 3600
QY 3575 CTTGTGAACCCAGGCCAAG-----GGCTTAGAGAGAGGCCAGGCCAGCTACCCAC 3629
Db 3601 CATGTCCGCTGAAGCTGAGTGTCCGCTGAGGCCCTGAGCGAGTGTCCAGCCAGGGCT 3660
QY 3630 CCCTCTCAGAGAGAGGCGCGTATACCAAGACAGAGCCCGCGCTCTCTGCTTC 3689
Db 3661 GAGTGTCCAGACACCTGCGCTCT-TCACTTCCCCACAGGCTGCGCTCCACCC 3719
QY 3690 CCAGTCAACCTCTCTGCGCTGACACTTTTCCAGCATCAGGAGGTTTCTGATCGGT 3749
Db 3720 AGGGCCAGCTTTCCTTCACAGGAGGCGCGCTTCCACTCCACATAGGAATAGTCCATC 3779
QY 3750 CTGAATTCAAGCATGTGAACCTGCGGCTGAGCTTAACAGCTTCTACTTCTGTTTC 3809
Db 3780 CCCAGATTC-GCCATTTGTCAACCCCTGCGCTGCTT-----CTTTGCTTCCACCC 3832
QY 3810 TTTCTGTGTGTGAGAGACCTGAGAGAGACCTTGAGAGCTCTGGGAATTTGAGTGAACA 3869
Db 3833 CACCATCCAGGTGAGAGACCTTGAGAGAGACCTTGAGAGCTCTGGGAATTTGAGTGAACA 3892
QY 3870 AAGGTGTGCTGTACACAGGCGAGGACCTGACCTGATGGGGTCCCTGTGGTCAA 3929
Db 3893 AAGGTGTGCTGTACACAGGCGAGGACCTGACCTGATGGGGTCCCTGTGGTCAA 3952
QY 3930 ATTGGGGGAGGTGCTGTGGAGTAATACTGAATATATAGTTTTCAGTTTGAATA 3989
Db 3953 ATTGGGGGAGGTGCTGTGGAGTAATACTGAATATATAGTTTTCAGTTTGAATA 4012
QY 3990 AAAAAAAAAAAAAAAAAAAAAA 4012
Db 4013 AAAAAAAAAAAAAAAAAAAAAA 4035

RESULT 3

AAV60320
ID AAV60320 standard; cDNA; 4023 BP.
XX AAV60320;
AC AAV60320;
XX 04-DEC-1998 (first entry)
DT Human telomerase gene referred to as hEST2.
DE
XX Catalytic subunit; human; telomerase; telomere maintenance; diagnosis;
KW treatment; cancer; ss.
XX

OS Homo sapiens.
XX Key Location/Qualifiers
FH CDS 59..3458
FT CDS /*tag= a
XX
XX W09837181-A2.
XX PD 27-AUG-1998.
XX
XX 20-FEB-1998; 98WO-US003404.
XX
XX 20-FEB-1997; 97US-0038750P.
XX 20-MAY-1997; 97US-0047151P.
XX 01-AUG-1997; 97US-0054549P.
XX 14-AUG-1997; 97US-0055762P.
XX 30-OCT-1997; 97US-0064322P.
XX
XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
XX Counter CM, Meyerson M, Weinberg RA;
XX
XX WPI; 1998-495367/42.
XX P-PSDB; AAW71376.
XX
XX New isolated human telomerase catalytic sub-unit gene - used to develop
XX products for increasing or reducing the life span of cells such as cancer
XX cells or transformed cells.
XX
XX Claim 5; Fig 5A-B; 96pp; English.
XX
XX The present sequence encodes the catalytic subunit of a human telomerase
XX holoenzyme. Disruption of the telomerase gene alters telomere
XX maintenance. The DNA is essential for telomerase activity, and the
XX protein is physically associated with telomerase and a constituent of
XX active telomerase complex. The products can be used for increasing or
XX reducing the lifespan of cells such as cancer cells or transformed cells.
XX They can also be used in the diagnosis and treatment of malignancies. In
XX addition, cells with a longer lifespan can be transplanted into or
XX grafted onto an individual (e.g. as skin grafts, as systems for delivery
XX of therapeutic proteins, such as hormones and enzymes), to whom they
XX provide therapeutic benefit
XX
XX Sequence 4023 BP; 668 A; 1363 C; 1277 G; 715 T; 0 U; 0 Other;
SQ
Query Match 82.5%; Score 3311.4; DB 2; Length 4023;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3624; Conservative 0; Mismatches 361; Indels 46; Gaps 5;
QY 5 CAGGACGCTGCTGCTGCTGCGACGTGGAAGCCCTGGCCCGGACCCCGGAT 64
Db 1 CAGGACGCTGCTGCTGCTGCGACGTGGAAGCCCTGGCCCGGACCCCGGAT 60
QY 65 GCCGCGCTGCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGACCACTACCGGAGT 124
Db 61 GCCGCGCTGCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGACCACTACCGGAGT 120
QY 125 GCTGCGCTGCGACAGTTGCTGCGGCGCTGGGGCCCAAGGCTGGCGGTGTGACGC 184
Db 121 GCTGCGCTGCGACAGTTGCTGCGGCGCTGGGGCCCAAGGCTGGCGGTGTGACGC 180
QY 185 CGGGACCGGCGGCTTCCGCGGCTGTGGCCCAAGTGTGTGCGTGGCTGGGA 244
Db 181 CGGGACCGGCGGCTTCCGCGGCTGTGGCCCAAGTGTGTGCGTGGCTGGGA 240
QY 245 CGACGCGCGCGCGCGCGCGCTTCCCTCCGACAGGTGTGCTGAGAGAGTGT 304
Db 241 CGACGCGCGCGCGCGCGCGCTTCCCTCCGACAGGTGTGCTGAGAGAGTGT 300
QY 305 GGCCTGAGTGTGAGAGGCTGTGCGAGCGCGCGGGAAGACGTGTGCTGCTTGGCTT 364
Db 301 GGCCTGAGTGTGAGAGGCTGTGCGAGCGCGCGGGAAGACGTGTGCTGCTTGGCTT 360

QY	365	CGCGCTGCTGGACGGGGGCCCCCCCCCGAGGCTTCAACCAAGCTGCGCAG	424
Db	361	CGCGCTGCTGGACGGGGGCCCCCCCCCGAGGCTTCAACCAAGCTGCGCAG	420
QY	425	CTACTGCCCCAACACCGGTGACCGGACTGCGGGGGAAGCGGGCGTGGGGGCTGTGCT	484
Db	421	CTACTGCCCCAACACCGGTGACCGGACTGCGGGGGAAGCGGGCGTGGGGGCTGTGTT	480
QY	485	GCGCGCGGTGGGCGACGAGCTGTGTTCACTGTGGACAGCTGCGGCTCTTGTGCT	544
Db	481	GCGCGCGGTGGGCGACGAGTGTGTTCACTGTGGACAGCTGCGGCTCTTGTGCT	540
QY	545	GGTGGCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGCGGCTGC	604
Db	541	GGTGGCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGCGGCTGC	600
QY	605	CACTAAGGCCCCGCCCCCGCCACACGCTAGTGAACCCGAAAGCGCTTGGGATGCGAAG	664
Db	601	CACTAAGGCCCCGCCCCCGCCACACGCTAGTGAACCCGAAAGCGCTTGGGATGCGAAG	660
QY	665	GGCTTGAACCATAGCGTCAGGGAAGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGC	724
Db	661	GGCTTGAACCATAGCGTCAGGGAAGCGGGGTCCCCCTGGGCTGCCAGCCCCGGGTGC	720
QY	725	GAGGAGCGCGCGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGCCCCAGGCTGG	784
Db	721	GAGGAGCGCGCGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGCCCCAGGCTGG	780
QY	785	CGCTGCCCCGTGAGCCGGAGCGGACGCCCGTTGGGCAAGGGTCTTGGGCCCAACCCGGGCAG	844
Db	781	CGCTGCCCCGTGAGCCGGAGCGGACGCCCGTTGGGCAAGGGTCTTGGGCCCAACCCGGGCAG	840
QY	845	GACGCGTGGAACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCCAGACCCGCCGAAGA	904
Db	841	GACGCGTGGAACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCCAGACCCGCCGAAGA	900
QY	905	AGCCACTCTTTGGAGGGTGCGCTCTCTGGCACGCGCACTCCCAACCATCCGTGGGCGG	964
Db	901	AGCCACTCTTTGGAGGGTGCGCTCTCTGGCACGCGCACTCCCAACCATCCGTGGGCGG	960
QY	965	CCAGCAACCACGCGGGCCCCCCCATCCACATCGCGGCCAACCAAGTCCCTGGGACACGCTTG	1024
Db	961	CCAGCAACCACGCGGGCCCCCCCATCCACATCGCGGCCAACCAAGTCCCTGGGACACGCTTG	1020
QY	1025	TCCCCCGGTGTACGCGCGAGAACCAACTTCTCTACTCTCAAGCGACAAGAGCAGCT	1084
Db	1021	TCCCCCGGTGTACGCGCGAGAACCAACTTCTCTACTCTCAAGCGACAAGAGCAGCT	1080
QY	1085	GCGGCGCTCTCTCTACTCAAGCTCTGTAGGCGCCAGCCTGAAGTGGCGCTCGAGGCTCGT	1144
Db	1081	GCGGCGCTCTCTCTACTCAAGCTCTGTAGGCGCCAGCCTGAAGTGGCGCTCGAGGCTCGT	1140
QY	1145	GGAAGACCATCTTCTGGGTTCAAGGCCCTGATGCAAGGGAATCCCCGCAAGTTGCCCG	1204
Db	1141	GGAAGACCATCTTCTGGGTTCAAGGCCCTGATGCAAGGGAATCCCCGCAAGTTGCCCG	1200
QY	1205	CCTGCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTCGAGAGCTCTTGGGAACCAAGC	1264
Db	1201	CCTGCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTCGAGAGCTCTTGGGAACCAAGC	1260
QY	1265	GCAAGTCCCCCTACGSGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCAACCC	1324
Db	1261	GCAAGTCCCCCTACGSGGTGCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCAACCC	1320
QY	1325	AGCAGCCGGTGTCTGTGCCCCGGAGAAAGCCCCCAAGGCTCTGTGCGCGGCCCCCCGAGAGGA	1384
Db	1321	AGCAGCCGGTGTCTGTGCCCCGGAGAAAGCCCCCAAGGCTCTGTGCGCGGCCCCCCGAGAGGA	1380
QY	1385	GGAACACAGACCCCCCGTGCCTGTGTGTCAGAGTGTCTCCGCCAGACACAGACCCCTGGCAGGT	1444
Db	1381	GGAACACAGACCCCCCGTGCCTGTGTGTCAGAGTGTCTCCGCCAGACACAGACCCCTGGCAGGT	1440
QY	1445	GTAACGGCTTCGTGCGGGCTGCTCGCGCGGCTGTGTGCCCCCAAGGCTCTGTGGGCTCCAG	1504

D	b	1441	GTACGGCTTCGTGCGGGCTTCCTGCGCCGGCTGGTGCCTCCAGGGCTCTGGGGTTCAG	1500
Q	y	1505	GCAACAAGAACGCGCTTCTCAGGAACCAAGAATTTCATCTCCCTGGGGAAGCATGC	1564
D	b	1501	GCACAACGAACGCGCTTCTCAGGAACCAAGAATTTCATCTCCCTGGGGAAGCATGC	1560
Q	y	1565	CAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGTCCGGACTGCCCTTGGCTGCC	1624
D	b	1561	CAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGACGTCCGGGCTGCCCTTGGCTGCC	1620
Q	y	1625	CAGGAGCCCAAGGGGTTGGCTGTTCCTCCGCCGACAGACCCGTCTGCGTGAAGATCCT	1684
D	b	1621	CAGGAGCCCAAGGGGTTGGCTGTTCCTCCGCCGACAGACCCGTCTGCGTGAAGATCCT	1680
Q	y	1685	GGCCAAGTTCCTGCACTGGCTGATGAGTGTGACGTCTGAGCTGCTCAGGTCTTCTT	1744
D	b	1681	GGCCAAGTTCCTGCACTGGCTGATGAGTGTGACGTCTGAGCTGCTCAGGTCTTCTT	1740
Q	y	1745	TTATGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTTTTTTCTACCGGAAGAGTGTCTG	1804
D	b	1741	TTATGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTTTTTTCTACCGGAAGAGTGTCTG	1800
Q	y	1805	GAGCAAGTTGCAAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTTGACGTGCGGAGCT	1864
D	b	1801	GAGCAAGTTGCAAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTTGACGTGCGGAGCT	1860
Q	y	1865	GTCGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGCCCGCCCTGCTGACGTCCAGACT	1924
D	b	1861	GTCGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGCCCGCCCTGCTGACGTCCAGACT	1920
Q	y	1925	CCGCTTCATCCCCCAAGCTGACGGGCTGCGGGCTGCGCCGATTGTGAACATGGACTACGTCTGTGG	1984
D	b	1921	CCGCTTCATCCCCCAAGCTGACGGGCTGCGGGCTGCGCCGATTGTGAACATGGACTACGTCTGTGG	1980
Q	y	1985	AGCCAGAACGTTCCGCGACAGAAAAGAGGGCCGACGCTCTACCTCGAGGGTGAAGGCACT	2044
D	b	1981	AGCCAGAACGTTCCGCGACAGAAAAGAGGGCCGACGCTCTACCTCGAGGGTGAAGGCACT	2040
Q	y	2045	GTTCAAGCGTGTCAACTACGAGCGGGCGCGCCCGGCTCTGCGCGGCTCTGTGCT	2104
D	b	2041	GTTCAAGCGTGTCAACTACGAGCGGGCGCGCCCGGCTCTGCGCGGCTCTGTGCT	2100
Q	y	2105	GGGCTTGACGATATCCACAGGGCTTGCGCGCACTTCTGCTGCGTGTGCGGGCCAGGA	2164
D	b	2101	GGGCTTGACGATATCCACAGGGCTTGCGCGCACTTCTGCTGCGTGTGCGGGCCAGGA	2160
Q	y	2165	CCCGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCC	2224
D	b	2161	CCCGCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCC	2220
Q	y	2225	CCAGGACAGGCTCAAGAGTTCATCGCCAGCATCAAAACCCAGAACAGTACTGCGT	2284
D	b	2221	CCAGGACAGGCTCAAGAGTTCATCGCCAGCATCAAAACCCAGAACAGTACTGCGT	2280
Q	y	2285	GCGTCGTATGCCGTGGTCCAGAAGGCCGCCATGGGACAGTCCGCAAGGCTTCAAGAG	2344
D	b	2281	GCGTCGTATGCCGTGGTCCAGAAGGCCGCCATGGGACAGTCCGCAAGGCTTCAAGAG	2340
Q	y	2345	CCACGTCTTACTTGAACAGACCTCCAGCCGTACATGCGACAGTTCTTGGCTCACCTGCA	2404
D	b	2341	CCACGTCTTACTTGAACAGACCTCCAGCCGTACATGCGACAGTTCTTGGCTCACCTGCA	2400
Q	y	2405	GGAAGACAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCTTCCCTGAATGAGGC	2464
D	b	2401	GGAAGACAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCTTCCCTGAATGAGGC	2460
Q	y	2465	CAGCAGTGGCTCTTGCACGTCTTCTTACGCTTCAATGTGCCAACACGCCGTGCCATCAG	2524
D	b	2461	CAGCAGTGGCTCTTGCACGTCTTCTTACGCTTCAATGTGCCAACACGCCGTGCCATCAG	2520
Q	y	2525	GGGCAAGTCTTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCT	2584

CC provided. The cell lines are also used as a diagnostic test for the
CC presence of a virus, such as human cytomegalovirus, and to determine the
CC efficacy of antiviral agents by testing the capability of a modified
CC virus containing a reporter gene to infect the cells. The cell lines have
CC the ability, which can be impaired in cell lines immortalised by other
CC methods, of being able to support viral replication. The cells remain
CC morphologically suitable for viral/vaccine cultivation

Sequence 4070 BP; 670 A; 1383 C; 1296 G; 721 T; 0 U; 0 Other;

Query Match	Score	DB	Length
82.4%	3307	6	4070

Matches 3619; Conservative 0; Mismatches 360; Indels 46; Gaps 5;

[illegible]

QY	906	GCACCTCTTTGAGGGTGCGCTCTCTGGCAGCGGCACTCCACCCATCCGTGGCGCG	965
Db	919	GCCACTCTTTGAGGGTGCGCTCTCTGGCAGCGGCACTCCACCCATCCGTGGCGCG	978
QY	966	CAGCACCAAGCGGGCCCCCATCCACATGCGGGCCACACGTCCCTGGGACACGCGCTGT	1025
Db	979	CAGCACCAAGCGGGCCCCCATCCACATGCGGGCCACACGTCCCTGGGACACGCGCTGT	1038
QY	1026	CCCCCGGTGTACGCGCGAGACCAAGCACTTCCCTCTACTCCTCAGGGGCAAGAGGACGCTG	1085
Db	1039	CCCCCGGTGTACGCGCGAGACCAAGCACTTCCCTCTACTCCTCAGGGGCAAGAGGACGCTG	1098
QY	1086	CGGCGCTCCTTCTCTACTCAGCTCTCTGAGGCCCCAGCGCTGACTGGCGCTCGGAGGCTCGTG	1145
Db	1099	CGGCGCTCCTTCTCTACTCAGCTCTCTGAGGCCCCAGCGCTGACTGGCGCTCGGAGGCTCGTG	1158
QY	1146	GAGACCATCTTTCTGGGTTCCAGGCCCTGAGATGCCAGGGACTCCCCGAGGTTGCCCGC	1205
Db	1159	GAGACCATCTTTCTGGGTTCCAGGCCCTGAGATGCCAGGGACTCCCCGAGGTTGCCCGC	1218
QY	1206	CTGCCCCAGCGCTACTGGCAATGCGGCCCGCTGTTTCTGAGCTGTGGGAAACAACGCG	1265
Db	1219	CTGCCCCAGCGCTACTGGCAATGCGGCCCGCTGTTTCTGAGCTGTGGGAAACAACGCG	1278
QY	1266	CAGTCCCCCTACGGGGTGCTCCTCAAGACGCATGCCCCGTGCGAGCTCGCGTCACCCCA	1325
Db	1279	CAGTCCCCCTACGGGGTGCTCCTCAAGACGCATGCCCCGTGCGAGCTCGCGTCACCCCA	1338
QY	1326	GCAGCCGSGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGAGAG	1385
Db	1339	GCAGCCGSGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGAGAG	1398
QY	1386	GACACAGACCCCCCGCTGCGCTGGTGTGACGTGTCTCCGCAAGACAGAGCCCCCTGGCAGGTG	1445
Db	1399	GACACAGACCCCCCGCTGCGCTGGTGTGACGTGTCTCCGCAAGACAGAGCCCCCTGGCAGGTG	1458
QY	1446	TACGGCTTCGTGCGGAGCTGCGCTGCGCGCGCTGTGTGCCCCCAGGCGCTCTGGGCTTCCAGG	1505
Db	1459	TACGGCTTCGTGCGGAGCTGCGCTGCGCGCGCTGTGTGCCCCCAGGCGCTCTGGGCTTCCAGG	1518
QY	1506	CACAACGAACGCCGCTTCTCAGGAAACAACAAGTTCAATCTCCCTGGGAAAGCATGCCC	1565
Db	1519	CACAACGAACGCCGCTTCTCAGGAAACAACAAGTTCAATCTCCCTGGGAAAGCATGCCC	1578
QY	1566	AAGCTCTCGCTGCAAGAGCTGACGTGAAAGATGACCGTGCGGGACTGCCCTTGGCTGCGC	1625
Db	1579	AAGCTCTCGCTGCAAGAGCTGACGTGAAAGATGACCGTGCGGGACTGCCCTTGGCTGCGC	1638
QY	1626	AGGAGCCCCAGGGGTTGGCTGTGTTCGGGCGCAGAGCAACCGTCTGCCGTGAGAGATCCTG	1685
Db	1639	AGGAGCCCCAGGGGTTGGCTGTGTTCGGGCGCAGAGCAACCGTCTGCCGTGAGAGATCCTG	1698
QY	1686	GCCAAAGTTCCTGCACTGGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTTTTCTTT	1745
Db	1699	GCCAAAGTTCCTGCACTGGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTTTTCTTT	1758
QY	1746	TATGTACCGGAGACCAACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGATGTCTGG	1805
Db	1759	TATGTACCGGAGACCAACGTTTCAAAAAGAACAGGCTCTTTTCTACCCGGAAGATGTCTGG	1818
QY	1806	AGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGTGACGTGCGGAGCTG	1865
Db	1819	AGCAAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGTGACGTGCGGAGCTG	1878
QY	1866	TCGGAAGCAGAGGTCAAGGACGATCGGGAAAGCCAGGCCCCCTGCTGACGTCCAAGACTC	1925
Db	1879	TCGGAAGCAGAGGTCAAGGACGATCGGGAAAGCCAGGCCCCCTGCTGACGTCCAAGACTC	1938
QY	1926	CGCTTCAATCCCCAAGCCTGACGGGCTGCGGCGCGATTGTGAACATGGACTACGTCTGGGA	1985
Db	1939	CGCTTCAATCCCCAAGCCTGACGGGCTGCGGCGCGATTGTGAACATGGACTACGTCTGGGA	1998

QY 1508 CAACGAACGCGCTTCTCAGGAACACCAAGATTCTCTCCCTGGGGAAGCATGCCAA 1567
DB 1501 CAACGAACGCGCTTCTCAGGAACACCAAGATTCTCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTCGCTGAGAGCTGACGTGGAAGATGAGCGTGGGGAAGTGGCTGGCGAG 1627
DB 1561 GCTCTCGCTGAGAGCTGACGTGGAAGATGAGCGTGGGGAAGTGGCTGGCGAG 1620
QY 1628 GAGCCCAAGGGTGGCTGTGTCCGGCCGAGAGCAAGCTGTGCGTGAAGAGATCTGGC 1687
DB 1621 GAGCCCAAGGGTGGCTGTGTCCGGCCGAGAGCAAGCTGTGCGTGAAGAGATCTGGC 1680
QY 1688 CAAGTTCTGCACTGCTGATGAGTGTGTACGTGCTGAGCTGTCAAGTCTTTCTTTA 1747
DB 1681 CAAGTTCTGCACTGCTGATGAGTGTGTACGTGCTGAGCTGTCAAGTCTTTCTTTA 1740
QY 1748 TGTCAAGGAGACCAAGTTCAAAAGAACAGGCTTTTCTTCTACCGGAAGAGTGTCTGAG 1807
DB 1741 TGTCAAGGAGACCAAGTTCAAAAGAACAGGCTTTTCTTCTACCGGAAGAGTGTCTGAG 1800
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DB 1801 CAAGTTGCAAGCATTTGGAATCAGACAGCATTTGAAGAGGGTGCAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAAGGAGCATCGGGAAGCCAGGCCCCCTGCTGACGTCCAGACTCCG 1927
DB 1861 GGAAGCAGAGGTCAAGGAGCATCGGGAAGCCAGGCCCCCTGCTGACGTCCAGACTCCG 1920
QY 1928 CTTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGAAACATGACATGCTGCTGGAGC 1987
DB 1921 CTTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGAAACATGACATGCTGCTGGAGC 1980
QY 1988 CAGAACGTTCCGAGAGAAAAGAGGGCCGAGGCTCTACCTCGAGGGTGAAGGCACTGTT 2047
DB 1981 CAGAACGTTCCGAGAGAAAAGAGGGCCGAGGCTCTACCTCGAGGGTGAAGGCACTGTT 2040
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DB 2341 CGTCTTACCTTGACAGACCTCCAGCCCTATGCGACAGTGTGCTGCTGAGAGGA 2400
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DB 2401 GACCAGCCCGCTGAGGAGTCCGTGCTATGAGCAGAGCTCTCTGATGAGGCGAG 2460
QY 2468 CAGTGCTCTTTCAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2527
DB 2461 CAGTGCTCTTTCAGCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
QY 2528 CAAGTCTACCTTACAGTGCAGGAGTCCCGAGGCTCCATCTCTCCACGCTGCTG 2587
DB 2521 CAAGTCTACCTTACAGTGCAGGAGTCCCGAGGCTCCATCTCTCCACGCTGCTG 2580

QY 2588 CAGCTGTGCTACGGGACATGAGAAACAAGTGTGCTGGGAGATTGGCGGAGCGGCT 2647
DB 2581 CAGCTGTGCTACGGGACATGAGAAACAAGTGTGCTGGGAGATTGGCGGAGCGGCT 2640
QY 2648 GCTCTCGCTTGGTGAATGATTTCTGTTGTGACACCTCACTCAACCGGAAAC 2707
DB 2641 GCTCTCGCTTGGTGAATGATTTCTGTTGTGACACCTCACTCAACCGGAAAC 2700
QY 2708 CTTCTCAGAACCTGATCCGAGGTGCTCCTGATGATGCTGCTGCTGCTGCTGCTG 2767
DB 2701 CTTCTCAGAACCTGATCCGAGGTGCTCCTGATGATGCTGCTGCTGCTGCTGCTG 2760
QY 2768 GACAGTGTGAACCTTCCCTGTAGAAGACAGGCCCCCTGGTGGACAGGCTTTTGT 2827
DB 2761 GACAGTGTGAACCTTCCCTGTAGAAGACAGGCCCCCTGGTGGACAGGCTTTTGT 2820
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QY 3575 CTTGTGCAAAACCGGCAAG-----GGCTTGAAGAGGAGGAGGAGGAGGAGGAG 3629
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QY 3630 CCGCTTCAGAGACAGAGGCGCGGTATCACACAGACAGAGCCCGCGCTCTGCTG 3689

Db	3661	GAGTGTCCAGCACACCTGCGCTCT-TCACCTTCCCCACAGGCTGGCGCTCGGCTCCACCCC	3719
QY	3690	CCAGTCACCGTCTCTGCCCCCTGGACACTTTGTCCAGCATCAGGAGGTTTCTGATCCGT	3749
Db	3720	AGGGCCAGCTTTTCTCTCACCCAGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATC	3779
QY	3750	CTGAATTCAGCCATGTGCAACCTGCGTCTGAGCTTAAACAGCTTCTACTTTCTGTTC	3809
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QY	3810	TTTCTGTGTTGTGAGACCCCTGAGAAGACCCCTGGAGCTCTGGGAATTTGAGTGACCA	3869
Db	3833	CACCATCCAGGTGAGACCTGAGAAGAACCCCTGGAGCTCTGGGAATTTGAGTGACCA	3892
QY	3870	AAGTGTGCCCTGTACACAGCGAGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAA	3929
Db	3893	AAGTGTGCCCTGTACACAGCGAGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAA	3952
QY	3930	ATTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTTCATAA	3989
Db	3953	ATTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTTCATAA	4012
QY	3990	AAA 3992	
Db	4013	AAA 4015	

RESULT 6
AAZ20279

ID	AAZ20279	standard;	CDNA;	4015	BP.
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7					

AC AAZ20279;

DT 17-JAN-2000 (first entry)

Human telomerase reverse transcriptase (hTERT) cDNA.

Telomerase reverse transcriptase; human; hTERT; cell proliferation;

OS Homo sapiens.

FH	Key	Location/Qualifiers
FM	and	23 3 174

FT / *tag= a

PN WO9950386-A2.

PD 07-OCT-1999

PF 31-MAR-1999; 99WO-US007097.
XX

PR	31-MAR-1998;	98US-00052864.
PR	03-APR-1998:	98US-00128354.

AA PA (GERB-) GERBON CORP

PI Morin GB:

DR WPI; 1999-610842/52.

[illegible]

PT catalytic activity in a cell.

PS Disclosure; Fig 2; 24pp; English.

CC This is the nucleotide sequence of cDNA encoding human telomerase reverse

CC diagnosing and treating diseases relating to cell proliferation and

CC of a cell. A claimed method for increasing the proliferative capacity of

CC a vertebrate cell, especially a human or other mammalian cell, involves
CC introducing into the cell a recombinant hTERT polynucleotide encoding an
CC hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-
CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
CC claimed method for reducing telomerase activity in a cell involves
CC introducing a recombinant polynucleotide encoding an hTERT variant having
CC a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT
CC coding sequence
CC
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match	82.4%	Score 3306.6;	DB 2;	Length 4015;
Best Local Similarity	89.9%;	Pred. No. 0;		
Matches 3618; Conservative	0;	Mismatches 359;	Indels 46;	Gaps 5;

QY 8 GCAGCGCTGCGTCTGCTGCTGCGCACGCTGGGAAGCCCTGGCCCCCGGCCACCCCCCGCATGCC 67

Db 1 GCAGCGCTGCGTCTGCTGCTGCGCACGCTGGGAAGCCCTGGCCCCCGGCCACCCCCCGCATGCC 60

QY 68 GCGCGTCCCCGCTGCGAGCCGTGCGTCCCTGCTGCGAGCCACTACCGCGAGGTGCT 127
 |||||
 Db 61 GCGCGCTCCCCGCTGCGAGCCGCTGCGTCCCTGCTGCGAGCCACTACCGCGAGGTGCT 120

125 GCGGCTGGCAGCTGCTGCGGCGCTGGAGGCGCCAGGCGGCTGGTGACGCGG 187
 121 GCGGCTGGCAGCTGCTGCGGCGCGCTGGAGGCCAGGAGCTGGCGCTGGTGACGCGG 180

Db 181 GGACCCGCGCTTTCGGCGCGCTGTGCCAGTGCTGTGTGCCTGGAGC 240

Db 241 ACGGGCCCCCGGGCCCCCTCTCCGCCAGGTGTCTGCTGAAGAGCTGTGGC 300

Db 301 CCGAGTGTGCAGAGCTGTGCGAGCGCGCGGCAAGACGTGCTTGGCTTGGC 360

Db 361 GCTGCTGACGGGGCCCCGGGGGGCCCCCGAGGCTTCACCAACGAGCGTGCAGCTA 420

Ov 428 CCTGCCAACACAGGTGACCGACGCACTGCGGGGGTAGCGGGGGCGTGGAGGAGCTGCTTGG 487

Db 421 C C T G C C C A A C A C G G T G A C C G A C G C A C T G C G G G G G A G C G G G C G T G G G G C T G C T G C G 480

OY 488 C C G C G T G G C C G A C G A C G T G C T G G T T C A C C T G C T G G C A C G C T G C G C G C T C T T T G T G C T G G T 547

Db 481 CCGCGTGGGCGACGAGTGTCTGGTTCACCTGTGGACGCTGGCGCTCTTTGTGTGGT 540

QY 548 GGCTCCACGCTGCGCCTTACAGGTGTGCGGCGCGCGCTGTACCAAGCTCGGCGCTGGCAC 607

Db 541 GGCTCCAGCTGCGCTACCAAGGTGTGCGGCGCGCTGTACCAGCTCGGCGTGCAC 600

QY 608 TCAGGCCCGGCCCGCCACACAGCTAGTGAACCCGAGAAGCGCTGGGATGCCAACGGGC 667

Db 601 TCAGGCCCCCCCCCGCCACACGCTAGTGCATCCCGAAGGCGTCTGGGATGCCAACGGGC 660

Qy 668 CTGGAACCATAGCGTCAAGGAGGCCGGGCTCCCTGGGCCCTGCCAGCCCCGGGTGCAG 727

DB 661 CTGGAACCAATAGCGTCAAGGAGGCCCGGGGTCCCGCTGGGCTGCCAGCCCCGGGTGCAG 720

QY 728 GAGGCGCGGGGCACTGCCAGCCGAAGTCTGCGCTTGCCCAAGAGGCCCAAGGCGTGCAGC 787

DB 121 GAGGCGGGGCGAGTGCACGCCGAAGTCGTCCGTTGCCCAAGAGGCCCCAGGCGGTGGCGC 780

QY 788 TGCCCTGAGCCGAGCGGACGCCCTTGGGCAAGGGTCTGTGCCCAACCCGGGCAAGAC 847

848 GCCTGACCGAGTGAACCGTTCTGTGTGTGTCAACTGCCAGAACCCGGCGAAGAAGC 907

[illegible]

Db	1921	CTTCATCCCAAGCCTGA	CGGGCTGCGGCGGATGTGAACATGGA	CTACGTGCGGAGC	1980	
QY	1988	CAGAACGTTCCG	CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT		2047	
Db	1981	CAGAACGTTCCG	CAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTT		2040	
QY	2048	CAGCGTGTCAA	CTACGAGCGGGCGCGCGCCCGCGCTCTGGGGCGCTCTGTGTGGG		2107	
Db	2041	CAGCGTGTCAA	CTACGAGCGGGCGCGCGCCCGCGCTCTGGGGCGCTCTGTGTGGG		2100	
QY	2108	CCTGACGATATCC	ACAGGGCCCTGGCGCACCTTCCTGCTGCGGTGTGCGGGCCAGAACCC		2167	
Db	2101	CCTGACGATATCC	ACAGGGCCCTGGCGCACCTTCCTGCTGCGGTGTGCGGGCCAGAACCC		2160	
QY	2168	GCCCGCTGAGCTG	TACTTTGTCAAGGTGATGTGACCGGGCGCGTACGACACCATCCCCCA		2227	
Db	2161	GCCCGCTGAGCTG	TACTTTGTCAAGGTGATGTGACCGGGCGCGTACGACACCATCCCCCA		2220	
QY	2228	GGAACAGGCTCA	CGGAGGTCA	TGCGCCAGCATCATCAAA	CCCCAGAACACGTTACTGCGTGGC	2287
Db	2221	GGAACAGGCTCA	CGGAGGTCA	TGCGCCAGCATCATCAAA	CCCCAGAACACGTTACTGCGTGGC	2280
QY	2288	TCCGTATGCCGTG	GTCTCAGAAAGGCCGCCCATGGGCA	CGTCCGCAAGGCTTCAAGAGCCA		2347
Db	2281	TCCGTATGCCGTG	GTCTCAGAAAGGCCGCCCATGGGCA	CGTCCGCAAGGCTTCAAGAGCCA		2340
QY	2348	CGTCTTACCTTG	ACAGACCTCCAGCCCGTACATGCGACAGTTGCTGCGTCACTGCGAGA		2407	
Db	2341	CGTCTTACCTTG	ACAGACCTCCAGCCCGTACATGCGACAGTTGCTGCGTCACTGCGAGA		2400	
QY	2408	GACCAGCCCGCT	GAGGGATGCCGCTGTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG		2467	
Db	2401	GACCAGCCCGCT	GAGGGATGCCGCTGTCATCGACAGAGCTCCTCCCTGAATGAGGCCAG		2460	
QY	2468	CAGTGGCCTCTT	CGACGCTCTTCCCTACGCTTCATGTGCCACACGCGCGTGCATCAGGGG		2527	
Db	2461	CAGTGGCCTCTT	CGACGCTCTTCCCTACGCTTCATGTGCCACACGCGCGTGCATCAGGGG		2520	
QY	2528	CAAGTCTACGT	CCAGTGCACAGGGGATCCCGCAGAGCTCCATCCTCTCCACGCTGCTGTG		2587	
Db	2521	CAAGTCTACGT	CCAGTGCACAGGGGATCCCGCAGAGCTCCATCCTCTCCACGCTGCTGTG		2580	
QY	2588	CAGCCTGTGCT	ACGCGACATGAGAACAAAGCTTTGCGGGGATTCGCGCGGACGGGCT		2647	
Db	2581	CAGCCTGTGCT	ACGCGACATGAGAACAAAGCTTTGCGGGGATTCGCGCGGACGGGCT		2640	
QY	2648	GCTCCTGCGTT	TGTTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGA	AAAC	2707	
Db	2641	GCTCCTGCGTT	TGTTGATGATTTCTTGTGTGACACCTCACCTCACCCACGCGA	AAAC	2700	
QY	2708	CTTCTCTCAG	AGACCTGATCCGAGGTGTCCCTAGATATGGCTGCGTGTGAACCTTGCGGA		2767	
Db	2701	CTTCTCTCAG	AGACCTGATCCGAGGTGTCCCTAGATATGGCTGCGTGTGAACCTTGCGGA		2760	
QY	2768	GACAGTGTGA	ACTTCCCTGTAGAAACGAGGCCCTGGGTGGCA	CGGCTTTTGTTCAGAT	2827	
Db	2761	GACAGTGTGA	ACTTCCCTGTAGAAACGAGGCCCTGGGTGGCA	CGGCTTTTGTTCAGAT	2820	
QY	2828	GCCGGCCCA	CGGCTATTTCCCTGTGTGCGGCTGTCTGTGATACCCGGA	CCCTGGAGGT	2887	
Db	2821	GCCGGCCCA	CGGCTATTTCCCTGTGTGCGGCTGTCTGTGATACCCGGA	CCCTGGAGGT	2880	
QY	2888	GCAGAGCGACT	ACTCCAGCTATATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG		2947	
Db	2881	GCAGAGCGACT	ACTCCAGCTATATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG		2940	
QY	2948	CGGCTTCAA	GCGTGGGAGAACATGCGTGGCAACTCTTTGGGGGTCTTGCGGCTGAAGTG		3007	
Db	2941	CGGCTTCAA	GCGTGGGAGAACATGCGTGGCAACTCTTTGGGGGTCTTGCGGCTGAAGTG		3000	
QY	3008	TCACAGCCTGTT	TCTGATTG	CAGGTGAACAGCCTCCAGACGGTGTGCAACCACTCTA	3067	
Db	3001	TCACAGCCTGTT	TCTGATTG	CAGGTGAACAGCCTCCAGACGGTGTGCAACCACTCTA	3060	

QY	3068	CAAGATCCTCCTGCTGCAAGCGGTACAGSTTTCAAGCATGTGTGCTGCAAGCTCCCATTTCA	3127
Db	3061	CAAGATCCTCCTGCTGCAAGCGGTACAGSTTTCAAGCATGTGTGCTGCAAGCTCCCATTTCA	3120
QY	3128	TCAGCAAGTTTGGAGAACCACATTTTCTCTGCGGCTCATCTGACACGGGCTCCCT	3187
Db	3121	TCAGCAAGTTTGGAGAACCACATTTTCTCTGCGGCTCATCTGACACGGGCTCCCT	3180
QY	3188	CTGCTACTCCATCCTGAAAGCCAAAGACGACGATATGT-----GCAGTGCCTGG	3237
Db	3181	CTGCTACTCCATCCTGAAAGCCAAAGACGACGATGTGCTGGGGGCCAAGGGCGCGC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTAGTGTGTCAGAGACTGAGTGAATCTG	3297
Db	3241	CGGCCCTGTCCCTCCGAGGCCGTGAGTGGCTGTGCCACACAGCATTCCTGCTCAAGCT	3300
QY	3298	GGCTTAGGAAGTTCTTACCCTTTTGCATCAGGAAGTGTGTTAACCAACCACTGTGAG	3357
Db	3301	GACTCGACACCGGTGTCACTACCTAGTGCCTCCTGGGTCATTCAGACAGCCCAAGCGCA	3360
QY	3358	GCTGCTGTCCCGCCTCTCGTGGGCTGAGCAGAGCACTGATGGAAGGACAGAGACTG	3417
Db	3361	GCTGATGTGGAAAGCTCCCGGGGACACGCTGACTGCTCCCTGAGAGCCGACGCCA	3420
QY	3418	TCTGGAGCTGCCATCCTTCCCACTTGCTCT-----GCTTG	3454
Db	3421	ACTGCCCTCAGACTTCAAGACCACTCTGGAATGAGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3455	GGGAAGCGCTGGGGGCGCTGTCTCTCTGTTTGCCCATGTGGGATTTGGGGGCGCTG	3514
Db	3481	GAGCAGACACCAAGCAGCCCTGTCAAGCCGGGCTCTACGTCCAGGGAAGGGGCGGCGC	3540
QY	3515	GCTCTCTCTGTTTGCCCTGTGTGGATTTGGGCTGTCTCCCGTCCATGGCACTTAGGCGC	3574
Db	3541	CACACCCAGGCGCCGACCCGCTGGAGTCTGAGGCTGAGTGAATGTTTGCCGAGGCGTG	3600
QY	3575	CTTGTGCAAAACCGGCCAAG----GGCTTAGGAGGAGGCCAGGCCAGGCTACCCCAAC	3629
Db	3601	CATGTCCGCGCTGAAGGCTGAGTGTCCGCGCTGAGGCTGAGTGAATGTTTCAAGCCAAAGGCT	3660
QY	3630	CCCTCTCAGGAGCAGAGGCGCGGTATCACCAAGCAGAGCGCCGCGCTCTGCTTC	3689
Db	3661	GAGTGTCCAGACACACTGCGCTCT-TCACTTCCCCACAGGCTGGCGCTCGGCTCCACCC	3719
QY	3690	CCAGTCAACCGTCTCTGCCCCCTGGAACACTTGTCCAGCATCAGGAGGTTTGTGATCCGT	3749
Db	3720	AGGGCCAGCTTTTCTCTCACCAAGAGCGCGCTTCCACTCCCAATAGAAATGTCATC	3779
QY	3750	CTGAATTCGAAGCCATGTGGAACCTGCGGCTCTGAGCTTAAACAGCTTCTACTTCTGTTC	3809
Db	3780	CCAGATTCGCCATGTGTAACCCCT-----CGCCCTGCGCTTCTTGCTTCCACCCC	3832
QY	3810	TTTCTGTGTGTGGAGACCCCTGAGAAGAACCCCTGGGAGCTCTGGGAATTTGAGTGACCA	3869
Db	3833	CACCATCCAGGTGAGACCCCTGAGAAGAACCCCTGGGAGCTCTGGGAATTTGAGTGACCA	3892
QY	3870	AAGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA	3929
Db	3893	AAGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA	3952
QY	3930	ATTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAA	3989
Db	3953	ATTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAA	4012
QY	3990	AAA 3992	
Db	4013	AAA 4015	

XX	AC	AAZ30154;
XX	DT	26-JAN-2000 (first entry)
XX	DE	CDNA encoding a human telomerase reverse transcriptase (TRT).
XX	KW	Human; telomerase reverse transcriptase; TRT; T lymphocyte activation; dendritic cell; telomerase activity; cancer cell; proliferating cell; immunological destruction; telomerase; cancer; proliferation disease; ss.
XX	OS	Homo sapiens.
FH	Key	Location/Qualifiers
FT	CDS	56..3454
FT		/tag= a
XX		/product= "telomerase reverse transcriptase"
PN		W09950392-A1.
XX	PD	07-OCT-1999.
XX	PF	30-MAR-1999; 99WO-US006898.
XX	PR	31-MAR-1998; 98US-0112006P.
PA		(GERO-) GERON CORP.
XX		Gaeta FCA;
XX	WI	WI; 1999-610845/52.
DR		P-PSDB; AAY43621.
PT		Eliciting an in vivo immune response for prevention and treatment of cancers.
XX		Disclosure; Fig 2; 26pp; English.
XX		The present sequence encodes a human telomerase reverse transcriptase (TRT) polypeptide. The protein is used in the method of the invention. The specification describes a method for activating a T lymphocyte, comprising contacting the T lymphocyte with a dendritic cell that expresses a TRT peptide in the context of an MHC class I or MHC class II molecule. The protein causes induction of an in vivo immunological response to telomerase activity. Cancer cells are characterized by expression of endogenous TRT gene and the presence of detectable telomerase activity. Therefore, by eliciting a specific immune response to TRT or to TRT-expressing cells, it is possible to selectively target proliferating cells for immunological destruction. The method is used for eliciting an in vivo immune response to telomerase by activating a T lymphocyte, and is useful for prevention and treatment of cancers and other proliferation diseases/conditions
XX		Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
XX		Query Match 82.4%; Score 3306.6; DB 2; Length 4015;
XX		Best Local Similarity 89.9%; Pred. No. 0;
XX		Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5
XX	Db	1 GCAGCGCTGCGTCCCTGCTGCGGACAGTGGAGCCCTGAGCCCGGACACCCCGCGATGCC 67
XX	XX	8 GCAGCGCTGCGTCCCTGCTGCGGACAGTGGAGCCCTGAGCCCGGACACCCCGCGATGCC 67
XX	XX	68 GCGCGCTCCCGCGCTGCGGACAGCCGTGCGTCCCTGCTGCGGACAGCCACTACCGGAGGTGCT 127
XX	XX	61 GCGCGCTCCCGCGCTGCGGACAGCCGTGCGTCCCTGCTGCGGACAGCCACTACCGGAGGTGCT 120
XX	XX	128 GCGCGCTGCGGACAGTGTGTCGGCGGCGCTGGGGGCCCGAGGCTGGCTGTGTCAGCGCGG 187
XX	XX	121 GCGCGCTGCGGACAGTGTGTCGGCGGCGCTGGGGGCCCGAGGCTGGCTGTGTCAGCGCGG 180
XX	XX	188 GAGCCCGCGGCTTCCGCGCGCTGTGTGCGCCAGTGGCTGTGTGCGTGTGCGTGTGCGGACGC 247

Db	181	GGACCCCGCGGCTTTCGCGCGCTGATGCGCAAGTGCCTGATGCGTGCCTTGGAGCGC	240
QY	248	ACGGCCGCCCCCGCGCCCCCTTCCTTCGCCAAGTGTCTGCTGCTGAAGAGCTGTGGC	307
Db	241	ACGGCCGCCCCCGCGCCCCCTTCCTTCGCCAAGTGTCTGCTGCTGAAGAGCTGTGGC	300
QY	308	CCGAGTGTCTCAGAGAGGCTGTGCGAGCGCGCGCGAAGAAGCTGTGCTGCTTCGCTTCGC	367
Db	301	CCGAGTGTCTCAGAGAGGCTGTGCGAGCGCGCGCGAAGAAGCTGTGCTGCTTCGCTTCGC	360
QY	368	GCTGTGGAACGGGGCCCGCGGGGGCCCCCGAGGCTTCACACCAAGCTGCGCAGCTA	427
Db	361	GCTGTGGAACGGGGCCCGCGGGGGCCCCCGAGGCTTCACACCAAGCTGCGCAGCTA	420
QY	428	CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAAGCGGGCGTGGGGCTGCTGCTCGC	487
Db	421	CCTGCCCAACACGGTGACCGACGCACTGCGGGGGAAGCGGGCGTGGGGCTGCTGCTCGC	480
QY	488	CCGCGTGGGCGACGACGTGCTGTTCACTGCTGCGACAGCTGCGCGCTTTGTGCTGTGT	547
Db	481	CCGCGTGGGCGACGACGTGCTGTTCACTGCTGCGACAGCTGCGCGCTTTGTGCTGTGT	540
QY	548	GGCTCCCAAGCTGCGCTTACCAAGGTGTGCGGGCCCGCGCTGTATCCAAGTTCGGCGTCCAC	607
Db	541	GGCTCCCAAGCTGCGCTTACCAAGGTGTGCGGGCCCGCGCTGTATCCAAGTTCGGCGTCCAC	600
QY	608	TCAAGCCCCGGCCCCCGCCACACGCTAGTGAACCCGGAAGCGCTTGGGATGCGAACGGGC	667
Db	601	TCAAGCCCCGGCCCCCGCCACACGCTAGTGAACCCGGAAGCGCTTGGGATGCGAACGGGC	660
QY	668	CTGGAACCATAGCGTCAGGGAGGCGCGGGTCCCCCTGGGCTTGCCAGCCCCGGGTGCGAG	727
Db	661	CTGGAACCATAGCGTCAGGGAGGCGCGGGTCCCCCTGGGCTTGCCAGCCCCGGGTGCGAG	720
QY	728	GAGCGCGGGGGGAGTGCACGCCGAAGTCTGCCGTTGCCCAAGAGCCCAAGCGTGGCGC	787
Db	721	GAGCGCGGGGGGAGTGCACGCCGAAGTCTGCCGTTGCCCAAGAGCCCAAGCGTGGCGC	780
QY	788	TGCCCTGAGCCCGAGCGGACGCCGTGGGAGGGGCTCTGGGCCCAACCGGACAGAC	847
Db	781	TGCCCTGAGCCCGAGCGGACGCCGTGGGAGGGGCTCTGGGCCCAACCGGACAGAC	840
QY	848	GCGTGAACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCCAGACCCGCCGAAGAAGC	907
Db	841	GCGTGAACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCCAGACCCGCCGAAGAAGC	900
QY	908	CACCTCTTTGAGGGTGCGCTTCTGGCAAGCGCCACTCCCAACCATCCGTGGGCGGCCA	967
Db	901	CACCTCTTTGAGGGTGCGCTTCTGGCAAGCGCCACTCCCAACCATCCGTGGGCGGCCA	960
QY	968	GCACCAAGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACAGCTTGTCC	1027
Db	961	GCACCAAGCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACAGCTTGTCC	1020
QY	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCTCAGGCAACAAGAGCAAGTGGC	1087
Db	1021	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCTCAGGCAACAAGAGCAAGTGGC	1080
QY	1088	GCCCTCCTTCTACTCAGCTCTCTGAGGCCACAGCTGACTGGGCTCGGAAGCTCGTGA	1147
Db	1081	GCCCTCCTTCTACTCAGCTCTCTGAGGCCACAGCTGACTGGGCTCGGAAGCTCGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAAGCCCTGAGATGCCAGGAGTCCCCGCAAGGTGCCCCGCTT	1207
Db	1141	GACCATCTTCTGGGTTCCAAGCCCTGAGATGCCAGGAGTCCCCGCAAGGTGCCCCGCTT	1200
QY	1208	GCCCCAAGCGCTACTGGCAATGCGGCCCTGTGTTCTGAGAGTCTTGGAAACCAAGCGCA	1267
Db	1201	GCCCCAAGCGCTACTGGCAATGCGGCCCTGTGTTCTGAGAGTCTTGGAAACCAAGCGCA	1260
QY	1268	GTGCCCCCTACGGGCTGCTCTCTCAAGACGCACTGCCCGCTGGAGCTGCGGTACACCCAGC	1327
Db	1261	GTGCCCCCTACGGGCTGCTCTCTCAAGACGCACTGCCCGCTGGAGCTGCGGTACACCCAGC	1320

QY	1328	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCCAGGGCTCTGTGCGGGCCCCCGAGGAGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCGGGAGAAAGCCCCAGGGCTCTGTGCGGGCCCCCGAGGAGAGGA	1380
QY	1388	CACAGACCCCCCGTCGCTGTGTGACAGCTGCTCCGCCAGCA CAGCAAGCCCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCCCGTCGCTGTGTGACAGCTGCTCCGCCAGCA CAGCAAGCCCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCGTGCGGGCCGTGCTGCGCCCGGGCTGTGTGCCCCAGGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGGCCGTGCTGCGCCCGGGCTGTGTGCCCCAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAAACCGCGCTTCTCAGGAAACACCAAGAGTTCACTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAAACCGCGCTTCTCAGGAAACACCAAGAGTTCACTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGGA CTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGGA CTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCACAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCTGAGAGAGATCCTGGC	1687
Db	1621	GAGCCACAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCTGAGAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGSTCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGSTCTTTCTTTTA	1740
QY	1748	TGTCAACGAGACCAACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGTGTCTGGAG	1807
Db	1741	TGTCAACGAGACCAACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGTGTCTGGAG	1800
QY	1808	CAAGTTCMAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTCMAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTGCGGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTGCGGGAGC	1980
QY	1988	CAGAACGTTCCGCAAGAAAGAGGGCCGAGCGTCTACCTCGAGGCTGAAGCACTGTT	2047
Db	1981	CAGAACGTTCCGCAAGAAAGAGGGCCGAGCGTCTACCTCGAGGCTGAAGCACTGTT	2040
QY	2048	CAGCGTGTCAACTACGAGCGGGCGCGGCCGCCCTCTCTGGGCCCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGGCCGCCCTCTCTGGGCCCTCTGTGCTGGG	2100
QY	2108	CCTGAGCATATCCACAGGGGCTGGCGCACTTTCGTGCTGCGTGTGCGGGGCCAGGACCC	2167
Db	2101	CCTGAGCATATCCACAGGGGCTGGCGCACTTTCGTGCTGCGTGTGCGGGGCCAGGACCC	2160
QY	2168	GCCGCCGTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGCGTACGACACCATCCCCCA	2227
Db	2161	GCCGCCGTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGCGTACGACACCATCCCCCA	2220
QY	2228	GGAACAGGCTACGGAAGTCAATGCGCAGCATCATAAACCCCAAGAACAGTACTGCGTGG	2287
Db	2221	GGAACAGGCTACGGAAGTCAATGCGCAGCATCATAAACCCCAAGAACAGTACTGCGTGG	2280
QY	2288	TCCGTATGCCGTGATCCAGAAAGGCCGCCCATGCGGCAAGGCTTTCAAGAGCCA	2347
Db	2281	TCCGTATGCCGTGATCCAGAAAGGCCGCCCATGCGGCAAGGCTTTCAAGAGCCA	2340
QY	2348	CGTCTCTACCTTGAACAGACCTCCAGCCGTTACATGCGACAGTTGCTGCTCACTGACAGA	2407
Db	2341	CGTCTCTACCTTGAACAGACCTCCAGCCGTTACATGCGACAGTTGCTGCTCACTGACAGA	2400

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Db 2401 GACCAGCCCGCTGAGGATGCGCTGCTCATGAGAGAGCTCTCCCTGAATGAGGCCAG 2460
QY 2468 CAGTGGCCTCTTGCAGCTCTTCTACGCTCATGTGCAACCAAGCCGCTGCGCATCAGGGG 2527
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QY 2528 CAAGTCTACGCTCCAGTGGCCAGGGGATCCCGCAGGGCTCCATCTCTTCAACGCTGCTTG 2587
Db 2521 CAAGTCTACGCTCCAGTGGCCAGGGGATCCCGCAGGGCTCCATCTCTTCAACGCTGCTTG 2580
QY 2588 CAGCCTGTGCTACCGCCGACATGAGAAACAAGCTGTTGCGGGGATTGGCGGGAGCGGGCT 2647
Db 2581 CAGCCTGTGCTACCGCCGACATGAGAAACAAGCTGTTGCGGGGATTGGCGGGAGCGGGCT 2640
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QY 2708 CTTCCTCAGAACCTGTGTCCGAGGTGTCCCTGATGATGGCTGCGTGAACCTTGGGAA 2767
Db 2701 CTTCCTCAGAACCTGTGTCCGAGGTGTCCCTGATGATGGCTGCGTGAACCTTGGGAA 2760
QY 2768 GACAGTGTGAACCTTCTCTGTAGAGAACGAGCCCTGGGTGCAAGCTTTGTTAGAT 2827
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Db 2821 GCCGGCCACGCGCTATTTCCCTGTGCGGCTGTGCTGTGATACCCGAGACCTGAGGT 2880
QY 2888 GCAGAGGCACTACTCAGACTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAACCG 2947
Db 2881 GCAGAGGCACTACTCAGACTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
QY 2948 CGGCTTCAAGGCTGGGAGAAACATGCGTGCAGAACTTTTGGGCTTTGCGGCTGAAGTG 3007
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Db 3001 TCACAGCCTGTTTCTGATTTGAGGTGAGAGAGCCTCCAGAGCGGTGCAACCAACATCTA 3060
QY 3068 CAAGATCCTCCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA 3127
Db 3061 CAAGATCCTCCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTCCCATTTCA 3120
QY 3128 TCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTCTGACAGCGGCTCCCT 3187
Db 3121 TCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGCTCATCTCTGACAGCGGCTCCCT 3180
QY 3188 CTGCTACTCCATCTCTGAAGCAAGCAAGCAAGGATGT-----GCAGGTGCTTG 3237
Db 3181 CTGCTACTCCATCTCTGAAGCAAGCAAGCAAGGATGTGCTGGGGCCAAAGGGCGCGC 3240
QY 3238 CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTAGTGTGTCAGAGACTAGTGAATCTG 3297
Db 3241 CGGCGCTCTGCTCCGAGGCGGTGAGTGTGTGTCAGAGACTAGTGAATCTG 3300
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Db 3301 GACTCGACACCGGTGACCTTACGTGCTCTTGGGGTCACTCAGAGACGCCCAAGCGCA 3360
QY 3358 GCTCGTGTGCGGCGCTCTGCTGAGGTGAGCAGACCTGATGAGGAGGAGAGAGCTG 3417
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QY 3418 TCTGGAGCTGCGCATCTTCCACCTTGTCT-----GCTTG 3454
Db 3421 ACTGCCCTCAGACTTCAAGACCATCTGGAATGAGCACCAGCCGCAAGGCGCGA 3480
QY 3455 GGGAAAGCGCTGGGGGCGCTGCTCTCTCTGTTTGGCCCATGTGAGATTGGGGGCGCTG 3514

Db 3481 GAGCAGACACACAGACGCTGTGTCAGCGCGGCTTACGTCCAGAGGAGGAGGCGGCC 3540
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Db 3541 CACACCCAGGCGCGCAGCTGGAGTGTGAGGCTGAGTGTGTTGGCGGAGGCTTG 3600
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Db 3601 CATGTCCGCTGAAGGTGAGTGTCCGCTGAGGCTGAGCGAGTGTCCAGCAAGGCT 3660
QY 3630 CCTCTCAGAGCAGAGCGCGGTATCACCAGACAGAGCCCGCGGCTCTGCTTC 3689
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QY 3690 CCAGTCAACGCTCTGCGCCCTGACACCTTGTCCAGCATCAGGAGTTCTGATCCGT 3749
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QY 3930 ATTGGGGGAGGTGCTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAATA 3989
Db 3953 ATTGGGGGAGGTGCTGTGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAATA 4012
QY 3990 AAA 3992
Db 4013 AAA 4015

RESULT 8
AAH45901
ID AAH45901 standard; DNA; 4015 BP.
XX AC AAH45901;
XX AC
DT 06-SEP-2001 (first entry)
XX DE
XX Human hTERT gene.
XX KW Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;
XX KW detection; beta-region; diagnosis; cancer; ds.
XX OS Homo sapiens.
FH XX
FH Key Location/Qualifiers
FT exon 1..274
FT /*tag= a
FT /number= 1
FT 275..1628
FT /*tag= b
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FT /number= 12
FT exon 3026. .3087
FT /tag= t
FT /number= 13
FT exon 3088. .3212
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FT exon 3351. .4015
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PN EPI108789-A2.
XX 20-JUN-2001.
PD 15-DEC-2000; 2000EP-00127228.
PF 16-DEC-1999; 99US-00465491.
XX (HOF) HOFFMANN LA ROCHE & CO AG F.
PA Chang SP, Santini CD;
PI WPI; 2001-376930/40.
XX
PT Quantitating expression of mRNA encoding hTERT, the catalytic subunit of
PT telomerase, as an indicator of cancer, by amplifying RNA using primers
PT complementary to hTERT gene sequence and quantitating amplified products.

XX Claim 1; Page 5-7; 29pp; English.
PS
XX The present sequence is that of the hTERT gene encoding the catalytic
CC subunit of the human telomerase, comprising 16 exons, which is useful in
CC a method for quantitating hTERT mRNA. The method is useful for detecting
CC the presence of beta-region (a 182 nucleotide region consisting of exons
CC 7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis
CC of cancer. The method provides an accurate measure of telomerase activity
CC by selectively measuring mRNA that encodes an active hTERT protein
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 82.4%; Score 3306.6; DB 4; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;
QY 8 GCAGCGCTGCTCTGCTGCGACAGTGGAGACCCCTGACCCCGGACACCCCGGATGCC 67
Db 1 GCAGCGCTGCTCTGCTGCGACAGTGGAGACCCCTGACCCCGGACACCCCGGATGCC 60
QY 68 GCGCGCTCCCGCTGCGAGCGTGGCTCCCTGCTGCGACGCACTACCGGAGTGCT 127
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QY 128 GCGCGTGGCAGCTTCTGCGGCGGCTGGGCGCCAGGCGTGGCGGCTGTGACGCGG 187
Db 121 GCGCGTGGCAGCTTCTGCGGCGGCTGGGCGCCAGGCGTGGCGGCTGTGACGCGG 180
QY 188 GGACCCGCGGCTTTCCGCGCGCTGTGTGCCAGTGGCTGTGTGTGCTGCGGACGC 247
Db 181 GGACCCGCGGCTTTCCGCGCGCTGTGTGCCAGTGGCTGTGTGTGCTGCGGACGC 240
QY 248 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 307
Db 241 ACGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
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Db 301 CCGAGTGTGACAGAGCTGTGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 368 GCTGTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 427
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QY 428 CCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGCGGCGGCGGCGGCGGCGGCGG 487
Db 421 CCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 488 CCGCGTGGCGGACGACGCTGTGTACCTGCTGGCACGCTGCGGCGCTCTTGTGCTGCT 547
Db 481 CCGCGTGGCGGACGACGCTGTGTACCTGCTGGCACGCTGCGGCGCTCTTGTGCTGCT 540
QY 548 GGTCCCAAGTGGCGCTTACCAAGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 607
Db 541 GGTCCCAAGTGGCGCTTACCAAGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
QY 608 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 667
Db 601 TCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
QY 668 CTGGAACCATAGCGCTCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 727
Db 661 CTGGAACCATAGCGCTCAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720
QY 728 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
Db 721 GAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
QY 788 TGCCCTGAGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 847
Db 781 TGCCCTGAGCGGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840

QY 848 GCGTGACCGAGTACCGTGGTTTCTGTGTGTGTCACCTGCCAGAACCCGCCGAGAAGC 907
DB 841 GCGTGACCGAGTACCGTGGTTTCTGTGTGTGTCACCTGCCAGAACCCGCCGAGAAGC 900
QY 908 CACCTCTTTGAGAGGTGCGCTCTCTGGACGCGGCCACTCCCAACCATCCCTGGGGCCCA 967
DB 901 CACCTCTTTGAGAGGTGCGCTCTCTGGACGCGGCCACTCCCAACCATCCCTGGGGCCCA 960
QY 968 GCAACACGCGGGCCCCCATCCACATCCGCGGCCACCATCCCTGGGACACGCTTGTCC 1027
DB 961 GCAACACGCGGGCCCCCATCCACATCCGCGGCCACCATCCCTGGGACACGCTTGTCC 1020
QY 1028 CCGCGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAGAGCAAGTGGC 1087
DB 1021 CCGCGTGTACGCGGAGACCAAGCACTTCTCTACTCTCAGGCGACAGAGCAAGTGGC 1080
QY 1088 GCGCTCTCTCTACTCAGCTCTCTGAGGCGCCAGCTGATGGCGCTCGAGAGCTGTGA 1147
DB 1081 GCGCTCTCTCTACTCAGCTCTCTGAGGCGCCAGCTGATGGCGCTCGAGAGCTGTGA 1140
QY 1148 GACCATCTTTCTGGGTTCAGAGCCCTGGATGCCAGGACTCCCGCAGGTGGCCGCCCT 1207
DB 1141 GACCATCTTTCTGGGTTCAGAGCCCTGGATGCCAGGACTCCCGCAGGTGGCCGCCCT 1200
QY 1208 GCGCCAGCGCTACTGGCAATGCGGCCCCCTGTCTGTGAGCTGTGGGAAACCAAGCGCA 1267
DB 1201 GCGCCAGCGCTACTGGCAATGCGGCCCCCTGTCTGTGAGCTGTGGGAAACCAAGCGCA 1260
QY 1268 GTGCCCTTACGAGGTGCTCTCAAGAGCGACCTGCGGCTGCGAGCTGCGGTCAACCCAGC 1327
DB 1261 GTGCCCTTACGAGGTGCTCTCAAGAGCGACCTGCGGCTGCGAGCTGCGGTCAACCCAGC 1320
QY 1328 AGCGGTGTCTGTGCGCGGAGAGAGCCCGAGGCTCTGTGGCGGCCCCGAGAGAGAGA 1387
DB 1321 AGCGGTGTCTGTGCGCGGAGAGAGCCCGAGGCTCTGTGGCGGCCCCGAGAGAGAGA 1380
QY 1388 CACAGACCCCGCTGCGCTGTGAGCTGTCTCCGCAAGACAGAGAGCCCTGGCAGGTGA 1447
DB 1381 CACAGACCCCGCTGCGCTGTGAGCTGTCTCCGCAAGACAGAGAGCCCTGGCAGGTGA 1440
QY 1448 CCGCTTCTGCGGCGCTGCGCTGCGCGGCTGTGCTCCCGAGGCTCTGGGGCTCCAGGCA 1507
DB 1441 CCGCTTCTGCGGCGCTGCGCTGCGCGGCTGTGCTCCCGAGGCTCTGGGGCTCCAGGCA 1500
QY 1508 CAACGAACGCGCTTCTCAAGAACCAAGATTCTCTCCCTGGGGAAGCATGCCAA 1567
DB 1501 CAACGAACGCGCTTCTCAAGAACCAAGATTCTCTCCCTGGGGAAGCATGCCAA 1560
QY 1568 GCTCTGCTGAGAGCTGAGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCCAG 1627
DB 1561 GCTCTGCTGAGAGCTGAGTGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCCAG 1620
QY 1628 GAGCCAGAGGTTGGCTGTGTTCCGCGGAGAGACACCGTCTGCGTGAAGATCTTGGC 1687
DB 1621 GAGCCAGAGGTTGGCTGTGTTCCGCGGAGAGACACCGTCTGCGTGAAGATCTTGGC 1680
QY 1688 CAAGTCTCTGACCTGCTGATGAGTGTGATGCTGAGCTGCTCAGGCTTCTTTTA 1747
DB 1681 CAAGTCTCTGACCTGCTGATGAGTGTGATGCTGAGCTGCTCAGGCTTCTTTTA 1740
QY 1748 TGTACGAGAGACAGTTTCAAAAGAACAGGCTTTTTTCTACCGAAGAGTGTCTGAG 1807
DB 1741 TGTACGAGAGACAGTTTCAAAAGAACAGGCTTTTTTCTACCGAAGAGTGTCTGAG 1800
QY 1808 CAAGTGAAGAGATTGAATCAGACAGCACTTGAAGAGGTTGAGCTGCGGAGCTGTC 1867
DB 1801 CAAGTGAAGAGATTGAATCAGACAGCACTTGAAGAGGTTGAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGGTCAAGCAGCATCGGAAGCAGAGCCCGCTGTGACCTCAGACTCCG 1927
DB 1861 GGAAGCAGAGGTCAAGCAGCATCGGAAGCAGAGCCCGCTGTGACCTCAGACTCCG 1920
QY 1928 CTTATCCCAAGCTTGAAGGCTGCGGCGGCTGTGACATGACTAGCTGTGGAGC 1987
DB 1921 CTTATCCCAAGCTTGAAGGCTGCGGCGGCTGTGACATGACTAGCTGTGGAGC 1980
QY 1988 CAGAAGTTCGAGAGAAAGAGGCGGAGCTCTCACTCGAGGTGAAGGCACTGTT 2047
DB 1981 CAGAAGTTCGAGAGAAAGAGGCGGAGCTCTCACTCGAGGTGAAGGCACTGTT 2040
QY 2048 CAGCGTCTCAACTACGAGCGGCGCGGCGCCCGCTCTGGGCGCTGTGCTGGG 2107
DB 2041 CAGCGTCTCAACTACGAGCGGCGCGGCGCCCGCTCTGGGCGCTGTGCTGGG 2100
QY 2108 CTTGAGCATATCCACAGGCGCTGGCGACCTTGTGCTGCTGTGCGGCGGAGAGCC 2167
DB 2101 CTTGAGCATATCCACAGGCGCTGGCGACCTTGTGCTGCTGTGCGGCGGAGAGCC 2160
QY 2168 GCGGCTGAGCTGACTTGTGCAAGGTGATGATGACGGGCGGCTACGACACCATCCCCA 2227
DB 2161 GCGGCTGAGCTGACTTGTGCAAGGTGATGATGACGGGCGGCTACGACACCATCCCCA 2220
QY 2228 GGAAGGCTCACGAGGTGATCGCCAGCATCATCAACCCAGAACACGTAAGTGGCG 2287
DB 2221 GGAAGGCTCACGAGGTGATCGCCAGCATCATCAACCCAGAACACGTAAGTGGCG 2280
QY 2288 TCGGTATGCGGTGTCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2347
DB 2281 TCGGTATGCGGTGTCCAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2340
QY 2348 CGTCTTACTTGAACAGACTCCAGCGGTACATGAGCAAGTTCGTGCTCAGCTGACGGA 2407
DB 2341 CGTCTTACTTGAACAGACTCCAGCGGTACATGAGCAAGTTCGTGCTCAGCTGACGGA 2400
QY 2408 GACCAAGCCGCTGAGGATGCGGCTGCTATGAGCAGAGCTCTCCCTGAATGAGGCGAG 2467
DB 2401 GACCAAGCCGCTGAGGATGCGGCTGCTATGAGCAGAGCTCTCCCTGAATGAGGCGAG 2460
QY 2468 CAGTGGCTCTTGAAGCTTCTTCAAGCTTATGATGAGCAGAGCGGCTGAGGAGG 2527
DB 2461 CAGTGGCTCTTGAAGCTTCTTCAAGCTTATGATGAGCAGAGCGGCTGAGGAGG 2520
QY 2528 CAAGTCTACGTCAGTGCCAGGAGATCCCGAGGCTCCATCTCTCCAGCTGCTG 2587
DB 2521 CAAGTCTACGTCAGTGCCAGGAGATCCCGAGGCTCCATCTCTCCAGCTGCTG 2580
QY 2588 CAGCTGTGTAAGGAGCATGAGAACAGCTGTTGCGGAGATTCGGGAGACGGGCT 2647
DB 2581 CAGCTGTGTAAGGAGCATGAGAACAGCTGTTGCGGAGATTCGGGAGACGGGCT 2640
QY 2648 GCTCTGCGTTGGTGAATTTCTTGTGTAACCTCACTCAACCGAAGAAC 2707
DB 2641 GCTCTGCGTTGGTGAATTTCTTGTGTAACCTCACTCAACCGAAGAAC 2700
QY 2708 CTTCTCAGAACCTGCTCCAGAGTGTCCCTGATGAGTGTGCTGCTGCTGCTGCTGCTG 2767
DB 2701 CTTCTCAGAACCTGCTCCAGAGTGTCCCTGATGAGTGTGCTGCTGCTGCTGCTGCTG 2760
QY 2768 GACAGTGAATCTTCCCTGTGAGAGAGAGCCCTGGTGGACAGGCTTGTTCAGAT 2827
DB 2761 GACAGTGAATCTTCCCTGTGAGAGAGAGCCCTGGTGGACAGGCTTGTTCAGAT 2820
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DB 2821 GCGGCGGAGGCTTATCCCTGTGAGGCGGCTGCTGCTGATACCGGAGCTTGGAGGT 2880
QY 2888 GCAAGGCACTATCCAGCTATGCGGAGCTCCATCAGAGCAGTCTCACTTCAACCG 2947
DB 2881 GCAAGGCACTATCCAGCTATGCGGAGCTCCATCAGAGCAGTCTCACTTCAACCG 2940
QY 2948 CCGCTTCAAGGCTGAGAGAAACATGCTGCAAACTCTTGGGCTTGGGCTGAAGTG 3007
DB 2941 CCGCTTCAAGGCTGAGAGAAACATGCTGCAAACTCTTGGGCTTGGGCTGAAGTG 3000
QY 3008 TCACAGCTGTTCTGATTTGAGGTGAACAGCTCCAGAGGTTGACCAACATCTA 3067

Db	3001	TCACAGCCTGTTTCTGTGATTGGACGGGTGAACAGCCTCCAGACGGGTGTGCACCAACATCTA	3060
QY	3068	CAGATCCTCCTGTGTGACAGGCGTACAGGTTTCAACGCATGTGTCTGACGCTCCCATTTCA	3127
Db	3061	CAGATCCTCCTGTGTGACAGGCGTACAGGTTTCAACGCATGTGTCTGACGCTCCCATTTCA	3120
QY	3128	TCAGCAAGTTTGGAGAACCACATTTTTCCTGCGCTCATCTGTGACACGCGCTCCCT	3187
Db	3121	TCAGCAAGTTTGGAGAACCACATTTTTCCTGCGCTCATCTGTGACACGCGCTCCCT	3180
QY	3188	CTGCTACTCCATCCTGAAAGCCAAGAACGAGGTATGT-----GCAGTGCCTGG	3237
Db	3181	CTGCTACTCCATCCTGAAAGCCAAGAACGAGGTATGTGGGGCCCAAGGGCGCTGC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTGTAGTGTGTGAGAGACTGAGTGAATCTG	3297
Db	3241	CGGCGCTCTGCGCTCCGAGGCGGTGCAGTGTGTGTGTGCAACCAAGCATTCCTGTCAAGT	3300
QY	3298	GGCTTAGGAAGTTCTTACCCCTTTTTCGCATCAGGAAGTGTTTAAACCAACACTGTACG	3357
Db	3301	GACTTCGACACCGTGTACCTTACGTATGCCACTCCTGGGTCACTCAGACAGCCACAGCA	3360
QY	3358	GCTGTGTGCCCCCGCTCTCGTGGGGGTGAGCAGAGCACTGATGGAAGGACAGAGAGCTG	3417
Db	3361	GCTTAGTGGGAAGCTCCCGGGGACAGCGCTGACTGCTGTGGAAGCGCAGCCAAACCGGC	3420
QY	3418	TCTGGAGCTGCCATCTTCCACCTTGCTCT-----GCTTG	3454
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTGTGACTGATGAGCCACCGCCACAGCCAGGCGCA	3480
QY	3455	GGAAGCGCTGGGGGCGCTGTGTCTCTCTGTGTTTGCCCATGTGGATTGGGGGCGTG	3514
Db	3481	GAGCAGACACCAAGCAGCCCTGTTCACGCGGGCTTACCTCCAGGGAGGAGGGGCGCC	3540
QY	3515	GCTCTCTCTGTTTGCCCTGTGTGGGATTGGCGTGTCCCGTCCATGACATTAGGACC	3574
Db	3541	CACACCCAGGCGCCGACCGCTGGAGTCTGAGGCTGAGTGAATGTTTGGCCGAGGCTG	3600
QY	3575	CTGTGCAAAACCCAGGCCAAG-----GGCTTAGAGAGGCCAGGCCAGGCTAACCAC	3629
Db	3601	CATGTCCGCTGAAGCTGATGTTCGGCTGAGGCTGAGCGAGTGTCCAGGCCAAGGCT	3660
QY	3630	CCCTCTCAGAGCAGAGGCGCGCTATACACAGACAGAGCCCGCGCTCTGTGCTTC	3689
Db	3661	GAGTGTCCAGACACACTGCCGTCT-TCACTTCCCAAGGCTGGCGTCCGCTCCACCC	3719
QY	3690	CCAGTCAACCGTCTGTGCCCTGGAACACTTGTGTCCAGCATCAGGAGTTTCTGATCCGT	3749
Db	3720	AGGGCCAGCTTTTCTTCAACAGAGACCCGCTTCCACTCCCAATAGGAATATGCCATC	3779
QY	3750	CTGAAATTCAGGCCATGTGAACTTGCGGTCTGAGCTTAAACAGCTTCTACTTTCTGTTC	3809
Db	3780	CCCAGATTGCCATTGTTCACCCCT-----CGCCCTGCGCTCTTGTGCTTCCACCC	3832
QY	3810	TTTCTGTGTGTGTGAGACCTTGAGAAGAACCCCTGGAGCTCTGGAAATTTGAGTGACCA	3869
Db	3833	CACCATCCAGGTGAGACCTTGAGAAGAACCCCTGGAGCTCTGGAAATTTGAGTGACCA	3892
QY	3870	AAGGTGTCCCTGTATACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA	3929
Db	3893	AAGGTGTCCCTGTATACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA	3952
QY	3930	ATTGGGGGGAGGTGCTGTGGGAGTAAATATACTGAATATATAGATTTTTCAGTTTGAATA	3989
Db	3953	ATTGGGGGGAGGTGCTGTGGGAGTAAATATACTGAATATATAGATTTTTCAGTTTGAATA	4012
QY	3990	AAA 3992	
Db	4013	AAA 4015	

ID	AAD46821 standard; cDNA; 4015 BP.	
XX		
AC	AAD46821;	
XX		
DT	27-JAN-2003 (first entry)	
XX		
DE	Human telomerase reverse transcriptase (TERT) cDNA.	
KM	Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;	
KM	transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;	
KW	telomerase reverse transcriptase; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	56..3454
FT		/*tag= a
FT		/product= "Human telomerase reverse transcriptase"
XX		
PN	WO200274948-A2.	
XX		
PD	26-SEP-2002.	
XX		
PF	21-MAR-2002; 2002WO-CA000378.	
XX		
PR	21-MAR-2001; 2001US-0277811P.	
XX		
PA	(GERO-) GERON CORP.	
XX		
PI	Denning C, Clark AJ, Schiff JM;	
XX		
DR	WPI; 2002-759895/82.	
DR	P-PSDB; AAE29226.	
XX		
PT	Mammalian cells, useful for producing animal tissues with carbohydrate	
PT	antigens that are compatible for transplantation into human patients.	
XX		
PS	Disclosure; Page 33-34; 71pp; English.	
XX		
CC	The invention relates to animal tissues with carbohydrate antigens that	
CC	are compatible for transplantation into human patients. The mammalian	
CC	cell is inactivated homozygously for expression of alpha(1,3)galactosyl-	
CC	transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-	
CC	fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue	
CC	with carbohydrate antigens that are compatible for transplantation into	
CC	human patients. The present sequence is human telomerase reverse	
CC	transcriptase (TERT) cDNA used in the invention	
XX		
SO	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;	
XX		

RESULT 9
AAD46821

[illegible]

QY	300	CCGAGTGTCTGACAGAGGCTGTGTCCGAGCGCGCGCGCAAGAACGTGTGGCTTCGGCTTCGC	367
Db	301	CCGAGTGTCTGACAGAGGCTGTGTCCGAGCGCGCGCGCAAGAACGTGTGGCTTCGGCTTCGC	360
QY	368	GCTGCTGGACGGGGCCCCCGGGGGGGCCCCCCCCGAGGCGCTTCACCAACGAGCGTGCAGCTA	427
Db	361	GCTGCTGGACGGGGCCCCCGGGGGGGCCCCCCCCGAGGCGCTTCACCAACGAGCGTGCAGCTA	420
QY	428	CCTGCCCAACACGGTGACCCGACCCACTGCGGGGAGACGGGGCGTGGGGGCTGCTGTGCG	487
Db	421	CCTGCCCAACACGGTGACCCGACCCACTGCGGGGAGACGGGGCGTGGGGGCTGCTGTGCG	480
QY	488	CCGCGTGGGGCGACGACGTGTGTGTCACTGTGGACAGCTGCGCGCTCTTGTGTGCTGCT	547
Db	481	CCGCGTGGGGCGACGACGTGTGTGTCACTGTGGACAGCTGCGCGCTCTTGTGTGCTGCT	540
QY	548	GGCTCCCAAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTGTACAGCTGCGCGCTGCGAC	607
Db	541	GGCTCCCAAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTGTACAGCTGCGCGCTGCGAC	600
QY	608	TCAGGCCCCGGCCCCCGCCACACGCTAGTGACCCCGAAGCGCTCTGGATGCGAACGGGC	667
Db	601	TCAGGCCCCGGCCCCCGCCACACGCTAGTGACCCCGAAGCGCTCTGGATGCGAACGGGC	660
QY	668	CTGGAACCATAGCGTCAAGGAGCGCGGGGTCCCCCTGGGCTTGACGCCCGGGTGCAG	727
Db	661	CTGGAACCATAGCGTCAAGGAGCGCGGGGTCCCCCTGGGCTTGACGCCCGGGTGCAG	720
QY	728	GAGGCGCGGGGCGAGTGCACGCGCAAGTCTGCCCTTGCCCAAGAGCCCGAGCGTGGCGC	787
Db	721	GAGGCGCGGGGCGAGTGCACGCGCAAGTCTGCCCTTGCCCAAGAGCCCGAGCGTGGCGC	780
QY	788	TGCCCCCTGAGCCGAGCGGACGCGCCGTTGGGCAAGGGTCTGGGCCACCCCGGGCAGGAC	847
Db	781	TGCCCCCTGAGCCGAGCGGACGCGCCGTTGGGCAAGGGTCTGGGCCACCCCGGGCAGGAC	840
QY	848	GCGTGAGCCGAGTGACCGTGTGTTCTGTGTGTGTCACTGCGCAGACCCGCGCAAGAAC	907
Db	841	GCGTGAGCCGAGTGACCGTGTGTTCTGTGTGTGTCACTGCGCAGACCCGCGCAAGAAC	900
QY	908	CACCTCTTTGAGAGGTGCGCTCTTGAGCAGCGCCACTCCACCCTCCGTGGGCGCGCA	967
Db	901	CACCTCTTTGAGAGGTGCGCTCTTGAGCAGCGCCACTCCACCCTCCGTGGGCGCGCA	960
QY	968	GCAACACGCGGGCCCCCCCCATCCATCGCGGCGCACCAACGTCCTGGGACACGCGCTGTCC	1027
Db	961	GCAACACGCGGGCCCCCCCCATCCATCGCGGCGCACCAACGTCCTGGGACACGCGCTGTCC	1020
QY	1028	CCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGGACAAAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGGACAAAGAGCAGCTGCG	1080
QY	1088	GCCCTCCTTCTACTCAGTCTCTGAGGCCCAAGCTGACTGGCGCTCGGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTACTCAGTCTCTGAGGCCCAAGCTGACTGGCGCTCGGAGGCTCGTGA	1140
QY	1148	GACCATCTTCTGTGGTTCCAGGCCCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGGCT	1207
Db	1141	GACCATCTTCTGTGGTTCCAGGCCCCCTGGATGCCAGGGACTCCCCGAGGTTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGAGCTGCTTGGGAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGAGCTGCTTGGGAACCAAGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCAACCCAGC	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTCAACCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCCGAGAGAGCCCCCAGGGCTGTGTGCGGGCCCCCGAGAGAGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCCGAGAGAGCCCCCAGGGCTGTGTGCGGGCCCCCGAGAGAGAGGA	1380

QY	1388	CACAGACCCCCCGCTGCGCTGGTGAGCTGCTCCGCGACAGACAGCAGCCCCCTGGCAGGTGTA	1444
Db	1381	CACAGACCCCCCGCTGCGCTGGTGAGCTGCTCCGCGACAGCAGCAGCCCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCGTGCGGGCCTGCGCTGCGCGCGGCTGTGTGCCCCCAGGCGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGGCCTGCGCTGCGCGCGGCTGTGTGCCCCCAGGCGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCCCGCTTCTCAGGAACACCAAGATTCAATCTCCCTGGGGAGCATGCCAA	1567
Db	1501	CAACGAACGCCCGCTTCTCAGGAACACCAAGATTCAATCTCCCTGGGGAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGGAGCTGACGTGGAGATGACGTGCGGGACTGCGCTTGCGTGGCGCAG	1627
Db	1561	GCTCTCGCTGCAGGAGCTGACGTGGAGATGACGTGCGGGACTGCGCTTGCGTGGCGCAG	1620
QY	1628	GAGCCACAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGAGATCCTGGC	1687
Db	1621	GAGCCACAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCATGCGCTGATGAGTGTGTACGTGTGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCATGCGCTGATGAGTGTGTACGTGTGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGAGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGAGAGACACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCCAGCATTCGGGAAGCCAGGCCCGCCCTGCTGACGTCACACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCCAGCATTCGGGAAGCCAGGCCCGCCCTGCTGACGTCACACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCCATTTGTGAACATGGACTACGTCTGTGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCCATTTGTGAACATGGACTACGTCTGTGGAGC	1980
QY	1988	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCTAACTACGAGCGGGCGCGCGCCCGGCTCTGTGGCGCCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCTAACTACGAGCGGGCGCGCGCCCGGCTCTGTGGCGCCTCTGTGCTGGG	2100
QY	2108	CCTGGACGATATCCACAGGGCCTGCGCACTTGTGCTGCGTGTGCGGGCCAGGACCC	2167
Db	2101	CCTGGACGATATCCACAGGGCCTGCGCACTTGTGCTGCGTGTGCGGGCCAGGACCC	2160
QY	2168	GCCGCGTGAAGTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA	2227
Db	2161	GCCGCGTGAAGTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA	2220
QY	2228	GGAACAGCTCACGGAGGTCATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCCGTGC	2287
Db	2221	GGAACAGCTCACGGAGGTCATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCCGTGC	2280
QY	2288	TCCGTATGCCGTGGTCCAGAAAGCGGCCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2347
Db	2281	TCCGTATGCCGTGGTCCAGAAAGCGGCCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTCTACCTTGAACAGACCTCCAGCCGTAATGCGACAGATTGCTGTGCTTCACTTGCA	2407
Db	2341	CGTCTCTACCTTGAACAGACCTCCAGCCGTAATGCGACAGATTGCTGTGCTTCACTTGCA	2400
QY	2408	GACCAAGCCCGCTGAGGGATGCCGTGCTCATTCGACAGAGAGCTCTCCCTGTAATGAGGCCAG	2467
Db	2401	GACCAAGCCCGCTGAGGGATGCCGTGCTCATTCGACAGAGAGCTCTCCCTGTAATGAGGCCAG	2460
QY	2468	CAGTGGCCTCTTGCACGCTCTTCTACGCTTCAATGTGCCACCAAGCCGCTGCGCATCAGGGG	2527

Db 2461 CAGTGGCTCTTGAAGCTCTTCTACGCTTATGTGCCACACCGCCGTGCGATCAGGGG 2520
QY 2528 CAGTCTTACGTCAGTGGCCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG 2587
Db 2521 CAGTCTTACGTCAGTGGCCAGGGGATCCCGAGGGCTCCATCTCTCCACGCTGCTCTG 2580
QY 2588 CAGCTGTGTACCGGCATGAGAACAGCTGTTGCGGGATTCGGGAGCGGCT 2647
Db 2581 CAGCTGTGTACCGGCATGAGAACAGCTGTTGCGGGATTCGGGAGCGGCT 2640
QY 2648 GCTCTGCGTTGTGATGATTTCTGTGTGACACCTCACCCTCAACCCAGGAAAC 2707
Db 2641 GCTCTGCGTTGTGATGATTTCTGTGTGACACCTCACCCTCAACCCAGGAAAC 2700
QY 2708 CTCTCTCAGACCTGTGCTCCGAGGTGCTCCCTGATGCTGCGTGAACCTTGCGAA 2767
Db 2701 CTCTCTCAGACCTGTGCTCCGAGGTGCTCCCTGATGCTGCGTGAACCTTGCGAA 2760
QY 2768 GACAGTGTGAACCTTCCCTGTAGAAGACGAGCCCTGGTGACAGCTTTTGTAGAT 2827
Db 2761 GACAGTGTGAACCTTCCCTGTAGAAGACGAGCCCTGGTGACAGCTTTTGTAGAT 2820
QY 2828 GCGGGCCACGCGCTATTCCCTGTGTGCGGCTGCTGTGATACCCGAGCCCTGAGGT 2887
Db 2821 GCGGGCCACGCGCTATTCCCTGTGTGCGGCTGCTGTGATACCCGAGCCCTGAGGT 2880
QY 2888 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACTTCAACG 2947
Db 2881 GCAGAGCGACTACTCCAGCTATGCCCCGAGCTCCATCAGAGCCAGTCTCACTTCAACG 2940
QY 2948 CCGCTTCAAGGCTGGGAGAACATGCGTCCGAACTCTTTGGGGTCTTGCGGCTGAAGT 3007
Db 2941 CCGCTTCAAGGCTGGGAGAACATGCGTCCGAACTCTTTGGGGTCTTGCGGCTGAAGT 3000
QY 3008 TCACAGCCTGTTTCTGGAATTGCAAGGTGAACAGCCTCCAGACGGGTGCAACCACTTA 3067
Db 3001 TCACAGCCTGTTTCTGGAATTGCAAGGTGAACAGCCTCCAGACGGGTGCAACCACTTA 3060
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QY 3128 TCAGCAAGTTTGAAGAACCACCATTTTCTGCGGCTCATCTTGAACAAGGCTCTCCCT 3187
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QY 3188 CTGCTACTCCATCTGAAAGCCCAAGACGAGTATGT-----GCAGTGCCTTG 3237
Db 3181 CTGCTACTCCATCTGAAAGCCCAAGACGAGTATGT-----GCAGTGCCTTG 3240
QY 3238 CTTAGTGGCAGCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3297
Db 3241 CCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3300
QY 3298 GAGCTTAGGAAGTTCTTACCCCTTTTTCGATCAGGAAGTGTGTTAACCAACCACTGTGAG 3357
Db 3301 GACTCGACACCGTGTACCTTACGTCACCTCTGCGGTCACTCAGACAGCCAGACGCA 3360
QY 3358 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3417
Db 3361 GCTGAGTCGGAAGCTCCCGGGGAGCAGACGCTGATGCTGAGGCGCAGCAACCCGCGC 3420
QY 3418 TCTGGAGCTGCTCATCTTCCACCTGCTCT-----GCTG 3454
Db 3421 ACTGCCCTCAGACTTGAAGACCATCTGATGATGCGCACCCGCCACAGCCAGGCGCA 3480
QY 3455 GGAAGCGCTGGGGGCTGCTGCTCTCTGTTGCCCCCATGTGGATTGGGGGCTG 3514
Db 3481 GAGCAGACACAGCAGCCTGTCTACGCGCGCTCTACGTCCTCAGGAGGAGGGGCGGCC 3540
QY 3515 GCCTCTCTGTTTGGCTGTGTGGATGGGCTGTCTCCGCTCATGCACTTAGGGCC 3574

Db 3541 CACACCCAGGCCCCGACCCGCTGGAGTCTGAGGCTGAGTGTGTCGCGAGGCTG 3600
QY 3575 CTTGTGCAAAACCCAGGCCAAG-----GGCTTAGAGAGAGGCCAGGCCATACCCAC 3629
Db 3601 CATGTCCGGCTGAAGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCAAGGCT 3660
QY 3630 CCCTCTCAGAGCAGAGGCGCGGTATTCACACGACAGAGCCCGCGCTCTGCTTC 3689
Db 3661 GAGTGTCCAGCAGACCTGCGCTCT-TCATTTCCCAAGCGCTGCGCTCCACCCC 3719
QY 3690 CCAATCACCCTCTCTGCCCCCTGACACTTTGTCCAGCATCAGGAGTTCGTATCCGT 3749
Db 3720 AGGCCAGCTTTCTCTCACCAGAGGCGCGCTTCCACTCCCAATAGGAATAGTCATC 3779
QY 3750 CTGAATTCAAGCCATGTGAACTGCGGCTGCTGAGCTTAACAGCTTCTACTTCTGTT 3809
Db 3780 CCCAGATTGCGCATGTTTCAACCCCT-----CGCCCTGCGCTCTTTCCTTCCACCCC 3832
QY 3810 TTTCTGTGTGTGAGACCCCTGAGAAAGACCCCTGGAGCTCTGGAAATTGAGTGACCA 3869
Db 3833 CACCATCAGGTGAGACCCCTGAGAAAGACCCCTGGAGCTCTGGAAATTGAGTGACCA 3892
QY 3870 AAGGTGTGCTGTGACACAGGCGAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAA 3929
Db 3893 AAGGTGTGCTGTGACACAGGCGAGGACCCCTGCACTGTGATGGGGTCCCTGTGGTCAA 3952
QY 3930 ATTGGGGGAGGTGCTGTGAGGATTAATACTGAATATATGAGTTTTCAGTTTGAATA 3989
Db 3953 ATTGGGGGAGGTGCTGTGAGGATTAATACTGAATATATGAGTTTTCAGTTTGAATA 4012
QY 3990 AAA 3992
Db 4013 AAA 4015

RESULT 10
ABA97534
ID ABA97534 standard; DNA; 4015 BP.
XX
AC ABA97534;
DT 05-APR-2002 (first entry)
XX
DE Cancer cell discrimination method related human DNA.
XX
KW Human; telomerase; enzyme; cancer cell discrimination; gene;
XX reverse transcriptase; ds.
OS Homo sapiens.
XX
PN JP2001309791-A.
XX
PD 06-NOV-2001.
XX
PF 02-MAY-2000; 2000JP-00138250.
XX
PR 02-MAY-2000; 2000JP-00138250.
XX
PA (KANE/) KANEUCHI H.
XX (KAMI/) KAMIMORI M.
XX
DR WPI; 2002-134853/18.
XX
PT Discrimination of a cancer cell in a sample tissue, comprises determining
PT the expression level of a reverse transcriptase component of telomerase
PT using a hybridization assay.
XX
PS Claim 2; Page 9-10; 16pp; Japanese.
XX
CC The present invention relates to a method for the discrimination of a
CC cancer cell in a sample tissue, which involves determining the expression
CC level of a reverse transcriptase component of telomerase in a cell
CC constituting the sample tissue by an in situ hybridization of the mRNA of

CC the enzyme, and judging a cell showing a higher expression level than
CC that of the reverse transcriptase component of telomerase in a normal
CC cell to be a cancer cell. The present sequence is a human DNA used in the
CC exemplification of the invention

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 82.4%; Score 3306.6; DB 6; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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QY 8 GCAGCGCTGCTCTCTGTCGCAAGTGGGAAAGCCCTGGCCCGGCAACCCCGCATGCC 67
DB 1 GCAGCGCTGCTCTCTGTCGCAAGTGGGAAAGCCCTGGCCCGGCAACCCCGCATGCC 60
QY 68 GCGCGCTCCCGCTGCGAGCCGCTGCTCTCTGTCGCAAGTGGGAAAGCCCTGGCCCG 127
DB 61 GCGCGCTCCCGCTGCGAGCCGCTGCTCTCTGTCGCAAGTGGGAAAGCCCTGGCCCG 120
QY 128 GCGCGCTGCGAGCTGCTGTCGCGCGCTGCGGAGCCCGCAAGGCTGCTGTCAGCGCG 187
DB 121 GCGCGCTGCGAGCTGCTGTCGCGCGCTGCGGAGCCCGCAAGGCTGCTGTCAGCGCG 180
QY 188 GGACCCGCGCGCTTTCGCGCGCTGCTGTCGCGAGTGCCTGCTGTCGTCGTCGTCG 247
DB 181 GGACCCGCGCGCTTTCGCGCGCTGCTGTCGCGAGTGCCTGCTGTCGTCGTCGTCG 240
QY 248 ACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
DB 241 ACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 308 CCGAGTGTGAGAGAGGCTGTGCGAGCGCGCGCGCGCGAGAAAGTGTGCTTCCGCTT 367
DB 301 CCGAGTGTGAGAGAGGCTGTGCGAGCGCGCGCGCGCGAGAAAGTGTGCTTCCGCTT 360
QY 368 GCTGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
DB 361 GCTGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 428 CCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGCG 487
DB 421 CCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGCG 480
QY 488 CCGCGTGGGCGACGACGCTGCTGTCACTGCTGCGACGCTGCGCGCTCTTGTGTGT 547
DB 481 CCGCGTGGGCGACGACGCTGCTGTCACTGCTGCGACGCTGCGCGCTCTTGTGTGT 540
QY 548 GGTCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTCGGCGTGCAC 607
DB 541 GGTCTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTCGGCGTGCAC 600
QY 608 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 667
DB 601 TCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
QY 668 CTGGAACCATAGCGTCAAGGAGCGCGGGGTCCCTCTGGGCTGCGCAAGCCCGGGTGCAG 727
DB 661 CTGGAACCATAGCGTCAAGGAGCGCGGGGTCCCTCTGGGCTGCGCAAGCCCGGGTGCAG 720
QY 728 GAGGCGCGGGGCGAGTGCAGCGCGAAGTCTGCGGTGCGCAAGAGGCGCGCAAGCGTGC 787
DB 721 GAGGCGCGGGGCGAGTGCAGCGCGAAGTCTGCGGTGCGCAAGAGGCGCGCAAGCGTGC 780
QY 788 TGCCCTTGAAGCGGAGCGGAGCGCGCTGGGCGAGGGGTCTGGGCGCGCAAGCGGAGAC 847
DB 781 TGCCCTTGAAGCGGAGCGGAGCGCGCTGGGCGAGGGGTCTGGGCGCGCAAGCGGAGAC 840
QY 848 GCGTGAAGCGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
DB 841 GCGTGAAGCGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGGGGTGCGCTCTGTGCAAGCGCGCACTCCCACTCCGTGGGCGCGCA 967
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DB 901 CACCTCTTTGAGGGGTGCGCTCTGTGCAAGCGCGCACTCCCACTCCGTGGGCGCGCA 960
QY 968 GCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027
DB 961 GCACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
QY 1028 CCCGCTGTCAGCGCGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1087
DB 1021 CCCGCTGTCAGCGCGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1088 GCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1147
DB 1081 GCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
QY 1148 GACCATCTTTCTGGGTTCCAGGCGCGTGGATGCGAGGACTCCCGCAGGTTGCCCGGCT 1207
DB 1141 GACCATCTTTCTGGGTTCCAGGCGCGTGGATGCGAGGACTCCCGCAGGTTGCCCGGCT 1200
QY 1208 GCCCAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
DB 1201 GCCCAGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGCCCTTACGGGGTGTCTCTCTCAAGACGCACTGCGCGCGCTGCGAGCTGCGTACC 1327
DB 1261 GTGCCCTTACGGGGTGTCTCTCTCAAGACGCACTGCGCGCGCTGCGAGCTGCGTACC 1320
QY 1328 AGCGGTGTCTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
DB 1321 AGCGGTGTCTGTGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCGCGCGCTGCGCTGTGTCAGCTGCTCCGCGAGCACAGACGCCCTTGCGAG 1447
DB 1381 CACAGACCGCGCGCTGCGCTGTGTCAGCTGCTCCGCGAGCACAGACGCCCTTGCGAG 1440
QY 1448 CGGCTTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1507
DB 1441 CGGCTTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
QY 1508 CAACGAACGCGCGCTTCTCTCAAGAACCAAGAAATTCATCTCTCTGGGAAAGCATG 1567
DB 1501 CAACGAACGCGCGCTTCTCTCAAGAACCAAGAAATTCATCTCTCTGGGAAAGCATG 1560
QY 1568 GCTCTGCTGAGAGGCTGACGCTGAAGATGAGCGTGCAGGCTGCGCTGCGCGAG 1627
DB 1561 GCTCTGCTGAGAGGCTGACGCTGAAGATGAGCGTGCAGGCTGCGCTGCGCGAG 1620
QY 1628 GAGCCAGGCGGTGCGTGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1687
DB 1621 GAGCCAGGCGGTGCGTGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1680
QY 1688 CAAGTCTCTGCACTGCGTGAATGATGTGTACGTCGTGAGCTGCTCAGGTCTTCTTT 1747
DB 1681 CAAGTCTCTGCACTGCGTGAATGATGTGTACGTCGTGAGCTGCTCAGGTCTTCTTT 1740
QY 1748 TGTACGAGACCAAGTTTCAAGAACAGAGCTCTTTTCTACCGAAGAGTGTCTGAG 1807
DB 1741 TGTACGAGACCAAGTTTCAAGAACAGAGCTCTTTTCTACCGAAGAGTGTCTGAG 1800
QY 1808 CAAGTTGCAAGCATTTGAATACAGCACTTGAAGAGGTCAGCTGCGGAGCTGTC 1867
DB 1801 CAAGTTGCAAGCATTTGAATACAGCACTTGAAGAGGTCAGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGTCAAGCAGCATCGGGAAGCAGCGCGCGCGCTGACGTCCAGACTCCG 1927
DB 1861 GGAAGCAGAGTCAAGCAGCATCGGGAAGCAGCGCGCGCGCTGACGTCCAGACTCCG 1920
QY 1928 CTTATCCCAAGCCTGACGCGGTGCGCGCGGATTTGTAATGACTAGTCTGTGGAGC 1987
DB 1921 CTTATCCCAAGCCTGACGCGGTGCGCGCGGATTTGTAATGACTAGTCTGTGGAGC 1980
QY 1988 CAGAACGTTCCGAGAGAAAGAGGCGCGAGCTCTCACTCGAGGTTGAAGGCACTGTT 2047
DB 1981 CAGAACGTTCCGAGAGAAAGAGGCGCGAGCTCTCACTCGAGGTTGAAGGCACTGTT 2040
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QY	2048	CAGCGTGTCACTACGAGCGGGCGCGGGCGCCCGGCGCTCTCTGGGGCGCTCTGTGTGGG	2107
Db	2041	CAGCGTGTCACTACGAGCGGGCGCGGGCGCCCGGCGCTCTCTGGGGCGCTCTGTGTGGG	2100
QY	2108	CCTGGACGATATCCACAGGGCGCTGGCGCACTTCGTGCTGCTGTGCGGGCCAGGACCC	2167
Db	2101	CCTGGACGATATCCACAGGGCGCTGGCGCACTTCGTGCTGCTGTGCGGGCCAGGACCC	2160
QY	2168	GCCGCGCTGAGCTGTACTTTGTTCAGGTGGATGTGACGGGGCGCGTACGACACCATCCCCA	2227
Db	2161	GCCGCGCTGAGCTGTACTTTGTTCAGGTGGATGTGACGGGGCGCGTACGACACCATCCCCA	2220
QY	2228	GGA CAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAAACACGTACTGCGTGGC	2287
Db	2221	GGA CAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAAACACGTACTGCGTGGC	2280
QY	2288	TCGGTATGCCGTGGTCCAGAAAGCGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA	2347
Db	2281	TCGGTATGCCGTGGTCCAGAAAGCGCCCATGGGCACGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGGCTCACCTGCAAGA	2407
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGGCTCACCTGCAAGA	2400
QY	2408	GACCAGCCCGCTGAGGGAGTGCCTGTCTATCGACAGAGCTCCTCCCTGAATGAGGCCAG	2467
Db	2401	GACCAGCCCGCTGAGGGAGTGCCTGTCTATCGACAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2468	CAGTGGCGCTCTTGACAGTCTTCTCAAGCTTCAATGTGCCAACAGCCGTGCGCATCAGGGG	2527
Db	2461	CAGTGGCGCTCTTGACAGTCTTCTCAAGCTTCAATGTGCCAACAGCCGTGCGCATCAGGGG	2520
QY	2528	CAAGTCTTACGTCCAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTG	2587
Db	2521	CAAGTCTTACGTCCAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCTCCACGCTGCTG	2580
QY	2588	CAGCCTGTGCTACCGCGCATGGAGAACAAAGCTGTTGCGGGGATTGCGCGGACGGGCT	2647
Db	2581	CAGCCTGTGCTACCGCGCATGGAGAACAAAGCTGTTGCGGGGATTGCGCGGACGGGCT	2640
QY	2648	GCTCCTGCGTTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCACCCAGCGGAAAAAC	2707
Db	2641	GCTCCTGCGTTTGTGTGATGATTTCTTGTGTGTGACACCTCACTCACCCAGCGGAAAAAC	2700
QY	2708	CTTCTCTCAGGACCCCTGGTCCGAGGTGTCCCTGAATAGCTGCTGTGTAACCTTGCGGAA	2767
Db	2701	CTTCTCTCAGGACCCCTGGTCCGAGGTGTCCCTGAATAGCTGCTGTGTAACCTTGCGGAA	2760
QY	2768	GACAGTGTGTAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACGCGTTTGTTCAGAT	2827
Db	2761	GACAGTGTGTAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACGCGTTTGTTCAGAT	2820
QY	2828	GCCGCGCCACGCGCTATTCCTGCTGTCGCGCTGCTGCTGATACCCGGAACCTTGAGGT	2887
Db	2821	GCCGCGCCACGCGCTATTCCTGCTGTCGCGCTGCTGCTGATACCCGGAACCTTGAGGT	2880
QY	2888	GCA GAGGCTACTCTCAAGTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2947
Db	2881	GCA GAGGCTACTCTCAAGTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940
QY	2948	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGCGGGCTGAAGTG	3007
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGCGGGCTGAAGTG	3000
QY	3008	TCACAGCCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGCAACCAATCTA	3067
Db	3001	TCACAGCCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGCAACCAATCTA	3060
QY	3068	CAAGATCTCTCTGCTGCAAGCGCTACAGTTTCAAGCATGTGTGCTGCAAGTCCCAATTCA	3127
Db	3061	CAAGATCTCTCTGCTGCAAGCGCTACAGTTTCAAGCATGTGTGCTGCAAGTCCCAATTCA	3120

QY	3128	TCAGCAGT	TTGAGAGAACCCACAT	TTTTTCTCGCGGCTCATCTCTGACACGGCTCCCT	3187
Db	3121	TCAGCAGT	TTGAGAGAACCCACAT	TTTTTCTCGCGGCTCATCTCTGACACGGCTCCCT	3180
QY	3188	CTGCTACT	CCATCTTGAAAGCCAGAACGCAAGTATGT	-----GCAGTGCCTGG	3237
Db	3181	CTGCTACT	CCATCTTGAAAGCCAGAACGCAAGTATGT	CGCTGGGGGCCAAGGCGCCGC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGGTGT	TTAGTGTGTCTCAGGAGACTGAGTGAATCTG	3297	
Db	3241	CGGCCCTCTG	CCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCAT	TTCTGTCTCAAGCT	3300
QY	3298	GGCTTAGGAAGTCTTA	ACCCCTTTTGGCATCAGGAAGTGT	TTAACCCACCACTGTCAAG	3357
Db	3301	GACTCGACACCGTGTCA	CTTACGTGCCACTCTGGGGTCACTCAGGACAGCCCAAGCGCA	3360	
QY	3358	GCTCGTCTGCCCCCTCTCGTGGGTGAGCGACGACCTGATGGAAGGACAGAGCTG	3417		
Db	3361	GCTGAGTCCGAAGCT	CCCCGGGAGCAGCGCTGACTGCTTGAGAGCCGCAAGCA	CCCCGGC	3420
QY	3418	TCTGGAGCTGCCAT	CTTCCCACTTGCTCT	-----GCCTG	3454
Db	3421	ACTGCCCTCAGACTTCA	AGACCATCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480	
QY	3455	GGGAAGCGCTGGGGGGCTGTGTCCTCTCTGTTTGCCCATGTGTGGATTGGGGGGCTG	3514		
Db	3481	GAGCAGACACCAAGCAGCCCTGTCA	CGCGGCTTACGTCCAGGAGGAGGGGCGGCC	3540	
QY	3515	GCCTCTCTGTTTGCCCTGTGTGTGGATTGGGCTGTCTCCCGTCCATGGCACTTAGGGCC	3574		
Db	3541	CACACCCAGGCCGCA	CCGCTGGAGTCTGAGGCTGAGTGAATGTTGGCCAGGCGCTG	3600	
QY	3575	CTTGTGCAAA	CCAGGCCAAG-----GCCTTAGAGAGAGGCCAGGCCAGGCTAACCCAC	3629	
Db	3601	CATGTCCGCTGAAGCTGAGTGTCCGGCTGAGGCTTGAGCGAGTGTCCAAGGAGGCT	3660		
QY	3630	CCCTCTCAGAGCAGAGCCCGGTATCACACGACAGAGCCCGCGCGTCTGTGCTTC	3689		
Db	3661	GAGTGTCCAGCACACCTGCGTCT-TCACTTCCCA	CAGGCTGCGCTCCACCCC	3719	
QY	3690	CCAGTACCGTCTCTGCCCCCTGACACTTTGTCCAGCATCAGGAGGTTCTGATCCGT	3749		
Db	3720	AGGGCCAGCTTTCTCACCAGAGAGCCGGCTTCCACTCCCA	CATAGAAATAGTCCATC	3779	
QY	3750	CTGAATTTCAAGCCATGT	CGAACCTGGGTCCTGAGCTTAACAGCTTCTACTTTCTGTTTC	3809	
Db	3780	CCCAGATTCCCATTTGTTCA	CCCCCT-----CGCCCTGCCCTCTTGCTTCCACCCC	3832	
QY	3810	TTTCTGTGTTGTGAGAGACCCCTGAGAGAACCCCTGGAGCTCTGGAAATTTGAGTGACCA	3869		
Db	3833	CACCATCCAGGTGAGAGACCCCTGAGAGAACCCCTGGAGCTCTGGAAATTTGAGTGACCA	3892		
QY	3870	AAGGTGTGCCCTGTACACAGGCGAGAACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA	3929		
Db	3893	AAGGTGTGCCCTGTACACAGGCGAGAACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA	3952		
QY	3930	ATTGGGGGGAGGTGCTGTGGAGTAATACTGAATATATGAGTTTTCAGTTTGA	3989		
Db	3953	ATTGGGGGGAGGTGCTGTGGAGTAATACTGAATATATGAGTTTTCAGTTTGA	4012		
QY	3990	AAA	3992		
Db	4013	AAA	4015		

RESULT	11
ACC58039	
ID	ACC58039 standard; cDNA; 4015 BP.
XX	
AC	ACC58039;
XX	
DT	11-AUG-2003 (first entry)
XX	

QY 1328 AGCCGGTGTCTGTGCCCCGGGAGAGAGCCCGGAGGCTCTGTGCGGCCCCCGGAGAGAGGA 1387
Db 1321 AGCCGGTGTCTGTGCCCCGGGAGAGAGCCCGGAGGCTCTGTGCGGCCCCCGGAGAGAGGA 1380
QY 1388 CACAGACCCCCCGTCCGCTGTGTGAGAGTGTCTCCGCGGAGAGAGAGAGAGAGAGAGAGAG 1447
Db 1381 CACAGACCCCCCGTCCGCTGTGTGAGAGTGTCTCCGCGGAGAGAGAGAGAGAGAGAGAG 1440
QY 1448 CGGCTTGTGCGGCGCTGCTGCGGCGGCTGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGG 1507
Db 1441 CGGCTTGTGCGGCGCTGCTGCGGCGGCTGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGG 1500
QY 1508 CACGAGACCGCGCTTCTCAGGAGACACCAAGAGTTCATCTCCCTGGGAGAGAGAGAGAGAG 1567
Db 1501 CACGAGACCGCGCTTCTCAGGAGACACCAAGAGTTCATCTCCCTGGGAGAGAGAGAGAGAG 1560
QY 1568 GCTCTGCTGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1627
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QY 1628 GAGCCCGAGGGGT 1687
Db 1621 GAGCCCGAGGGGT 1680
QY 1688 CAGGTTCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1747
Db 1681 CAGGTTCTGCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1748 TGTCAAGAGAGACAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1807
Db 1741 TGTCAAGAGAGACAGCTTTCAG 1800
QY 1808 CAGGTTGCAAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1867
Db 1801 CAGGTTGCAAGAGATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
QY 1868 GGAAGCAGAGAGTCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1927
Db 1861 GGAAGCAGAGAGTCAAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
QY 1928 CTTCACTCCCAAGCTGAGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCT 1987
Db 1921 CTTCACTCCCAAGCTGAGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCTGCGGCGGCT 1980
QY 1988 CAGAACGTTCCGAG 2047
Db 1981 CAGAACGTTCCGAG 2040
QY 2048 CAGCGTGTCAACTAG 2107
Db 2041 CAGCGTGTCAACTAG 2100
QY 2108 CTTGAGCAGATATCAAG 2167
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QY 2168 GCGCGCTGAGCTGATCTTGTCAAGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2227
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Db 2221 GGAAGAGCTCAAGAGAGTCAAG 2280
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Db 2281 TCGGTATGCGGTGTCCAG 2340
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QY 2588 CAGCTGTGCTACAG 2647
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Db 2641 GCTCTGCGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2700
QY 2708 CTTCTCAG 2767
Db 2701 CTTCTCAG 2760
QY 2768 GACAGTGTGATCTTCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2827
Db 2761 GACAGTGTGATCTTCCCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820
QY 2828 GCGGCGGAG 2887
Db 2821 GCGGCGGAG 2880
QY 2888 GCAAG 2947
Db 2881 GCAAG 2940
QY 2948 CGGCTTCAAG 3007
Db 2941 CGGCTTCAAG 3000
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QY 3068 CAGAGTCTCTGCTGAG 3127
Db 3061 CAGAGTCTCTGCTGAG 3120
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Db 3121 TCAGCAAGTTGGAAG 3180
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Db 3241 CTTCAAGTGGAG 3300
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Db 3301 GCGCTTGAAGAGTCTTACCCCTTTTCCAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360
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Db 3421 ACTGCCCTCAGAGAGTCAAG 3480
QY 3455 GGAAGCGCTGAG 3514


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Db 3481 GAGCAGACACAGCAGCCCTGTCAAGCCGGCTCTACGTCCAGGAGGAGGCGGCC 3540
QY 3515 GCCTCTCTCTTTTCCCTGTGGGATTTGGGCTGTCTCCCATGGCATTAGGCC 3574
Db 3541 CACACCCAGGCCCCGACCCGCTGGAGTCTGAGGCCCTGAGTGTGTTGGCCGAGCCTG 3600
QY 3575 CTGTGCAACCCAGGCCAAG-----GGCTTAGAGAGGCCAGGCCAGGCTACCCAC 3629
Db 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAGGGCT 3660
QY 3630 CCCTCTCAGAGCAGAGAGCCCGCTATCAACCAAGAGCCCGCCGCTCTCTGCTTC 3689
Db 3661 GAGTGTCCAGCAGACACCTGCGCTT-TCACTTCCCAAGGCTGGCGCTCCAGCCCC 3719
QY 3690 CCAATCAACCGTCTCTCTGCCCCCTGGAACACTTGTCCAGCATCAGGAGTTTGTATCCGT 3749
Db 3720 AGGGCCAGCTTTCTCTCAACAGAGCCCGGCTTCCACTCCCAATAGATGTCATC 3779
QY 3750 CTGAATTCAGCCCATGTGGAACCTGCGGTCTGAGCTTAACAGCTTCTACTTTCTGTC 3809
Db 3780 CCCAGATTCCCATTTGTTCAACCTT-----CGCCCTGCTCTTGTCCATCCACC 3832
QY 3810 TTTCTGTGTGTGAGAGACCTTGAGAGAGACCTTGGAAGTCTGGAATTGAGTGACCA 3869
Db 3833 CACCATTCAGGTGAGAGACCTTGAGAGAGACCTTGGAAGTCTGGAATTGAGTGACCA 3892
QY 3870 AAGTGTGCTCTGTACACAGGCGAGAGACCTTGACCTGATGGGGTCTCTGAGTCAA 3929
Db 3893 AAGTGTGCTCTGTACACAGGCGAGAGACCTTGACCTGATGGGGTCTCTGAGTCAA 3952
QY 3930 ATTGGGGGAGGTGCTGTGGAGTAATACTGAATATATGAGTTTTCAGTTTGAAGA 3989
Db 3953 ATTGGGGGAGGTGCTGTGGAGTAATACTGAATATATGAGTTTTCAGTTTGAAGA 4012
QY 3990 AAA 3992
Db 4013 AAA 4015
```

RESULT 12

ACC57552 standard; cDNA; 4015 BP.

ACC57552;

28-JUL-2003 (first entry)

Human telomerase reverse transcriptase cDNA.

XX Telomerase reverse transcriptase; TERT: enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytosolic; contraceptive;
KW immunosuppressive; antifertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy; gene; ss.

Homo sapiens.

XX Key Location/Qualifiers
FH CDS 56..3454
FT /*tag= a
FT /product= "TERT"

WO2003034985-A2.

01-MAY-2003.

16-OCT-2002; 2002WO-US033146.

PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.

(UTRP) UNIV ROCHESTER.

PI Rowley PT;
XX
DR WPI; 2003-403289/38.
DR P-PSDB; ABR42063.
XX
PT Novel nucleic acid encoding or comprising interfering RNAs which target
telomerase RNA, useful for inhibiting telomerase activity for treating
cancer, infertility and disorders of the immune system.
XX
PS Disclosure; Fig 3; 52pp; English.

CC The present sequence is that of human telomerase reverse transcriptase
CC (TERT) cDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy

SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 82.4%; Score 3306.6; DB 7; Length 4015;

Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 8 GCAGGCTGCGTCTGCTGCGCAGCTGGGAGCCCTGAGCCCGGCAACCCCGGATGCC 67
Db 1 GCAGGCTGCGTCTGCTGCGCAGCTGGGAGCCCTGAGCCCGGCAACCCCGGATGCC 60

QY 68 GCGGCTCCCCGCTGCGCAGCCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 127
Db 61 GCGGCTCCCCGCTGCGCAGCCGCTGCGCTCCCTGCTGCGCAGCCACTACCGGAGTGT 120

QY 128 GCGGCTGCGCAGCTTCTGCGCGCGCTGCGCGCCCGGCTGCGCGCTGCGCGCGG 187
Db 121 GCGGCTGCGCAGCTTCTGCGCGCGCTGCGCGCCCGGCTGCGCGCTGCGCGCGG 180

QY 188 GGAACCGGCGCTTTCGCGCGCGCTGCGCGCCAGTGTGCTGCTGCGCGCGG 247
Db 181 GGAACCGGCGCTTTCGCGCGCGCTGCGCGCCAGTGTGCTGCTGCGCGCGG 240

QY 248 ACGGCGCGCGCGCGCGCGCGCTTCCGCGAGTGTCTGCTGAGAGAGTGTGCG 307
Db 241 ACGGCGCGCGCGCGCGCGCGCTTCCGCGAGTGTCTGCTGAGAGAGTGTGCG 300

QY 308 CCGAGTGTGAGAGGTGTGCGAGCGCGCGCGGAGAGAGAGTGTGCTGCGCTTGC 367
Db 301 CCGAGTGTGAGAGGTGTGCGAGCGCGCGCGGAGAGAGAGTGTGCTGCGCTTGC 360

QY 368 GCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCAACACAGCGCGAGCTA 427
Db 361 GCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCAACACAGCGCGAGCTA 420

QY 428 CTTGCCAACAACGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 487
Db 421 CTTGCCAACAACGCTGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 480

QY 488 CCGGCTGGGCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
Db 481 CCGGCTGGGCGAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 548 GGGTCCAGCTGCGCTACAGGTGTGCGCGCGCGCGCTGTACAGCTCGCGCTGCCAC 607
Db 541 GGGTCCAGCTGCGCTACAGGTGTGCGCGCGCGCGCTGTACAGCTCGCGCTGCCAC 600

QY 608 TCAGGCG 667

Db 601 TCAGGCCGCCCCGCCACACGCTAGTAGACCCCGAAGCGCTGTGGATGCGAACGGGC 660
QY 668 CTGGAACCATAGCGTCAAGGAGCGCGGTCCCTGGGCTGCGACGCCCGGGTGGAG 727
Db 661 CTGGAACCATAGCGTCAAGGAGCGCGGTCCCTGGGCTGCGACGCCCGGGTGGAG 720
QY 728 GAGGCGCGGGGCACTGCGACCGAAGTCTGCCGTGGCCCAAGAGGCCCGGCTGGCG 787
Db 721 GAGGCGCGGGGCACTGCGACCGAAGTCTGCCGTGGCCCAAGAGGCCCGGCTGGCG 780
QY 788 TGCCCTGAGCCGAGCGGAGCGCCCGTTGGGCAAGGGTCTGGGCCCAACCGGCGAGAG 847
Db 781 TGCCCTGAGCCGAGCGGAGCGCCCGTTGGGCAAGGGTCTGGGCCCAACCGGCGAGAG 840
QY 848 GCGTGGACCGAGTGAACGCTGCTTCTGTGTGTCACTGCGCAGACCCCGCGAAGAGC 907
Db 841 GCGTGGACCGAGTGAACGCTGCTTCTGTGTGTCACTGCGCAGACCCCGCGAAGAGC 900
QY 908 CACCTCTTTGAGGGGTGCGCTCTGTGCAACGCGCCACTCCCAACCCATCCGTGGCGCCA 967
Db 901 CACCTCTTTGAGGGGTGCGCTCTGTGCAACGCGCCACTCCCAACCCATCCGTGGCGCCA 960
QY 968 GCACCAACGCGGCGCCCGCATCCACATCGCGGCCCAACGTCCTCCGGAACAACGCTTGTCC 1027
Db 961 GCACCAACGCGGCGCCCGCATCCACATCGCGGCCCAACGTCCTCCGGAACAACGCTTGTCC 1020
QY 1028 CCGGCTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAAGGCGACAAGAGCAAGTGGC 1087
Db 1021 CCGGCTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAAGGCGACAAGAGCAAGTGGC 1080
QY 1088 GCGCTCTCTCTACTAGCTCTGTGAGGCGCGAGCTGAGCGCTGGAGAGGCTGTGGA 1147
Db 1081 GCGCTCTCTCTACTAGCTCTGTGAGGCGCGAGCTGAGCGCTGGAGAGGCTGTGGA 1140
QY 1148 GACCATCTTCTGGGTTCCAGGCGCTGATGCGAGGGACTCCCGCAGAGTTGCCCGGCT 1207
Db 1141 GACCATCTTCTGGGTTCCAGGCGCTGATGCGAGGGACTCCCGCAGAGTTGCCCGGCT 1200
QY 1208 GCGCCAGCGCTACTGCGAATGCGGCGCTGTTCTGTGAGCTGCTTGGGAACCAACGCGCA 1267
Db 1201 GCGCCAGCGCTACTGCGAATGCGGCGCTGTTCTGTGAGCTGCTTGGGAACCAACGCGCA 1260
QY 1268 GTGCGCTTACGCGGTCTCTCAAGAGCACTGCGCGCTGCGAGCTGCGTCAACCCAGC 1327
Db 1261 GTGCGCTTACGCGGTCTCTCAAGAGCACTGCGCGCTGCGAGCTGCGTCAACCCAGC 1320
QY 1328 AGCGGTGTGTGCGCGGAGAGAGCGCGCTGTGTGCGCGCGCGCGAGAGAGGA 1387
Db 1321 AGCGGTGTGTGCGCGGAGAGAGCGCGCTGTGTGCGCGCGCGCGAGAGAGGA 1380
QY 1388 CACAGACCCCGCTGCGCTGTGAGCTGCTGCGCAGACAGACAGCGCTTGGCAGGTGA 1447
Db 1381 CACAGACCCCGCTGCGCTGTGAGCTGCTGCGCAGACAGACAGCGCTTGGCAGGTGA 1440
QY 1448 CGGCTTGTGCGGCGCTGCGCTGCGCGCGCTGTGTGCGCGCTTGGGCTCCAGGCA 1507
Db 1441 CGGCTTGTGCGGCGCTGCGCTGCGCGCGCTGTGTGCGCGCTTGGGCTCCAGGCA 1500
QY 1508 CAACGAACGCGCTTCTCAAGAACCAAGATTCTCTCTGGGGAAGCATGCGAA 1567
Db 1501 CAACGAACGCGCTTCTCAAGAACCAAGATTCTCTCTGGGGAAGCATGCGAA 1560
QY 1568 GCTCTGCTGAGAGCTGAGCTGGAAGTGAAGCTGCGGAGCTGCTTGGCTGCGAG 1627
Db 1561 GCTCTGCTGAGAGCTGAGCTGGAAGTGAAGCTGCGGAGCTGCTTGGCTGCGAG 1620
QY 1628 GAGCCAGAGGTTGGTGTGTTCCGCGCGAGAGACCGTCTGCGTGAAGATCTGCG 1687
Db 1621 GAGCCAGAGGTTGGTGTGTTCCGCGCGAGAGACCGTCTGCGTGAAGATCTGCG 1680
QY 1688 CAAGTCTCTGACTGCTGATGAGTGTGATGCTGCTGAGCTGCTCAGGCTTTCTTTA 1747
Db 1681 CAAGTCTCTGACTGCTGATGAGTGTGATGCTGCTGAGCTGCTCAGGCTTTCTTTA 1740

QY 1748 TGTACGAGAGACCAAGTTTCAAAAAGAGAGCTTTTCTACCGAAGAGTGTCTGAG 1807
Db 1741 TGTACGAGAGACCAAGTTTCAAAAAGAGAGCTTTTCTACCGAAGAGTGTCTGAG 1800
QY 1808 CAAGTTGCAAGACATTGGAATCAGACAGCACTTGAAGAGGCTGCGGAGCTGTC 1867
Db 1801 CAAGTTGCAAGACATTGGAATCAGACAGCACTTGAAGAGGCTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGTCAAGCAGCATCGGAAGCAAGCCCGCTGTGACGTCCAGACTCCG 1927
Db 1861 GGAAGCAGAGTCAAGCAGCATCGGAAGCAAGCCCGCTGTGACGTCCAGACTCCG 1920
QY 1928 CTTATCCCAAGCTTGAAGCGGCTGCGCGGCTTGTGAACATGAATACTGCTGAGAGC 1987
Db 1921 CTTATCCCAAGCTTGAAGCGGCTGCGCGGCTTGTGAACATGAATACTGCTGAGAGC 1980
QY 1988 CAGAACGTTCCGAGAGAAAAGAGGCGGAGCTCTACCTCGAGGTTGAAGCACTGTT 2047
Db 1981 CAGAACGTTCCGAGAGAAAAGAGGCGGAGCTCTACCTCGAGGTTGAAGCACTGTT 2040
QY 2048 CAGCGTCTCAACTACAGAGCGGCGCGCGCGCGCGCTCTGCGCGCTCTGTGCTGG 2107
Db 2041 CAGCGTCTCAACTACAGAGCGGCGCGCGCGCGCGCGCTCTGCGCGCTCTGTGCTGG 2100
QY 2108 CTTGAGCATATCCACAGGCGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2167
Db 2101 CTTGAGCATATCCACAGGCGCTGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
QY 2168 GCGGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGCGGCGCTGACACCATCCCCA 2227
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QY 2228 GGAAGAGCTCAAGAGGTCATGCGCAGCATCAAAACCCAGAAACGTAAGTGGTGG 2287
Db 2221 GGAAGAGCTCAAGAGGTCATGCGCAGCATCAAAACCCAGAAACGTAAGTGGTGG 2280
QY 2288 TCGGTATGCGGTGTCAGAGAGCGCGCATGGGCAAGTCCGCAAGGCTTCAAGAGCA 2347
Db 2281 TCGGTATGCGGTGTCAGAGAGCGCGCATGGGCAAGTCCGCAAGGCTTCAAGAGCA 2340
QY 2348 CGTCTTACCTTGAAGACCTCCAGCGCTATGCGACAGATTGCTGCTCACTGACGGA 2407
Db 2341 CGTCTTACCTTGAAGACCTCCAGCGCTATGCGACAGATTGCTGCTCACTGACGGA 2400
QY 2408 GACCAAGCGCTGAGAGGATGCGCTGCTATGAGCAGAGCTCTCTCTGAATGAGGCCAG 2467
Db 2401 GACCAAGCGCTGAGAGGATGCGCTGCTATGAGCAGAGCTCTCTCTGAATGAGGCCAG 2460
QY 2468 CAGTGGCTCTTGAAGCTTCTCTACGCTTATGTGCAACCAAGCGCTGCGCATGAGGG 2527
Db 2461 CAGTGGCTCTTGAAGCTTCTCTACGCTTATGTGCAACCAAGCGCTGCGCATGAGGG 2520
QY 2528 CAAGTCTTACGTCAGTGTGCGAGGGATGCGCAGAGGCTCCATCTCTTCCACGCTGCTG 2587
Db 2521 CAAGTCTTACGTCAGTGTGCGAGGGATGCGCAGAGGCTCCATCTCTTCCACGCTGCTG 2580
QY 2588 CAGCTGTGTCAGGCGCAGATGAGAACAGCTGTTGCGGGGATTCGGCGGAGCGGCT 2647
Db 2581 CAGCTGTGTCAGGCGCAGATGAGAACAGCTGTTGCGGGGATTCGGCGGAGCGGCT 2640
QY 2648 GCTCTGCGTTGTGATGATTTCTTGTGTGACACCTCACTTCAACCAAGCGGAAAC 2707
Db 2641 GCTCTGCGTTGTGATGATTTCTTGTGTGACACCTCACTTCAACCAAGCGGAAAC 2700
QY 2708 CTTCTCAGAGACCTGCTCGAGGTTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 2767
Db 2701 CTTCTCAGAGACCTGCTCGAGGTTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 2760
QY 2768 GACAGTGTGAATCTTCTCTGTAGAACAGAGGCGCTGCGTGGTGGTCTTGTTCAGAT 2827
Db 2761 GACAGTGTGAATCTTCTCTGTAGAACAGAGGCGCTGCGTGGTGGTCTTGTTCAGAT 2820

QY 2828 GCCGCCCAACGCGCTATATCCCTGCTGCGCCTGCTGCTGATACCCGACCTGGAGGT 2887
DB 2821 GCCGCCCAACGCGCTATATCCCTGCTGCGCCTGCTGCTGATACCCGACCTGGAGGT 2880
QY 2888 GCAGAGCAGTACTTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAGCTTCAACCG 2947
DB 2881 GCAGAGCAGTACTTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAGCTTCAACCG 2940
QY 2948 CGGCTTCAAGGCTGGAGGAAATGCGTCCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3007
DB 2941 CGGCTTCAAGGCTGGAGGAAATGCGTCCAAACTCTTTGGGGTCTTGCGGCTGAAGTG 3000
QY 3008 TCACAGCTGTTTCTGATTTGAGGTGACACAGCCTCCAGACGGTGTGCACCAACATCTA 3067
DB 3001 TCACAGCTGTTTCTGATTTGAGGTGACACAGCCTCCAGACGGTGTGCACCAACATCTA 3060
QY 3068 CAAGATCCTCTCTGCTGACAGGCTTACAGGTTTACCGCATGTGTCTGCAGCTCCATTTC 3127
DB 3061 CAAGATCCTCTCTGCTGACAGGCTTACAGGTTTACCGCATGTGTCTGCAGCTCCATTTC 3120
QY 3128 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACACGCGCTCCCT 3187
DB 3121 TCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTCTGACACGCGCTCCCT 3180
QY 3188 CTGCTACTCCATCTCTGAAGAACCAAGACGACGATGT-----GCAGGTGCTTGG 3237
DB 3181 CTGCTACTCCATCTCTGAAGAACCAAGACGACGATGTGGGGGCCAAAGGCGCGCGC 3240
QY 3238 CCTCAGTGGCAGCAGAGTCCCTGCTGCTGTGTGTTAGTGTGACAGACTGATGAAATCTG 3297
DB 3241 CGGCCCTCTGCCCTCCGAGGCGGTGACGTGCTGTGCGCAACCAAGCATTCCTGCTCAAGCT 3300
QY 3298 GCGTTAAGGAAGTCTTACCCCTTTTTCGATCAGAGAGTGTGTTAACCCCAACCTGTCA 3357
DB 3301 GACTGACACACCGTGTACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
QY 3358 GCTGCTGCTGCGCGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3417
DB 3361 GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCTGAGGCGCGCAACCGCGC 3420
QY 3418 TCTGGAGAGCTGCCATCTTCCCACTTGTCT-----GCCTG 3454
DB 3421 ACTGCCCTCAGACTTCAAGACCACTCTGACTGATGAGCCACCGCCACAGCCAGCGCGA 3480
QY 3455 GGGAAAGCGCTGGGGGCGCTGCTCTCTCTGCTTTGCCCATGCTGGAATTTGGGGCGCTG 3514
DB 3481 GAGCAGACACACGAGCAGCCTGCTGACGCGCGCTTACGCTCCAGGAGGAGGGGCGCGC 3540
QY 3515 GCCTCTCTGTTTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3574
DB 3541 CACACCCAGGCGCGCAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3600
QY 3575 CTGTGCAAAACCCAGGCCAAG-----GCGTTAGAGAGGAGCCAGGCCAGCTAACCCAC 3629
DB 3601 CATGTCCGCTGAGGCTGAGTGTCCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 3660
QY 3630 CCTCTCAGGAGCAGAGCGCGCTATCACCACGACAGAGCCCGCGCGCTCTGCTTTC 3689
DB 3661 GAGTGTCCAGCAGACCTGCTGCT-TCATTTCCCAACAGGCTGCGCTGCGCTCCACCCC 3719
QY 3690 CCAGTCAACGCTCTGCGCGCTGACACTTTGTCAGCATCAGGAGGTTTCTGATCGT 3749
DB 3720 AGGGCCAGCTTTTCTCAACAGAGCGCGCTTCCACTCCCAATAGGAATAGTCATC 3779
QY 3750 CTGAATTTCAAGCCATGTCGAACCTGCGGTCTGAGCTTAAAGCTTCTTCTGTTTC 3809
DB 3780 CCCAGATTGCGCATTTTCAACCT-----CGCCTGCGCTCTTGGCTTCCACCCC 3832
QY 3810 TTTCTGTGTGAGAGCCTGAGAGAGCCTGAGAGCTCTGGAATTTGAGTGACCA 3869
DB 3833 CACCATCCAGTGTGAGAGCCTGAGAGAGCCTGAGAGCTCTGGAATTTGAGTGACCA 3892
QY 3870 AAGGTGTGCTGTACACAGGCGAGGACCTGCACTGATGGGGTCTGTGCTCA 3929

DB 3893 AAGGTGTGCTGTACACAGGCGAGGACCTGACCTGATGGGGTCTGTGCTCA 3952
QY 3930 ATTGGGGGAGGTGCTGTGGAGTAATACTGAATATAGATTTCAGTTTGAATAA 3989
DB 3953 ATTGGGGGAGGTGCTGTGGAGTAATACTGAATATAGATTTCAGTTTGAATAA 4012
QY 3990 AAA 3992
DB 4013 AAA 4015
RESULT 13
ABZ22474
ID ABZ22474 standard; cDNA; 4015 BP.
XX
AC ABZ22474;
XX
DT 25-MAR-2003 (first entry)
XX
DE Human telomerase reverse transcriptase encoding cDNA SEQ ID NO:1.
XX
KW Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
KW vulnery; antitumor; epithelial cell migration promoter; wound;
KW epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
KW epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "human telomerase reverse transcriptase"
XX
PN WO200291999-A2.
XX
PD 21-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014867.
XX
PR 09-MAY-2001; 2001US-0289903P.
XX
PA (GERO-) GERON CORP.
XX
PI Jiang X, Chiu C, Harley CB;
XX
DR WPI; 2003-120591/11.
XX
DR P-PSDB; ABB56676.
XX
PT Composition for treating wounds and enhancing epithelialization of a skin
PT surface, comprises vector encoding telomerase reverse transcriptase or
PT telomerized epithelial cells on a microparticle or a matrix.
XX
PS Disclosure; Page 31-32; 68pp; English.
XX
CC The present invention describes a pharmaceutical composition (I) comprising a vector encoding telomerase reverse transcriptase (TERT) in an excipient or device, or comprises telomerized epithelial cells on a microparticle or a matrix suitable for topical administration or administration to a wound site. (I) has vulnery and antitumor activities and can be used to promote epithelial cell migration. (I) is useful for treating a wound and enhancing epithelialization of a skin surface. The wound is especially skin wound including acute lesion such as traumatic lesion, burn, or surgical incision, chronic lesion such as chronic venous ulcer, diabetic ulcer or compression ulcer and the wound expression is increased in epithelial cells at the site of treatment and also in fibroblasts or endothelial cells at the site of treatment. The TERT is useful for the preparation of a medicament for treatment of a wound or an epithelial surface in a human or animal. An epithelial cell with increased telomerase activity or increased expression of TERT is useful for preparation of a medicament for the treatment of a wound in a

CC human or animal. (I) is also useful for treating wounds of other
CC epidermal surfaces including mucosal surfaces such as bronchus, mouth,
CC nose, oesophagus, stomach, or intestine. The present sequence encodes
CC human TERT (hTERT), which is given in the exemplification of the present
CC invention. hTERT is located to chromosome 5

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 82.4%; Score 3306.6; DB 7; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 8 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCCCGCCACCCCGCATGCC 67
DB 1 GCAGCGCTGCTCTGCTGCGACGTGGGAAGCCCTGGCCCCCGCCACCCCGCATGCC 60
QY 68 GCGCGCTCCCCGCTGCGAGCGGTGCGCTCCCTGCTGGCAGCCACTACCGGAGTGTCT 127
DB 61 GCGCGCTCCCCGCTGCGAGCGGTGCGCTCCCTGCTGGCAGCCACTACCGGAGTGTCT 120
QY 128 GCGCGTGGCCACGTTCTGTCGGCGCTGCGGCCCCCAAGGGCTGGCGGCTGTGCAAGCGCG 187
DB 121 GCGCGTGGCCACGTTCTGTCGGCGCTGCGGCCCCCAAGGGCTGGCGGCTGTGCAAGCGCG 180
QY 188 GGACCCCGCGGCTTTCCGCGCGCTGTGGCCCAATGCTGTGTGCTGCTGCTGGAGCGC 247
DB 181 GGACCCCGCGGCTTTCCGCGCGCTGTGGCCCAATGCTGTGTGCTGCTGCTGGAGCGC 240
QY 248 ACGGCGCGCCCCCGCGCCCCCTCTTCCGCGAGGTGCTGCTGTAAGAGCTGTGTGC 307
DB 241 ACGGCGCGCCCCCGCGCCCCCTCTTCCGCGAGGTGCTGCTGTAAGAGCTGTGTGC 300
QY 308 CCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCGAAGACGTGTGCTGCTTCCGCTTCCG 367
DB 301 CCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCGAAGACGTGTGCTGCTTCCGCTTCCG 360
QY 368 GCTGTGTGACAGCG 427
DB 361 GCTGTGTGACAGCG 420
QY 428 CTTGCCCAACACAGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGTGCTGCG 487
DB 421 CTTGCCCAACACAGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGTGCTGCG 480
QY 488 CCGCGTGGGCGACGAGCTGTGCTGCTTCACTGTGCGACGCTGCGCGCTTGTGTGTGT 547
DB 481 CCGCGTGGGCGACGAGCTGTGCTGCTTCACTGTGCGACGCTGCGCGCTTGTGTGTGT 540
QY 548 GGCTCCCGAGCTGCGCTTACAGGTGTGCGCGCGCGCGCTGTACAGCTGCGCGCTGCCAC 607
DB 541 GGCTCCCGAGCTGCGCTTACAGGTGTGCGCGCGCGCGCTGTACAGCTGCGCGCTGCCAC 600
QY 608 TCAGGCG 667
DB 601 TCAGGCG 660
QY 668 CTGGAACCATAGCGTCAAGGAGGCGCGGCTCCCTGCGCTGCGCGCGCGCGCGCGCGG 727
DB 661 CTGGAACCATAGCGTCAAGGAGGCGCGGCTCCCTGCGCTGCGCGCGCGCGCGCGG 720
QY 728 GAGGCG 787
DB 721 GAGGCG 780
QY 788 TGCCCCCTGAGCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
DB 781 TGCCCCCTGAGCGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GCGTGAACGAGTGAAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907
DB 841 GCGTGAACGAGTGAAGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
QY 908 CACCTCTTTGAGGCTGCGCTCTGTGACGCGCGCACTCCACCACTCCGTGGCGCGCA 967

DB 901 CACTCTTTGAGGCTGCGCTCTGTGACGCGCGCACTCCACCATCCGTGGCGCGCA 960
QY 968 GCACACG 1027
DB 961 GCACACG 1020
QY 1028 CCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGACCAAGAGAGCTGCG 1087
DB 1021 CCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGACCAAGAGAGCTGCG 1080
QY 1088 GCCCTCTCTCTACT 1147
DB 1081 GCCCTCTCTCTACT 1140
QY 1148 GACCATTTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1207
DB 1141 GACCATTTTCTGAGTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 1200
QY 1208 GCGCCAGCGCTACTGCGAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1267
DB 1201 GCGCCAGCGCTACTGCGAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 1260
QY 1268 GTGCCCTTACGCGGCTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCAGC 1327
DB 1261 GTGCCCTTACGCGGCTCTCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCAGC 1320
QY 1328 AGCGGCTGTCTGTGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387
DB 1321 AGCGGCTGTCTGTGCGCGCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
QY 1388 CACAGACCCCGCTGCGCTGTGTGACAGTGTCTCCGCGACACAGAGCGCGCGCGCGAGTGA 1447
DB 1381 CACAGACCCCGCTGCGCTGTGTGACAGTGTCTCCGCGACACAGAGCGCGCGCGAGTGA 1440
QY 1448 CGGCTTGTGCGGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1507
DB 1441 CGGCTTGTGCGGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
QY 1508 CACAGACCGCGCTTCTCTCAAGACCAAGAGTTCATCTCCCTGGGAGAGCATGCCAA 1567
DB 1501 CACAGACCGCGCTTCTCTCAAGACCAAGAGTTCATCTCCCTGGGAGAGCATGCCAA 1560
QY 1568 GCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGGCAG 1627
DB 1561 GCTCTGCTGACAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGGCAG 1620
QY 1628 GAGCCCGAGGGTGGCTGTGTTCCGCGCGCGAGACACCGCTGCGGTGAGAGATCTGGC 1687
DB 1621 GAGCCCGAGGGTGGCTGTGTTCCGCGCGCGAGAGACCGCTGCGGTGAGAGATCTGGC 1680
QY 1688 CAGTTCCTGACCTGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 1747
DB 1681 CAGTTCCTGACCTGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTG 1740
QY 1748 TGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTTTTCTTACCGGAGAGTGTCTGAG 1807
DB 1741 TGTCAAGGAGACCAAGTTTCAAAAGAACAGGCTTTTCTTACCGGAGAGTGTCTGAG 1800
QY 1808 CAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGAGTGT 1867
DB 1801 CAGTTCGAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAGAGTGT 1860
QY 1868 GGAAGCAGAGGTGAGGAGCAGATCGGGAAGCGAGCGCGCGCGCGCGCGCGCGCGCG 1927
DB 1861 GGAAGCAGAGGTGAGGAGCAGATCGGGAAGCGAGCGCGCGCGCGCGCGCGCGCGCG 1920
QY 1928 CTTATCCCGCAAGCTTACGCGGCTGCGCGCGGATTTGTAACATGACATGCTGTGGAGC 1987
DB 1921 CTTATCCCGCAAGCTTACGCGGCTGCGCGCGGATTTGTAACATGACATGCTGTGGAGC 1980
QY 1988 CAGACGTTCCGAGAGAAAGAGGCGGAGCGTCTACCTGAGGCTGAAGGCACTGTT 2047

D	b	1981	CAGAACGTTCCGACAGAGAAAAGAGGGCCGAGCGTCTCACCTTGAGGGGTGAAGGCACCTGTT	204
Q	y	2048	CAGCGTGTCACTACGAGCGGGCGGGCGCCCGCCGCTCTGTGGGCGCCTCTGTGTGGG	2107
D	b	2041	CAGCGTGTCACTACGAGCGGGCGGGCGCCCGCCGCTCTGTGGGCGCCTCTGTGTGGG	2100
Q	y	2108	CTTGACGATATCCACAGGGGCTTGGCGCACCTTGTGTGTGGGTGTGGGGCCAGGACCC	2167
D	b	2101	CTTGACGATATCCACAGGGGCTTGGCGCACCTTGTGTGTGGGTGTGGGGCCAGGACCC	2160
Q	y	2168	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGCGTACGACACCATCCCCA	2227
D	b	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGGCGCGTACGACACCATCCCCA	2220
Q	y	2228	GGACAGGCTCACGGAGTCATGCGCAGCATCATCAAAACCCAGAAACAGTACTGCGTCCG	2287
D	b	2221	GGACAGGCTCACGGAGTCATGCGCAGCATCATCAAAACCCAGAAACAGTACTGCGTCCG	2280
Q	y	2288	TCGGTATGCCGTGTCCAGAAAGCCGCCATGAGGACGTCGCGCAAGGCTTCAAGAGCA	2347
D	b	2281	TCGGTATGCCGTGTCCAGAAAGCCGCCATGAGGACGTCGCGCAAGGCTTCAAGAGCA	2340
Q	y	2348	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCACCTGACGA	2407
D	b	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCACCTGACGA	2400
Q	y	2408	GACCAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2467
D	b	2401	GACCAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
Q	y	2468	CAGTGGCCTCTTGACGCTCTTCTACGCTTCATGTGCGCAACAGCCGCTGCCATCAGGGG	2527
D	b	2461	CAGTGGCCTCTTGACGCTCTTCTACGCTTCATGTGCGCAACAGCCGCTGCCATCAGGGG	2520
Q	y	2528	CAAGTCTTACGTCCAGTGCACAGGGGATCCCGCAGGGGCTCCATCTCTCCACGCTGCTG	2587
D	b	2521	CAAGTCTTACGTCCAGTGCACAGGGGATCCCGCAGGGGCTCCATCTCTCCACGCTGCTG	2580
Q	y	2588	CAGCCTGTGCTACGGCGCACATGAGAAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT	2647
D	b	2581	CAGCCTGTGCTACGGCGCACATGAGAAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT	2640
Q	y	2648	GCTCCTGCGTTTGGTGAATGATTTCTTGTGTGACACCTCACTCAACCCACGGCAAAAC	2707
D	b	2641	GCTCCTGCGTTTGGTGAATGATTTCTTGTGTGACACCTCACTCAACCCACGGCAAAAC	2700
Q	y	2708	CTTCTCAGGACCCCTGTGTCGAGGTGTCCCTGAGTATGCTGCGTGTGAATTCGGAA	2767
D	b	2701	CTTCTCAGGACCCCTGTGTCGAGGTGTCCCTGAGTATGCTGCGTGTGAATTCGGAA	2760
Q	y	2768	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGACAGGCTTTGTTCAGAT	2827
D	b	2761	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGACAGGCTTTGTTCAGAT	2820
Q	y	2828	GCCGGCCACGGCCTATTCCTGTCGCGGCTGCTGTGATACCCGACCTTGAGAGT	2887
D	b	2821	GCCGGCCACGGCCTATTCCTGTCGCGGCTGCTGTGATACCCGACCTTGAGAGT	2880
Q	y	2888	GCAGAGCGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCTTCAACCG	2947
D	b	2881	GCAGAGCGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
Q	y	2948	CGGCTTCAAGGCTGGAGGAAACATGCGTGCAGAACTCTTTGGGGTCTTGCGGCTGAAGTG	3007
D	b	2941	CGGCTTCAAGGCTGGAGGAAACATGCGTGCAGAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
Q	y	3008	TCACAGCCTGTTTCTGATTTGAGGTGAACAGCCTCCAGACGGTGTGACACCAACATCTA	3067
D	b	3001	TCACAGCCTGTTTCTGATTTGAGGTGAACAGCCTCCAGACGGTGTGACACCAACATCTA	3060
Q	y	3068	CAAGATCTCTCTGCTGACGGCGTACAGTTTCAACGATGTGTGCTGACAGTCCCATTTTCA	3127
D	b	3061	CAAGATCTCTCTGCTGACGGCGTACAGTTTCAACGATGTGTGCTGACAGTCCCATTTTCA	3120

QY	3128	TCAGCAAGTTTGGAGAAGCCCAACATTTTTCCTGGCGTCATCTCTGACACGGCTCCCT	3187
Db	3121	TCAGCAAGTTTGGAGAAGCCCAACATTTTTCCTGGCGTCATCTCTGACACGGCTCCCT	3180
QY	3188	CTGCTACTCCATCCTGAAAGCCCAAGACCGCAGTATGT-----GCAGTGTCTGG	3237
Db	3181	CTGCTACTCCATCCTGAAAGCCCAAGACCGCAGGATGTCTGCTGGGGGCCAAGGCGCCGC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTACTGTGTCAAGAGACTGAGTAATCTG	3297
Db	3241	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTCAAGCT	3300
QY	3298	GGCTTAGGAAGTTCTTACCCCTTTTCGCATCAAGAAAGTGGTTTAAACCAACCACTGTCAAG	3357
Db	3301	GACTCGACACCGTGTCACTACGTGCCACTCTGGGGGTCACTCAGACAGCCCAAGACGCA	3360
QY	3358	GCTCGTCTGCCCGCCCTCTCGTGGGTGAGCAGACCACTGATGGAAGGACAGGAGCTG	3417
Db	3361	GCTGAGTCGGAAGCTCTCCGGGGACGACGCTGACTGTCCCTTGAGGCCGCGACCAACCCGGC	3420
QY	3418	TCTGGAGCTGCCATCTCTCCACCTGTCT-----GCCTG	3454
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3455	GGGAAGCGCTGGGGGCTGTCTCTCTGTTTCCCATGTTGGATTTGGGGGCTG	3514
Db	3481	GAGCAGACACAGCAGCCCTGTCAAGCCGGGCTTAAGTCCAGGAGGAGGAGGGCGGCC	3540
QY	3515	GCCTCTCTGTTTGGCCCTGTGTGGAGTGGGCTGTCTCCGTCATGCACTTAAGGCC	3574
Db	3541	CACACCCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTAGTGTGGCCGAGGCTG	3600
QY	3575	CTGTGCAAAACCAGGCCAAG----GGCTTAGAGAGAGGCCAGGCCCAAGCTAACCCAC	3629
Db	3601	CATGTCCGCTGAAGGCTGAGTGTCCGGCTGAGGCTTGAAGGAGTGTCCAGCCAAAGGCT	3660
QY	3630	CCCTCTCAGAGCAGAGGCCGCGTATCACCAAGACAGAGCCCGCGCGTCTGTCTTC	3689
Db	3661	GAGTGTCCAGACACACTGCCGTCT-TCACTTCCCAAGGCTGCGCTCCACCCC	3719
QY	3690	CCAGTACCCGTCTCTGCCCTGACACTTTGTCAGCATCAGGAGTTCTGATCCGT	3749
Db	3720	AGGGCAGCTTTCTCTCACAGAGAGCCGGCTTCACTCCCAATAGATATGCCATC	3779
QY	3750	CTGAATTCAGCCATGTGGAACCTGCGTCTGAGCTTAACAGCTTCTACTTCTGTTTC	3809
Db	3780	CCCAAGTTCCGCAATTGTTCAACCCCT-----CGCCCTGCCCTCTTGCCTTCCACCCC	3832
QY	3810	TTTCTGTGTGTGAGAGACCCCTGAGAGAACCCCTGGAGCTCTGGGAATTTGAAGTACCA	3869
Db	3833	CACCATCCAGGTGAGAGACCCCTGAGAGAACCCCTGGAGCTCTGGGAATTTGAAGTACCA	3892
QY	3870	AAAGTGTGCCCTGTAACACAGGCGAGGACCTCTGCACTGGATGGGGTCCCTGTGGGTCAA	3929
Db	3893	AAAGTGTGCCCTGTAACACAGGCGAGGACCTCTGCACTGGATGGGGTCCCTGTGGGTCAA	3952
QY	3930	ATTGGGGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAA	3989
Db	3953	ATTGGGGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAA	4012
QY	3990	AAA 3992	
Db	4013	AAA 4015	

RESULT 14	
ACC44482	
ID	ACC44482 standard; DNA; 4015 BP.
XX	
AC	ACC44482;
XX	
DT	29-AUG-2003 (first entry)

29-AUG-2003 (first entry)

XX Human telomerase reverse transcriptase gene.
XX Gene; ds; human; telomerase reverse transcriptase; adipogenic capacity;
KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
XX anorectic; adiponectin; insulin.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "telomerase reverse transcriptase"
XX WO2003031640-A2.
XX 17-APR-2003.
XX 07-OCT-2002; 2002WO-US031635.
XX 06-OCT-2001; 2001US-0327650P.
XX 06-OCT-2001; 2001US-0327651P.
XX (BOST-) BOSTON MEDICAL CENT CORP.
XX Kirkland J, Tchkonja T;
XX WPI; 2003-421278/39.
XX P-PSDB; ABR58045.
XX New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assays,
PT clinical applications, and in the administration of therapeutic agents,
PT particularly for obesity.
XX
XX Disclosure; Page 11-13; 53pp; English.
XX The invention relates to the generation of primary preadipocyte cell
CC strains that express telomerase reverse transcriptase (TERT- the
CC catalytic subunit of telomerase), and maintain and/or enhance replicative
CC potential and maintain adipogenic capacity of the cell. This sequence
CC represents the gene encoding the TERT protein. The cell strain can be
CC used in research to study all aspect of adipogenesis, especially in
CC relation to researching treatments for e.g. obesity. The cell can also be
CC used to identify adipogenesis modulators for use as therapeutic agents
CC such as hormones, growth factors, cytokines, enzymes, cholesterol binding
CC proteins, cholesterol removing proteins or their combinations.
CC Alternatively, the therapeutic agent may be an adipocytokine, preferably
CC adiponectin, or insulin
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
Query Match 82.4%; Score 3306.6; DB 7; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;
QY 8 GCAGCGCTGCTGCTGCTGCGACGTGGAGACCCCTGGCCCCCGGCAACCCCGGATGCC 67
DB 1 GCAGCGCTGCTGCTGCTGCGACGTGGAGACCCCTGGCCCCCGGCAACCCCGGATGCC 60
QY 68 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGACGCCACTACCGGAGTGTCT 127
DB 61 GCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGACGCCACTACCGGAGTGTCT 120
QY 128 GCGCGTGGCCACGTTCTGCGGCGCCCTGGGAGCCCAAGGCTGGCGCTGTGCAAGCGCG 187
DB 121 GCGCGTGGCCACGTTCTGCGGCGCCCTGGGAGCCCAAGGCTGGCGCTGTGCAAGCGCG 180
QY 188 GGAACCGGCGGCTTCCGCGCGCTGTGCGGCGCAAGTGCCTGTGTGCGTGCCTGGAGCGC 247
DB 181 GGAACCGGCGGCTTCCGCGCGCTGTGCGGCGCAAGTGCCTGTGTGCGTGCCTGGAGCGC 240
QY 248 AGGCGCGCGCGCGCGCGCGCGCGCTCTTCCGCCACAGGTGTCTGCTGAAGAGAGTGTGCG 307

DB 241 ACGCGCGCGCGCGCGCGCGCGCGCTCTTCCGCCACAGGTGTCTGCTGAAGAGAGTGTGCG 300
QY 308 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGGAGAGACGTGTGCTGCTGCGCTTCCG 367
DB 301 CCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGGAGAGACGTGTGCTGCTGCGCTTCCG 360
QY 368 GCTGTGACAGCG 427
DB 361 GCTGTGACAGCG 420
QY 428 CCTGCCCAACACAGGTGACCGGACCGGACCGGAGCGGCGCGCGCGCGCGCGCGCGCG 487
DB 421 CCTGCCCAACACAGGTGACCGGACCGGACCGGAGCGGCGCGCGCGCGCGCGCGCGCG 480
QY 488 CCGCGTGGCGGACGACGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
DB 481 CCGCGTGGCGGACGACGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GCGTCCCAAGCTGCGGCTTACGAGGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
DB 541 GCGTCCCAAGCTGCGGCTTACGAGGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
QY 608 TCAGGCG 667
DB 601 TCAGGCG 660
QY 668 CTGAACCATATAGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
DB 661 CTGAACCATATAGCTCAGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 728 GAGGCG 787
DB 721 GAGGCG 780
QY 788 TGCCCTGTAGCGCGGAGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
DB 781 TGCCCTGTAGCGCGGAGCGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
QY 848 GCGTGAACCGGAGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 907
DB 841 GCGTGAACCGGAGCGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 900
QY 908 CACCTCTTTGAGAGGTGCGCTCTGTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
DB 901 CACCTCTTTGAGAGGTGCGCTCTGTGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
QY 968 GCACACG 1027
DB 961 GCACACG 1020
QY 1028 CCGGCTGTAGCGCGGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1087
DB 1021 CCGGCTGTAGCGCGGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1080
QY 1088 GCGCT 1147
DB 1081 GCGCT 1140
QY 1148 GACCATCTTTCTGAGTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1207
DB 1141 GACCATCTTTCTGAGTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
QY 1208 GCGCGAGCGCTACTGCAAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
DB 1201 GCGCGAGCGCTACTGCAAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1260
QY 1268 GTGCGCGTACGCGGTGCTCTCTCAAGACGACGTGCGCGCGCGCGCGCGCGCGCGCG 1327
DB 1261 GTGCGCGTACGCGGTGCTCTCTCAAGACGACGTGCGCGCGCGCGCGCGCGCGCGCG 1320
QY 1328 AGCGGTGTGTGCG 1387

Db 1321 AGCCGCTGTCTGTGCCCCGGGAGAACCCCAAGGCTCTGTGGCGGCCCCCGAGAGAGGA 1380
QY 1388 CACAGACCCCCCGTCCGCTGTGTGCACTGTCTCCGCGACAGACAGCCCCCTGGCAGGTGTA 1447
Db 1381 CACAGACCCCCCGTCCGCTGTGTGCACTGTCTCCGCGACAGACAGCCCCCTGGCAGGTGTA 1440
QY 1448 CGGCTTCTGTGCGGCGCTGCTGCGCCGCGCTGTGTGCCCCAGGCTCTGGGGTCCAGGCA 1507
Db 1441 CGGCTTCTGTGCGGCGCTGCTGCGCCGCGCTGTGTGCCCCAGGCTCTGGGGTCCAGGCA 1500
QY 1508 CAACGAACCGCCGCTTCTCTAGAGAACACCAAGAGTTTCTCTCCCTGGGGAAGCATGCGAA 1567
Db 1501 CAACGAACCGCCGCTTCTCTAGAGAACACCAAGAGTTTCTCTCCCTGGGGAAGCATGCGAA 1560
QY 1568 GCTCTCGCTGACAGAGCTGACGTGGAAGATGAGCGTGGGGAATGCGCTTGGCTGCGCAG 1627
Db 1561 GCTCTCGCTGACAGAGCTGACGTGGAAGATGAGCGTGGGGAATGCGCTTGGCTGCGCAG 1620
QY 1628 GAGCCCAAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAAGAGATCCTGGC 1687
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QY 1688 CAAGTTCTGCACTGCGCTGATGAGTGTGTACGTGTCAGCTGCTCAGGTCTTTCTTTTA 1747
Db 1681 CAAGTTCTGCACTGCGCTGATGAGTGTGTACGTGTCAGCTGCTCAGGTCTTTCTTTTA 1740
QY 1748 TGTCAAGGAGACCAAGCTTTTCAAAAGAACAGGCTTTTCTTCTACCGGAAGATGTCTGAG 1807
Db 1741 TGTCAAGGAGACCAAGCTTTTCAAAAGAACAGGCTTTTCTTCTACCGGAAGATGTCTGAG 1800
QY 1808 CAAGTTGCAAGCATTTGGAATCAGACAGACATTGAAGAGGGTGAAGTGGAGCTGTGTC 1867
Db 1801 CAAGTTGCAAGCATTTGGAATCAGACAGACATTGAAGAGGGTGAAGTGGAGCTGTGTC 1860
QY 1868 GGAAGCAGAGGTGAGGACGATCGGGAAGCCAGGCCCCGCTGCTGAGCTCAGACTCCG 1927
Db 1861 GGAAGCAGAGGTGAGGACGATCGGGAAGCCAGGCCCCGCTGCTGAGCTCAGACTCCG 1920
QY 1928 CTTTATCCCCCAAGCTGACGGGCTGCGCGCATTTGTGAACATGATGATGCTGGAGC 1987
Db 1921 CTTTATCCCCCAAGCTGACGGGCTGCGCGCATTTGTGAACATGATGATGCTGGAGC 1980
QY 1988 CAGAACTTCCGACAGAAAGAGGCGCGGCTCTACCTCGAGGTGAAGCACTGTT 2047
Db 1981 CAGAACTTCCGACAGAAAGAGGCGCGGCTCTACCTCGAGGTGAAGCACTGTT 2040
QY 2048 CAGCGTCTCAACTACGAGCGGGCGCGCGCGGCTCTGCGGCTCTGTGCTGG 2107
Db 2041 CAGCGTCTCAACTACGAGCGGGCGCGCGCGGCTCTGCGGCTCTGTGCTGG 2100
QY 2108 CCTGGACGATATCCACAGGGGCTGCGCGCACTTCTGTGCTGCTGTGCGGGGCCAGAGACC 2167
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QY 2168 GCGGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA 2227
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Db 2221 GGAACAGGCTCAGGAGGTCACTGCGCAGCATCAAAACCCAGAACACGTACTGCGTGG 2280
QY 2288 TCGGTATGCGGTGTCCAGAAAGGCGCGCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA 2347
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QY 2348 CGTCTCTACTTGAACAGACCTCCAGGCGGTACATGCGACAGTTGCTGCTCAGCTGACGA 2407
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QY 2408 GACCAAGCCGCTGAGGGGATGCGGTGTATGAGCAGAGCTCTCTCTGATGAGGCGAG 2467
Db 2401 GACCAAGCCGCTGAGGGGATGCGGTGTATGAGCAGAGCTCTCTCTGATGAGGCGAG 2460

QY 2468 CAGTGGCTCTTTCAGACGTTCTTCTTCTACGCTTCAATGTGCCAACACCGCGTGGCATGAGGG 2527
Db 2461 CAGTGGCTCTTTCAGACGTTCTTCTTCTACGCTTCAATGTGCCAACACCGCGTGGCATGAGGG 2520
QY 2528 CAAGTCTTACGTCAGTGGCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGTCTG 2587
Db 2521 CAAGTCTTACGTCAGTGGCAGGGGATCCCGCAGGGCTCCATCTCTCCAGCTGTCTG 2580
QY 2588 CAGCTGTGCTACGCGGACATGGAAGAACAGCTGTTTCCGGGATTCGCGGACGGGCT 2647
Db 2581 CAGCTGTGCTACGCGGACATGGAAGAACAGCTGTTTCCGGGATTCGCGGACGGGCT 2640
QY 2648 GCTCTGCGTTTGGTGAATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAAC 2707
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Db 2701 CTTCTCAGGACCCCTGCTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGTAACCTTGGGAA 2760
QY 2768 GACAGTGTGAACCTTCCCTGTAGAAGACAGAGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2827
Db 2761 GACAGTGTGAACCTTCCCTGTAGAAGACAGAGCCCTGGGTGGCACGGCTTTTGTTCAGAT 2820
QY 2828 GCGGCGCCCAAGGCTTATCCCTGTGTGCGGCTGTGCTGTGATACCCGACCTGAGGT 2887
Db 2821 GCGGCGCCCAAGGCTTATCCCTGTGTGCGGCTGTGCTGTGATACCCGACCTGAGGT 2880
QY 2888 GAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2947
Db 2881 GAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCG 2940
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QY 3068 CAAGTCTCTCTGTCAGAGCGTACAGGTTTCAAGCATGTGTGCTGAGCTCCATTCA 3127
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Db 3181 CTGCTACTCATCTGAAAGCCAGAGACGAGATGTGCTGGGGCCAAAGGCGCGC 3240
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Db 3241 CCGGCTCTGCGCTCCGAGGCGCGTGCAGTGGCTGTGCCAACAGCATTCCTGCTCAAGCT 3300
QY 3298 GGGTTAGGAAGTTTACCCTTTTCCGATCAGGAAGTGTGTTAACCAACCACTGTGAG 3357
Db 3301 GACTGACACCGGTGTACCTACGTGCACCTCTGCGGTCACTCAGGACAGCCAGACGCA 3360
QY 3358 GCTGCTGCGCGCGCTCTGCTGCGGTGAGACAGACCTGATGAAAGGACAGAGCTG 3417
Db 3361 GCTGAGTGGGAAGCTTCCGCGGACGACGCTGATGCGCCAGGCGCGCAACCGCGC 3420
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Db 3421 ACTGCGCTGAGACTTCAAGACCATCTGAGACTGATGCGCACCGCGCGCAAGCGCGCA 3480
QY 3455 GGAAGCGCTGGGGGCGCTGTCTCTCTGTTTGGCCCATGTGGGATTTGGGGGCGCTG 3514
Db 3481 GAGCAGACACAGACGCGCTGTACGCGCGGCTTACGTCCAGGAGGAGGCGCGCC 3540

QY 3515 GCCTCTCCTGTTTCCCTGTGTGGATTGGCTGTCTCCCTCCATGGCACTTAGGGCC 3574
DB 3541 CACACCCAGGCCCCGACCGCTGGAGTCTGAGGCTGAGTGTGTCGAGGCGCTG 3600
QY 3575 CTTGTGCAAAACCCAGGCCAAG-----GGCTTAGAGGAGGCCAGGCCAGGCTACCCAC 3629
DB 3601 CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAGGCT 3660
QY 3630 CCCTCTCAGAGCAGAGCGCCGCTATCACCACAGAGAGCCCGCGCTCTCTGCTTC 3689
DB 3661 GAGTGTCCAGCACACCTGCGCTCT-TCACTTCCCCACAGGCTGCGCTCGCTCCACCC 3719
QY 3690 CCAGTCACCGCTCTCTGCCCCCTGACACTTGTCCAGCATCAGGAGGTTTCTGATCCGT 3749
DB 3720 AGGGCCAGCTTTTCTTCCACAGAGAGCCCGCTTCCACTCCCCACATAGGAATAGTCCATC 3779
QY 3750 CTGAAATTCAGCCATGTCGAACCTGCGCTGAGCTTAACAGCTTCTACTTCTGTTTC 3809
DB 3780 CCCAGATTCCCATTTGTTCAACCCCT-----CGCCCTGCGCTCTTGTCTCCACCC 3832
QY 3810 TTCTGTGTGTGAGAGCCCTGAGAAGAGCCCTGGAGCTCTGGAAATTTGAGTGACCA 3869
DB 3833 CACCATCCAGTGGAGACCTTGAGAAGAGACCTGGAGCTCTGGAAATTTGAGTGACCA 3892
QY 3870 AAGGTGTGCTGTACACAGGCGAGAGCCCTGACCTGGATGGGGTCCCTGTGCTCAA 3929
DB 3893 AAGGTGTGCTGTACACAGGCGAGAGCCCTGACCTGGATGGGGTCCCTGTGCTCAA 3952
QY 3930 ATTGGGGGAGGTGCTGTGGAGTAAATACTGAATATATAGTATTTCAGTTTGAATA 3989
DB 3953 ATTGGGGGAGGTGCTGTGGAGTAAATACTGAATATATAGTATTTCAGTTTGAATA 4012
QY 3990 AAA 3992
DB 4013 AAA 4015

RESULT 15
AAZ08150
ID AAZ08150 standard; cDNA; 4015 BP.
XX
AC AAZ08150;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human telomerase reverse transcriptase cDNA.
XX
KW Human telomerase reverse transcriptase; hTERT; telomerase; hEST2;
KW catalytic protein component; cell proliferative capacity;
KW cell immortality; neoplastic phenotype; diagnostic application;
KW prognostic application; telomerase related condition; cancer;
KW therapeutic agent; telomerase expression; telomerase activity; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "Human telomerase reverse transcriptase"
FT /transl_except= (pos:1877..1879, aa:Gln)
XX

PN WO950279-A1.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US007160.
XX
PR 31-MAR-1998; 98US-00052919.
XX
PA (GERO-) GERON CORP.
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Cech TR, Lingner J, Nakamura T, Chapman KB, Morin GB, Harley CB;

PI Andrews WH;
XX
XX WPI: 1999-610834/52.
DR P-PSDB; AAY28881.
XX
PT Antisense polynucleotides for human telomerase reverse transcriptase used
PT for diagnosing or treating cancer.
XX
PS Claim 1; Fig 1; 31pp; English.
XX
CC The present sequence encodes for human telomerase reverse transcriptase
CC (hTERT). This is the catalytic protein component of telomerase and is also
CC referred to as hEST2. This correlates with cell proliferative capacity,
CC cell immortality, and the development of a neoplastic phenotype. Human
CC TRT antisense oligonucleotides are useful for diagnostic or prognostic
CC applications to telomerase related conditions, including cancer. They are
CC also useful as therapeutic agents, for inhibition of telomerase
CC expression and activity
XX
SQ Sequence 4015 BP; 663 A; 1364 C; 1274 G; 714 T; 0 U; 0 Other;

Query Match 82.4%; Score 3305; DB 2; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3617; Conservative 0; Mismatches 360; Indels 46; Gaps 5;

QY 8 GCAGCGCTGCTCTCTCTGCTGCGACGTTGGAGAGCCCTGGCCCGCCGCGATGCC 67
DB 1 GCAGCGCTGCTCTCTCTCTGCTGCGACGTTGGAGAGCCCTGGCCCGCCGCGATGCC 60
QY 68 GCGCGCTCCCGCTGCGAGCGCGCTCTCTCTGCTGCGACGTTGGAGAGCCCTGGCCCG 127
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QY 188 GGAACCGCGCGCTTTCGCGCGCTGTCGCGCGCGCTGTCGCGCGCTGTCGCGCG 247
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 19:45:38 ; Search time 8132.11 Seconds
(without alignments)
17359.183 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3333.6	83.1	4042	20	US-09-424-686B-1	Sequence 1, Appli
3	3333.6	83.1	4042	20	US-09-424-686F-1	Sequence 1, Appli
4	3333.6	83.1	4042	24	US-09-582-246-2	Sequence 2, Appli
5	3320.2	82.8	4037	13	US-08-974-549-343	Sequence 343, App
6	3320.2	82.8	4037	20	US-09-432-503-343	Sequence 343, App
7	3320.2	82.8	4037	31	US-09-721-477-343	Sequence 343, App
8	3320.2	82.8	4037	31	US-09-721-506-343	Sequence 343, App
9	3320.2	82.8	4037	49	US-10-325-810-343	Sequence 343, App
10	3320.2	82.8	4038	13	US-08-974-524E-117	Sequence 117, App
11	3320.2	82.8	4038	13	US-08-974-584C-117	Sequence 117, App
12	3311.4	82.5	4023	14	US-09-026-981-35	Sequence 35, Appli
13	3307	82.4	7029	13	US-08-911-312-1	Sequence 1, Appli
14	3307	82.4	7029	13	US-08-911-312A-1	Sequence 1, Appli
15	3306.6	82.4	4015	1	PCT-US01-15774-3	Sequence 3, Appli
16	3306.6	82.4	4015	1	PCT-US02-14867-1	Sequence 1, Appli
17	3306.6	82.4	4015	1	PCT-US02-31635-1	Sequence 1, Appli
18	3306.6	82.4	4015	1	PCT-US02-33146-19	Sequence 19, Appli
19	3306.6	82.4	4015	1	PCT-US03-19844-1	Sequence 1, Appli
20	3306.6	82.4	4015	1	PCT-US99-.06898-1	Sequence 1, Appli
21	3306.6	82.4	4015	1	PCT-US99-.07097-1	Sequence 1, Appli
22	3306.6	82.4	4015	1	PCT-US99-.07160-1	Sequence 1, Appli
23	3306.6	82.4	4015	13	US-08-974-549-1	Sequence 1, Appli
24	3306.6	82.4	4015	14	US-09-052-864-1	Sequence 1, Appli
25	3306.6	82.4	4015	20	US-09-432-503-1	Sequence 1, Appli
26	3306.6	82.4	4015	25	US-09-601-645-10	Sequence 10, Appli
27	3306.6	82.4	4015	25	US-09-601-645A-10	Sequence 10, Appli
28	3306.6	82.4	4015	31	US-09-721-477-1	Sequence 1, Appli
29	3306.6	82.4	4015	31	US-09-721-506-1	Sequence 1, Appli
30	3306.6	82.4	4015	34	US-09-843-676-224	Sequence 224, App
31	3306.6	82.4	4015	39	US-09-949-016-455	Sequence 455, App
32	3306.6	82.4	4015	42	US-09-990-080-1	Sequence 1, Appli
33	3306.6	82.4	4015	43	US-10-044-539-1	Sequence 1, Appli
34	3306.6	82.4	4015	43	US-10-044-692-1	Sequence 1, Appli
35	3306.6	82.4	4015	44	US-10-053-758-224	Sequence 224, App
36	3306.6	82.4	4015	44	US-10-054-295-224	Sequence 224, App
37	3306.6	82.4	4015	44	US-10-054-611-224	Sequence 224, App
38	3306.6	82.4	4015	45	US-10-105-963-1	Sequence 1, Appli
39	3306.6	82.4	4015	45	US-10-143-536-1	Sequence 1, Appli
40	3306.6	82.4	4015	47	US-10-208-243-1	Sequence 1, Appli
41	3306.6	82.4	4015	49	US-10-325-810-1	Sequence 1, Appli
42	3306.6	82.4	4015	50	US-10-388-578-1	Sequence 1, Appli
43	3306.6	82.4	4015	50	US-10-389-431-1	Sequence 1, Appli
44	3306.6	82.4	4015	51	US-10-449-565-1	Sequence 1, Appli
45	3306.6	82.4	4015	53	US-10-602-441-1	Sequence 1, Appli

ALIGNMENTS

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; RESULT 1
; US-09-424-686F-12
; Sequence 12, Application US/09424686F
; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Siegmund, Hans-Ulrich
; APPLICANT: Weichel, Walter
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Therap
; TITLE OF INVENTION: Use
; FILE REFERENCE: Bayer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686F
; CURRENT FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/EP98/03468
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Word
; SEQ ID NO 12

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; LENGTH: 4012
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4012)
; OTHER INFORMATION: Nucleotide positions 1-1782 and 3872 to 4012 are identical to th
; OTHER INFORMATION: same sequences in SEQ ID NO: 1; nucleotide positions from 1783
; OTHER INFORMATION: to 3871 are according to SEQ ID NO: 7.
US-09-424-686F-12

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Query Match	100.0%;	Score 4012;	DB 20;	Length 4012;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4012;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY	1	GTTCAGGACGCGCTGCCTCCTGTCGACAGTGGGAAGCCCTGGCCCCGGCCACCCCGG	60
Db	1	GTTTCAGGACGCGCTGCCTCCTGTCGACAGTGGGAAGCCCTGGCCCCGGCCACCCCGG	60
QY	61	CGATGCCCGCGCGCTCCCCCGCTGCCGAGCCGCTGCCTCTGTCGCGACGCACTACCGCG	120
Db	61	CGATGCCCGCGCGCTCCCCCGCTGCCGAGCCGCTGCCTCTGTCGCGACGCACTACCGCG	120
QY	121	AGGTGCTGCGCGCTGGCCACGTTGCTGCGGCGCCTGGGGGCCCCAAGGGCTGGCGGCTGCTG	180
Db	121	AGGTGCTGCGCGCTGGCCACGTTGCTGCGGCGCCTGGGGGCCCCAAGGGCTGGCGGCTGCTG	180
QY	181	AGCGCGGGGACCCCGCGCTTCCCGCGCGCTGCTGAGCCCAAGTGCCTGGTGTGCGTCCCT	240
Db	181	AGCGCGGGGACCCCGCGCTTCCCGCGCGCTGCTGAGCCCAAGTGCCTGGTGTGCGTCCCT	240
QY	241	GGGACGACG	300
Db	241	GGGACGACG	300
QY	301	TGCTGCGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGCTGGCCTTCG	360
Db	301	TGCTGCGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGCTGGCCTTCG	360
QY	361	GCTTGCCTGCTGTGACCGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	420
Db	361	GCTTGCCTGCTGTGACCGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	420
QY	421	GCAGCTACTGCCCCAACACCGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGC	480
Db	421	GCAGCTACTGCCCCAACACCGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGC	480
QY	481	TGCTGCGCGCGGTGGGCGACGCTGTGTTCACTGCTGGACAGCTGCGGCTCTTTG	540
Db	481	TGCTGCGCGCGGTGGGCGACGCTGTGTTCACTGCTGGACAGCTGCGGCTCTTTG	540
QY	541	TGCTGTGCTCTCCAGCTGCGCTACCAAGTGTGCGGGCGCGCTGTACCAAGCTGCGCG	600
Db	541	TGCTGTGCTCTCCAGCTGCGCTACCAAGTGTGCGGGCGCGCTGTACCAAGCTGCGCG	600
QY	601	CTGCCACTCAGGCGCGCGCGCGCCACACGCTAGTGAACCCGAAGCGTCTGGATGCG	660
Db	601	CTGCCACTCAGGCGCGCGCGCGCCACACGCTAGTGAACCCGAAGCGTCTGGATGCG	660
QY	661	AACGGGCTGGAACCATAGCGTCAAGGAGCGCGGGTCCCCCTGGGCTGCGACGCCCGG	720
Db	661	AACGGGCTGGAACCATAGCGTCAAGGAGCGCGGGTCCCCCTGGGCTGCGACGCCCGG	720
QY	721	GTGCGAGGAGCGCGCGGGCGAGTGCAGCCGAAGTGTGCGTTGCCCAAGAGGCCAAGC	780
Db	721	GTGCGAGGAGCGCGCGGGCGAGTGCAGCCGAAGTGTGCGTTGCCCAAGAGGCCAAGC	780
QY	781	GTGCGCTGCCCTGAGCCGAGCGGACGCCCTTGGGCAAGGGTCTGGGCCACCCCG	840
Db	781	GTGCGCTGCCCTGAGCCGAGCGGACGCCCTTGGGCAAGGGTCTGGGCCACCCCG	840
QY	841	GCAGACCGCTGACCGAGTGAACGTGTTCTGTGTGTCACTGCGCAGACCGCGCG	900

Db 841 GCAGGACGCTGACCCGAGTGAACCTGTTCTGTGTGTGTCACTGCGCAGACCCGCCG 900
QY 901 AAGAGCCACTCTTTGGAGGCTGCTCTGTGCAACGCGCACTCCACCCTATCCGTGG 960
Db 901 AAGAGCCACTCTTTGGAGGCTGCTCTGTGCAACGCGCACTCCACCCTATCCGTGG 960
QY 961 GCGCCGACGACCAACGCGGCGCCCATCCACATCGCGGCCACCACTCCCTGGGACACGC 1020
Db 961 GCGCCGACGACCAACGCGGCGCCCATCCACATCGCGGCCACCACTCCCTGGGACACGC 1020
QY 1021 CTTGTCCCCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGCGCAGCAAGAGC 1080
Db 1021 CTTGTCCCCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGCGCAGCAAGAGC 1080
QY 1081 AGCTGCGGCGCTCTCTCTACTAGCTCTGTAGGCGCCAGCTGACTGCGCTCGAGGC 1140
Db 1081 AGCTGCGGCGCTCTCTCTACTAGCTCTGTAGGCGCCAGCTGACTGCGCTCGAGGC 1140
QY 1141 TCGTGAGACCATCTTCTGTGGTTCCAGGCGCTGATGCGAGGACTCCCGCAGGTTGC 1200
Db 1141 TCGTGAGACCATCTTCTGTGGTTCCAGGCGCTGATGCGAGGACTCCCGCAGGTTGC 1200
QY 1201 CCGCGCTGCGCCAGCGCTACTGCGAAATGCGGCGCTGTTTCTGAGCTGTGGAAAC 1260
Db 1201 CCGCGCTGCGCCAGCGCTACTGCGAAATGCGGCGCTGTTTCTGAGCTGTGGAAAC 1260
QY 1261 ACGCGAGTGCGCTCTAGCGGCTGCTCAAGACGCACTGCGCGCTGCGAGCTGCGTCA 1320
Db 1261 ACGCGAGTGCGCTCTAGCGGCTGCTCAAGACGCACTGCGCGCTGCGAGCTGCGTCA 1320
QY 1321 CCGCAGACGCGGTGTGTGTGCGCGGAGAGAGCGCGCTGTGTGCGCGCGCGAGG 1380
Db 1321 CCGCAGACGCGGTGTGTGTGCGCGGAGAGAGCGCGCTGTGTGCGCGCGCGAGG 1380
QY 1381 AGGAGGACACAGACCCCGCTGCTGTGAGCTGTCTCGCAGCAGCAGCAGCAGCAGC 1440
Db 1381 AGGAGGACACAGACCCCGCTGCTGTGAGCTGTCTCGCAGCAGCAGCAGCAGCAGC 1440
QY 1441 AGGTGTACGCTTCTGTGCGGCTGCTGCGCGCGCTGTGCGCGCGCTGTGCGGCT 1500
Db 1441 AGGTGTACGCTTCTGTGCGGCTGCTGCGCGCGCTGTGCGCGCGCTGTGCGGCT 1500
QY 1501 CAGGACACAGACCGCGCTTCTCAGGAACACCAAGTTCTCTCTGGGGAAGC 1560
Db 1501 CAGGACACAGACCGCGCTTCTCAGGAACACCAAGTTCTCTCTGGGGAAGC 1560
QY 1561 ATGCCAAGCTTCTGCTGAGAGCTGACGTGAAGATGAGCTGCGGACTGCGCTTGGC 1620
Db 1561 ATGCCAAGCTTCTGCTGAGAGCTGACGTGAAGATGAGCTGCGGACTGCGCTTGGC 1620
QY 1621 TGGCGAGGAGCCAGGCGTGTGTTCGCGCGCAGAGCAGCAGCTGCGTGAAGAGA 1680
Db 1621 TGGCGAGGAGCCAGGCGTGTGTTCGCGCGCAGAGCAGCAGCTGCGTGAAGAGA 1680
QY 1681 TCGTGCGCAAGTCTCTGCACTGCTGATGATGTGTACGTCTGAGCTGCTCAGTCTT 1740
Db 1681 TCGTGCGCAAGTCTCTGCACTGCTGATGATGTGTACGTCTGAGCTGCTCAGTCTT 1740
QY 1741 TCTTTTATGTACCGAGACCACTTCAAAAGAACAGCTCTTTTCTACCGAAAGAGTG 1800
Db 1741 TCTTTTATGTACCGAGACCACTTCAAAAGAACAGCTCTTTTCTACCGAAAGAGTG 1800
QY 1801 TCTGAGCAAGTGTGCAAGCAATTGGAATCAGACAGCACTTGAAGAGGCTGAGCTGCGG 1860
Db 1801 TCTGAGCAAGTGTGCAAGCAATTGGAATCAGACAGCACTTGAAGAGGCTGAGCTGCGG 1860
QY 1861 AGCTGTGCGAAGCAGAGCTGAGCAGCATCGGGAAGCCAGGCGCGCTGCTGAGCTCA 1920
Db 1861 AGCTGTGCGAAGCAGAGCTGAGCAGCATCGGGAAGCCAGGCGCGCTGCTGAGCTCA 1920
QY 1921 GACTCCGCTTCACTCCCAAGCTGACGCGCTGCGGCGGCTGCTGAACTGAGCTACGTCG 1980
Db 1921 GACTCCGCTTCACTCCCAAGCTGACGCGCTGCGGCGGCTGCTGAACTGAGCTACGTCG 1980

QY 1981 TGGAGCCAGAACGTTCCGACAGAAAGAGGCGCGAGGCTCACTCGAGGTTGAAG 2040
Db 1981 TGGAGCCAGAACGTTCCGACAGAAAGAGGCGCGAGGCTCACTCGAGGTTGAAG 2040
QY 2041 CACTGTTAGCGTGTCTCACTACAGCGGCGCGCGCGCGCTCTGGCGCTCTG 2100
Db 2041 CACTGTTAGCGTGTCTCACTACAGCGGCGCGCGCGCGCTCTGGCGCTCTG 2100
QY 2101 TGCTGGGCTGAGCAGATATCCAGAGGCGCTGCGCACCTTGCTGCTGCTGCGGCGCC 2160
Db 2101 TGCTGGGCTGAGCAGATATCCAGAGGCGCTGCGCACCTTGCTGCTGCTGCGGCGCC 2160
QY 2161 AGGACCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGACGCGCGCTACGACCA 2220
Db 2161 AGGACCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGACGCGCGCTACGACCA 2220
QY 2221 TCCCGCAGACAGGCTACCGAGGTCTACGCGCATCTAAACCCAGAACAGTACT 2280
Db 2221 TCCCGCAGACAGGCTACCGAGGTCTACGCGCATCTAAACCCAGAACAGTACT 2280
QY 2281 GCGTGCCTGCTATGCGGTGTGTCAGAGGCGCGCGCGCGCGCGCGCGCTTCA 2340
Db 2281 GCGTGCCTGCTATGCGGTGTGTCAGAGGCGCGCGCGCGCGCGCGCGCGCTTCA 2340
QY 2341 AGAGCCAGCTCTCTACTTGAAGACCTCCAGCGCTACATGCGACAGTTCGTGCTTACC 2400
Db 2341 AGAGCCAGCTCTCTACTTGAAGACCTCCAGCGCTACATGCGACAGTTCGTGCTTACC 2400
QY 2401 TGCAGGACACAGCGCGCTGAGGAGTCCCGTGTCTATGAGCAGAGCTCTCTCTGATG 2460
Db 2401 TGCAGGACACAGCGCGCTGAGGAGTCCCGTGTCTATGAGCAGAGCTCTCTCTGATG 2460
QY 2461 AGGCGCAGGTGCGCTCTTCAAGCTCTTCTACGCTTCAATGTCACACAGCGCGTGC 2520
Db 2461 AGGCGCAGGTGCGCTCTTCAAGCTCTTCTACGCTTCAATGTCACACAGCGCGTGC 2520
QY 2521 TCAAGGCAAGTCTCTACGCTGAGTCCAGGAGTCCCGAGGCTCCATCTCTTCAAGC 2580
Db 2521 TCAAGGCAAGTCTCTACGCTGAGTCCAGGAGTCCCGAGGCTCCATCTCTTCAAGC 2580
QY 2581 TGTCTGACGCTGTGTACGCGCAGATGAGAAACAAGCTGTTGCGGAGTTGCGGCG 2640
Db 2581 TGTCTGACGCTGTGTACGCGCAGATGAGAAACAAGCTGTTGCGGAGTTGCGGCG 2640
QY 2641 ACGGCTGCTCTGCGTGTGTGATGATTTCTTGTGTGACACCTCACTCACTCAAGC 2700
Db 2641 ACGGCTGCTCTGCGTGTGTGATGATTTCTTGTGTGACACCTCACTCACTCAAGC 2700
QY 2701 CGAAACCTTCTCTACAGACCTGTGCGAGTGTCCCTGATGAGTGTGCTGCTGCTG 2760
Db 2701 CGAAACCTTCTCTACAGACCTGTGCGAGTGTCCCTGATGAGTGTGCTGCTGCTG 2760
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Db 2821 TTTAGATGCGCGCCAGCGCTATTCCCTGTGCGGCGCTGCTGCTGATACCGGAGCC 2880
QY 2881 TGGAGGTGACAGAGCACTACTCAGCTATGCGCGACCTCCATCAGAGCGAGTCACT 2940
Db 2881 TGGAGGTGACAGAGCACTACTCAGCTATGCGCGACCTCCATCAGAGCGAGTCACT 2940
QY 2941 TCAACCGCGCTTCAAGGCTGGAGAGAACATGCGTCAAACTCTTTGGGCTTGGCGC 3000
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QY 3001 TGAAGTGTACAGCTGTTCTGATTTGAGTGAACAGCTCCAGACGCTGTCACCA 3060
Db 3001 TGAAGTGTACAGCTGTTCTGATTTGAGTGAACAGCTCCAGACGCTGTCACCA 3060

QY 3061 ACATCTACAGATCTCTCTGTCAGGCGTACAGGTTTTCAGCATGTGTGTGCTGCACTCC 3120
DB 3061 ACATCTACAGATCTCTCTGTCAGGCGTACAGGTTTTCAGCATGTGTGTGCTGCACTCC 3120
QY 3121 CATTTCAACAGCAAGTTTGAAGAAGCCCAATTTTCTGCGGCTCATCTCTGACACGG 3180
DB 3121 CATTTCAACAGCAAGTTTGAAGAAGCCCAATTTTCTGCGGCTCATCTCTGACACGG 3180
QY 3181 CCTCCCTGCTACTCCATCTCTGAAAGCCCAAGACGAGTATGTGAGAGTGTGCTGCTGCT 3240
DB 3181 CCTCCCTGCTACTCCATCTCTGAAAGCCCAAGACGAGTATGTGAGAGTGTGCTGCTGCT 3240
QY 3241 CAGTGGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
DB 3241 CAGTGGCAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
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DB 3301 TTAGGAAGTCTTACCCCTTTTTCGCAACAGGAAGTGTGTTTAAACCAACCTGTGAGGCT 3360
QY 3361 CGTCTGCCCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
DB 3361 CGTCTGCCCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
QY 3421 GGGAGCTGCACTCTCTCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
DB 3421 GGGAGCTGCACTCTCTCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3481 CCTGTTGCCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
DB 3481 CCTGTTGCCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
QY 3541 ATTGGGCTGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
DB 3541 ATTGGGCTGCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3600
QY 3601 AGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3660
DB 3601 AGGAGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3660
QY 3661 CGACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3720
DB 3661 CGACAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3720
QY 3721 GTCCAGCATCAGGAGGTTTCTGATCCGCTGTAATTCAGGCAATGTGCAACTGTGCGGTC 3780
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DB 3781 CTGAGCTTAACAGCTTCTACTTCTGTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTG 3840
QY 3841 CTGGAAGCTCTGGGAATTTTGAAGTGAAGGTTGCTGCTGTTACACAGGCGAGGACCTT 3900
DB 3841 CTGGAAGCTCTGGGAATTTTGAAGTGAAGGTTGCTGCTGTTACACAGGCGAGGACCTT 3900
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DB 3901 GCACCTGATGGGGGTTCCCTGTGGGTCAATTTGGGGGAGGTTGCTGTGGAGTAAATAC 3960
QY 3961 TGAATATATAGTTTTCAGTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4012
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RESULT 2

US-09-424-686B-1

; Sequence 1, Application US/09424686B

; GENERAL INFORMATION:

; APPLICANT: Hagen, Gustav

; APPLICANT: Siegmund, Hans-Ulrich

; APPLICANT: Weichel, Walter

; APPLICANT: Wick, Mareba

; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and
; TITLE OF INVENTION: Therapeutic Use
; FILE REFERENCE: Beyer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686B
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/BP98/03468
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-686B-1

Query Match 83.1%; Score 333.6; DB 20; Length 4042;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 1 GTTTCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
DB 1 GTTTCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 61 CGATGCGCGCGCTCCCGCTGCGAGCGCGCTGCGCTCCCTGCTGCGAGCCACTACCGCG 120
DB 61 CGATGCGCGCGCTCCCGCTGCGAGCGCGCTGCGCTCCCTGCTGCGAGCCACTACCGCG 120
QY 121 AGTGTGCGCGCTGCGCACGTTTCGTCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 180
DB 121 AGTGTGCGCGCTGCGCACGTTTCGTCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 180
QY 181 AGCGCGGAGACCCCGCGCTTCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 AGCGCGGAGACCCCGCGCTTCCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 GGGAGCGACG 300
DB 241 GGGAGCGACG 300
QY 301 TGTGCGCGCGAGTCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 301 TGTGCGCGCGAGTCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
QY 361 GCTTCGCGCTGCTGAGCGGCG 420
DB 361 GCTTCGCGCTGCTGAGCGGCG 420
QY 421 GCAGCTACTGCGCCCAACACCGGTGACGACGCACTGCGGCGGAGCGGCGGCGGCGGCGGCG 480
DB 421 GCAGCTACTGCGCCCAACACCGGTGACGACGCACTGCGGCGGAGCGGCGGCGGCGGCGGCG 480
QY 481 TGCTGCGCGCGGTGGGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 TGCTGCGCGCGGTGGGCGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 TGCT 600
DB 541 TGCT 600
QY 601 CTGCACTACAGGCG 660
DB 601 CTGCACTACAGGCG 660
QY 661 AACGGGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
DB 661 AACGGGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 721 GTGCGAGGAGCG 780
DB 721 GTGCGAGGAGCG 780
QY 781 GTGCGCGCTGCGCGCTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840

Db 781 GTGGCGTGGCCCTGAGCCGAGGCGGACGCCGTTGGGAGGGGTCTGGGCCACCCGG 840
QY 841 GCAGAGCGGTGACCGAGTGCCTGTTTCTGTGTGTGTCACCTGCAGACCCGGCG 900
Db 841 GCAGAGCGGTGACCGAGTGCCTGTTTCTGTGTGTGTCACCTGCAGACCCGGCG 900
QY 901 AAGAAGCACTCTTTGAGGGTGCCTCTCTGACGCGCCACTCCACCACTCCGTGG 960
Db 901 AAGAAGCACTCTTTGAGGGTGCCTCTCTGACGCGCCACTCCACCACTCCGTGG 960
QY 961 GCCGCAAGCAACGCGGCGCCCATCCACATCGCGCCACCACTCCGTGGCAACGC 1020
Db 961 GCCGCAAGCAACGCGGCGCCCATCCACATCGCGCCACCACTCCGTGGCAACGC 1020
QY 1021 CTTGTCCCGGTGTAGCGCGGAGCAAGCACTCTCTACTCTCAGCGGAGAGAGC 1080
Db 1021 CTTGTCCCGGTGTAGCGCGGAGCAAGCACTCTCTACTCTCAGCGGAGAGAGC 1080
QY 1081 AGCTGGCGCTCTCTCTACTAGCTCTTGAGGCGCCAGCTGAGCGCTGGAGGC 1140
Db 1081 AGCTGGCGCTCTCTCTACTAGCTCTTGAGGCGCCAGCTGAGCGCTGGAGGC 1140
QY 1141 TCGTGAGAACATTTCTGTGGTTCCAGGCGCTGATGCCAGGACTCCCGGAGTTGC 1200
Db 1141 TCGTGAGAACATTTCTGTGGTTCCAGGCGCTGATGCCAGGACTCCCGGAGTTGC 1200
QY 1201 CCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTTTCTGAGCTGTTGGGAAC 1260
Db 1201 CCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTTTCTGAGCTGTTGGGAAC 1260
QY 1261 ACGCGAGTGGCCCTACGCGGTGCTCTCAAGACGCACTGCGCCGCTGCGAGTGGTCA 1320
Db 1261 ACGCGAGTGGCCCTACGCGGTGCTCTCAAGACGCACTGCGCCGCTGCGAGTGGTCA 1320
QY 1321 CCCGAGAGCGGTGTCTGTGCGCGGAGAGAGCCCGGAGCTCTGTGGCGCCCGAGG 1380
Db 1321 CCCGAGAGCGGTGTCTGTGCGCGGAGAGAGCCCGGAGCTCTGTGGCGCCCGAGG 1380
QY 1381 AGGAGGACACAGACCCCGCTGCTGTGAGAGCTGCTCGCCAGACAGACAGCCCTGGC 1440
Db 1381 AGGAGGACACAGACCCCGCTGCTGTGAGAGCTGCTCGCCAGACAGACAGCCCTGGC 1440
QY 1441 AGGTGTACGGCTTCTGTGCGGCGCTGCTGCGCGGCTGCTGCGCGCTTGGGCT 1500
Db 1441 AGGTGTACGGCTTCTGTGCGGCGCTGCTGCGCGGCTGCTGCGCGCTTGGGCT 1500
QY 1501 CCAGGCAACGAAAGCGCGCTTCTCAAGAACCAAGAGTTCTCTCCGAGGAGC 1560
Db 1501 CCAGGCAACGAAAGCGCGCTTCTCAAGAACCAAGAGTTCTCTCCGAGGAGC 1560
QY 1561 ATGCCAAGCTCTGCTGAGAGAGCTGAGCTGGAAGATGAGCTGCGGAGCTGGCTGGC 1620
Db 1561 ATGCCAAGCTCTGCTGAGAGAGCTGAGCTGGAAGATGAGCTGCGGAGCTGGCTGGC 1620
QY 1621 TGGCAGAGAGCGCGGTTGGCTGTGTTCCGCGCGAGAGCACTGCTGAGAGAGA 1680
Db 1621 TGGCAGAGAGCGCGGTTGGCTGTGTTCCGCGCGAGAGCACTGCTGAGAGAGA 1680
QY 1681 TCCTGGCAAGTCTCTGACAGCTGATGAGTGTGAGCTGCTGAGCTGCTGAGCTT 1740
Db 1681 TCCTGGCAAGTCTCTGACAGCTGATGAGTGTGAGCTGCTGAGCTGCTGAGCTT 1740
QY 1741 TCTTTATGTCAAGAGACAGCTTCAAAAGAACAGGCTTTTCTACCGAAGAGTG 1800
Db 1741 TCTTTATGTCAAGAGACAGCTTCAAAAGAACAGGCTTTTCTACCGAAGAGTG 1800
QY 1801 TCTGAGCAAGTGTCAAGCAATGGAATCAGACAGCACTTGAAGAGGAGTGGCGG 1860
Db 1801 TCTGAGCAAGTGTCAAGCAATGGAATCAGACAGCACTTGAAGAGGAGTGGCGG 1860
QY 1861 AGCTGTGGAAGCAGAGGTGAGGAGCACTGCGGAGGCGCGCTGCTGAGCTCA 1920

Db 1861 AGCTGTGGAAGCAGAGGTGAGGAGCACTGCGGAGGCGCGCTGCTGAGCTCA 1920
QY 1921 GACTCCGTTTCAATCCCAAGCTGACGGGCTGCGGCGGATTTGAACATGACTACGTG 1980
Db 1921 GACTCCGTTTCAATCCCAAGCTGACGGGCTGCGGCGGATTTGAACATGACTACGTG 1980
QY 1981 TGGAGGCAAGAGCTTCCGAGAGAAAGAGGGCCGAGGCTCTCACTCGAGGAGAGG 2040
Db 1981 TGGAGGCAAGAGCTTCCGAGAGAAAGAGGGCCGAGGCTCTCACTCGAGGAGAGG 2040
QY 2041 CACTGTTACGCTGCTCAACTACAGCGGGCGGGCGGGCGGGCTCTCTGGCGGCTTG 2100
Db 2041 CACTGTTACGCTGCTCAACTACAGCGGGCGGGCGGGCGGGCTCTCTGGCGGCTTG 2100
QY 2101 TGTGGGCTGAGAGATATCCAGGGGCTGCGGCACTTCTGCTGCTGCTGCGGCGC 2160
Db 2101 TGTGGGCTGAGAGATATCCAGGGGCTGCGGCACTTCTGCTGCTGCTGCGGCGC 2160
QY 2161 AGACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGAGCGGGCGGTACAGACA 2220
Db 2161 AGACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGAGCGGGCGGTACAGACA 2220
QY 2221 TCCCGCAGAGCAGGCTCAGGAGGTATGCGGAGCATCAAAACCCAGAACAGTACT 2280
Db 2221 TCCCGCAGAGCAGGCTCAGGAGGTATGCGGAGCATCAAAACCCAGAACAGTACT 2280
QY 2281 GCGTGTGCTGTATGCGGTGTGTCAGAGAGGCGCCCATGAGCACTCCGAGGCTTCA 2340
Db 2281 GCGTGTGCTGTATGCGGTGTGTCAGAGAGGCGCCCATGAGCACTCCGAGGCTTCA 2340
QY 2341 AGAGCAGCTCTCTACCTTGAAGACCTCCAGCGGTAATGCAAGTCTGCTGAGC 2400
Db 2341 AGAGCAGCTCTCTACCTTGAAGACCTCCAGCGGTAATGCAAGTCTGCTGAGC 2400
QY 2401 TGCAAGAGACAGCGCGCTGAGGAGTGCGGTGATGAGAGAGAGCTCTCCGTAATG 2460
Db 2401 TGCAAGAGACAGCGCGCTGAGGAGTGCGGTGATGAGAGAGAGCTCTCCGTAATG 2460
QY 2461 AGGCAAGAGTGGCTCTTGAAGTCTTCTACGCTTCACTGAGCAAGAGCGGCGCA 2520
Db 2461 AGGCAAGAGTGGCTCTTGAAGTCTTCTACGCTTCACTGAGCAAGAGCGGCGCA 2520
QY 2521 TCAAGGAGAGTCTTACGTCAGTGCAGGAGGATCCCGAGGCTCCATCTCTCAAGC 2580
Db 2521 TCAAGGAGAGTCTTACGTCAGTGCAGGAGGATCCCGAGGCTCCATCTCTCAAGC 2580
QY 2581 TGCTCTGAGCCTGTGCTACGCGGACATGAGAACAGAGCTTTGCGGGGATTCGGCGG 2640
Db 2581 TGCTCTGAGCCTGTGCTACGCGGACATGAGAACAGAGCTTTGCGGGGATTCGGCGG 2640
QY 2641 ACGGCTGCTCTGCGTTTGTGAGATTTCTTGTGTTGATGACACTCACTCAAGCAG 2700
Db 2641 ACGGCTGCTCTGCGTTTGTGAGATTTCTTGTGTTGATGACACTCACTCAAGCAG 2700
QY 2701 CGAAACCTTCTCAGGACCTCTGTCGAGGAGTCTCTGAGTATGGCTGCTGTAAT 2760
Db 2701 CGAAACCTTCTCAGGACCTCTGTCGAGGAGTCTCTGAGTATGGCTGCTGTAAT 2760
QY 2761 TGGGAGAGACAGTGTGTAATTTCCCTGTAGAGACAGAGGCTTGGTGACGGCTTTG 2820
Db 2761 TGGGAGAGACAGTGTGTAATTTCCCTGTAGAGACAGAGGCTTGGTGACGGCTTTG 2820
QY 2821 TTCAATGCGCGGCGGCTTATCCCTGTGAGGCTGCTGCTGATACCCGAGACC 2880
Db 2821 TTCAATGCGCGGCGGCTTATCCCTGTGAGGCTGCTGCTGATACCCGAGACC 2880
QY 2881 TGGAGGTGAGAGAGCACTACTCAAGCTATGCGCGGAGCTCCATCAGAGCAAGTCACT 2940
Db 2881 TGGAGGTGAGAGAGCACTACTCAAGCTATGCGCGGAGCTCCATCAGAGCAAGTCACT 2940
QY 2941 TCAACGCGGCTTCAAGGCTGGGAGGAGCACTGCTGCAAACTTTTGGGGTCTTGGCGC 3000
Db 2941 TCAACGCGGCTTCAAGGCTGGGAGGAGCACTGCTGCAAACTTTTGGGGTCTTGGCGC 3000

QY	3001	TGAAGTGTACAGACCCCTGTTTCTCGATTGTCAGAGTGAACAGCCTCCAGACCGGTGTGCACCA	3060
Db	3001	TGAAGTGTACAGACCCCTGTTTCTCGATTGTCAGAGTGAACAGCCTCCAGACCGGTGTGCACCA	3060
QY	3061	ACATCTACAGAGATCCTCCTGCTGACAGCGCTACAGGTTTTCACGCAATGTGTCTGCAGCTCC	3120
Db	3061	ACATCTACAGAGATCCTCCTGCTGACAGCGCTACAGGTTTTCACGCAATGTGTCTGCAGCTCC	3120
QY	3121	CATTTCATCAGCAAGTTTGGAGAACCCCAATTTTTCCTGCGCGTCATCTCTGCACACGG	3180
Db	3121	CATTTCATCAGCAAGTTTGGAGAACCCCAATTTTTCCTGCGCGTCATCTCTGCACACGG	3180
QY	3181	CCTCCCTCTGCTACTCCATCCTGAAAGCCCAAGAACGACAGTATGT-----GCAGG	3230
Db	3181	CCTCCCTCTGCTACTCCATCCTGAAAGCCCAAGAACGACAGTATGT-----GCAGG	3240
QY	3231	TGCGTGGCCTCAGTGGCAGCAGTGCCTGCCTGCTGTGTAGTGTGTCAGGAGACTGAGT	3290
Db	3241	GCGCGCGCGCGCCTCTGCGCTCCGAGGCGCGTGAGTGTGTGCCAACCAAGCATTCCTGC	3300
QY	3291	GAACTCTGGGCTTAGGAAGTTCTTAACCCCTTTTCGCATCAGGAAGTGTTTAACCAACCA	3350
Db	3301	TCAAGCTGACTGCACACCGTGTCACTTACGTGCCACTCTGGGGTCACTCAGACAGACCC	3360
QY	3351	CTGTCAAGCTCGTCTGCGCGCGCTCTCGTGGGTGAGCAGACCACTGATGGAAGGACA	3410
Db	3361	AGACGAGCTGAGTGGAAAGTCCCGGGACGACGCTGACTGCCCTGGAGCCGACGCCA	3420
QY	3411	GGAAGCTGTCTGGAGCTGCCATCCTTCCACCTTGTCT-----	3449
Db	3421	ACCGGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGAGCCACCGCCACAGCC	3480
QY	3450	--GCCTGGGGAAGCGCTGGGGGCGCTGTGTCCTCTCTGTTTGCCTCATGTGGATTGGG	3507
Db	3481	AGGCCGAGAGCAGACACCAAGCAGCCTGTGCACGCGGGCTCTACGTCCAGGAGGGAGG	3540
QY	3508	GGGCTGTGCTCTCTGTTTGGCTGTGTGGATTGGCTGTCTCCGTCATGGCACT	3567
Db	3541	GGCGGCCACACCCAGGCGCGCACCGCTGGAGTCTGAGGCTGAGTGAAGTTTGGCCG	3600
QY	3568	TAGGGCCCTTGTGCAACCCAGGCCAAG-----GGCTTAGGAGAGGCCAGGCCAGGCT	3622
Db	3601	AGGCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTAGGCTGAGCGAGTGTCCAGCC	3660
QY	3623	ACCCCAACCCCTCTCAGAGCAGAGGCGCGTATCACCAAGACAGAGCCCGCGCGCTCT	3682
Db	3661	AAGGCTGAGTGTCCAGACACACTGCGCTCT-TCACTTCCCCACAGGCTGCGCGCTGGCT	3719
QY	3683	CTGCTTCCAGTCAACCGTCTCTGCCCCGTGACACTTTGTCCAGCATCAGGAGTTTCT	3742
Db	3720	CCACCCCAAGGCGCAGCTTTTCTCACCAGAGGCCGCGCTTCCACTCCCCACATAGGATA	3779
QY	3743	GATCCGTCTGAAATTCAAGCCATGTGGAACCTGCGGTCTGAGCTTAACAGCTTCTACTT	3802
Db	3780	GTCCATCCCCAGATTGCGCATTTGTCAACCCCTC-----GCCCTGCCCTCCTTGGCTT	3832
QY	3803	TCTGTTCTTTCTGTTGTGGAGACCCCTGAGAAGAACCCCTGGAGCTCTGGGAATTTGA	3862
Db	3833	CCACCCCAACCATCAAGGTGGAGAACCCCTGAGAAGAACCCCTGGAGCTCTGGGAATTTGA	3892
QY	3863	GTGACCAAGGTGTGCTCTGTACACAGGCGAGGACCTGCACCTGGATGGGGTCCCTGT	3922
Db	3893	GTGACCAAGGTGTGCTCTGTACACAGGCGAGGACCTGCACCTGGATGGGGTCCCTGT	3952
QY	3923	GGGTCAATTTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTT	3982
Db	3953	GGGTCAATTTGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTT	4012
QY	3983	TTGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA	4012
Db	4013	TTGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA	4042

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RESULT 3
US-09-424-686F-1
; Sequence 1, Application US/09424686F
; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Siegmund, Hans-Ulrich
; APPLICANT: Weichsel, Walter
; APPLICANT: Wick, Mareisa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Thera
; TITLE OF INVENTION: Use
; FILE REFERENCE: Bayer 10, 203
; CURRENT APPLICATION NUMBER: US/09/424, 686F
; PRIOR FILING DATE: 1999-11-29
; PRIORITY APPLICATION NUMBER: PCT/EP98/03468
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-424-686F-1

Query Match      83.1%; Score 3333.6; DB 20; Length 4042;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY      1 GTTTCAGGCAGCGCTGCTCCTCTGTGGCCACGTGGGAAGCCCTGGCCCCGCCACCCTCG 60
Db      1 GTTTCAGGCAGCGCTGCTCCTCTGTGGCCACGTGGGAAGCCCTGGCCCCGCCACCCTCG 60
QY      61 CGATGCCGCGCGCTCCCGCTGCGGAGCCGTGGCTCCCTGTGCGCAGCCACTAACCGCG 120
Db      61 CGATGCCGCGCGCTCCCGCTGCGGAGCCGTGGCTCCCTGTGCGCAGCCACTAACCGCG 120
QY      121 AGGTGCTGCCGTGGCCACGTTGCTGCGCGCTGGGGCCCAAGGGCTGGCGCTGATGC 180
Db      121 AGGTGCTGCCGTGGCCACGTTGCTGCGCGCTGGGGCCCAAGGGCTGGCGCTGATGC 180
QY      181 AGCGCGGGGACCGCGCGCTTTCGCGCGCTGCTGGCCCAAGTGCTGTGCTGCTGCT 240
Db      181 AGCGCGGGGACCGCGCGCTTTCGCGCGCTGCTGGCCCAAGTGCTGTGCTGCTGCT 240
QY      241 GGGACGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db      241 GGGACGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY      301 TGGTGGCCCGAGTGTGTGAGAAGGCTGTGCGAAGCGCGCGCGCGCGCGCGCGCGCG 360
Db      301 TGGTGGCCCGAGTGTGTGAGAAGGCTGTGCGAAGCGCGCGCGCGCGCGCGCGCGCG 360
QY      361 GCTTCGCGCTGTGAACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db      361 GCTTCGCGCTGTGAACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY      421 GCAGCTACCTGCCCACAACAGGTGACCGACGCACTGCGGGGGGAGCGGGCGTGGGGGCTGC 480
Db      421 GCAGCTACCTGCCCACAACAGGTGACCGACGCACTGCGGGGGGAGCGGGCGTGGGGGCTGC 480
QY      481 TGCTGCGCGCGCTGGGGCGACGAGCTGTGTTCACCTGCTGGCACGCTGCGCGCTCTTG 540
Db      481 TGCTGCGCGCGCTGGGGCGACGAGCTGTGTTCACCTGCTGGCACGCTGCGCGCTCTTG 540
QY      541 TGCTGTGCTTCCAAGCTGCGCTTACCAAGGTGTGCGGGCGCGCGCTGTACCAAGCTCGCG 600
Db      541 TGCTGTGCTTCCAAGCTGCGCTTACCAAGGTGTGCGGGCGCGCGCTGTACCAAGCTCGCG 600
QY      601 CTGCCACTCAGGCCCCGGCCCCCGCCACACGCTAGTGAACCCCGAAGCGCTTGGGATGCG 660
Db      601 CTGCCACTCAGGCCCCGGCCCCCGCCACACGCTAGTGAACCCCGAAGCGCTTGGGATGCG 660

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QY	661	AA	CGGCGCTGGAACCATAGGCTCAGGGAGGCCGGGGTCCCGCTGGCGCTGCAAGCCCCG	720
Db	661	AA	CGGCGCTGGAACCATAGGCTCAGGGAGGCCGGGGTCCCGCTGGCGCTGCAAGCCCCG	720
QY	721	GT	CGAGGAGGCGCGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGC	780
Db	721	GT	CGAGGAGGCGCGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCAGGC	780
QY	781	GT	GCGCGCTGCCCCCTGAGCCGGAGCGGACGCCCGTTGGGAGAGGGGTCTTGCGCCACCCGG	840
Db	781	GT	GCGCGCTGCCCCCTGAGCCGGAGCGGACGCCCGTTGGGAGAGGGGTCTTGCGCCACCCGG	840
QY	841	GC	AGGACCGCGTGGACCGGAGTGACCGTGTTCTGTGTGTCTACCTGCGCAGACCCCG	900
Db	841	GC	AGGACCGCGTGGACCGGAGTGACCGTGTTCTGTGTGTCTACCTGCGCAGACCCCG	900
QY	901	AAGA	AGCCACTCTTTGAGGAGTGCGCTCTTGCAACGCGCACTCCACCCATCCGTGG	960
Db	901	AAGA	AGCCACTCTTTGAGGAGTGCGCTCTTGCAACGCGCACTCCACCCATCCGTGG	960
QY	961	GCCG	CAGCACCGCGGCGCCCCCATCCACATCGCGCCACCAAGTCCCTGGGACAGC	1020
Db	961	GCCG	CAGCACCGCGGCGCCCCCATCCACATCGCGCCACCAAGTCCCTGGGACAGC	1020
QY	1021	CT	TGCCCCCGGTGACGCGGAGACCAAGCACTTCTACTCTCCTCAGCGACAAGAGC	1080
Db	1021	CT	TGCCCCCGGTGACGCGGAGACCAAGCACTTCTACTCTCCTCAGCGACAAGAGC	1080
QY	1081	AG	TGCGCGCCCTCCTCCTACTAGCTCTTGAGGCCAGCCTGACTGGCGCTCGAGGC	1140
Db	1081	AG	TGCGCGCGCCCTCCTCCTACTAGCTCTTGAGGCCAGCCTGACTGGCGCTCGAGGC	1140
QY	1141	TC	TGAGAGACCATCTTCTGGGTTCCAGGCGCTGATGCCAGGACTCCCCGCAAGTTGC	1200
Db	1141	TC	TGAGAGACCATCTTCTGGGTTCCAGGCGCTGATGCCAGGACTCCCCGCAAGTTGC	1200
QY	1201	CC	CGCGTGGCCCAAGCGCTACTGGCAATGCGGCCCTGTTCTGAGCTGCTTGGGAACC	1260
Db	1201	CC	CGCGTGGCCCAAGCGCTACTGGCAATGCGGCCCTGTTCTGAGCTGCTTGGGAACC	1260
QY	1261	AC	CGCAGTGCCTTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGTGGGTCA	1320
Db	1261	AC	CGCAGTGCCTTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGTGGGTCA	1320
QY	1321	CCC	CAGCAGCGCGGTGTGTGCCCGGAGAAAGCCCCAGGCTGTGTGCGGCCCGAGG	1380
Db	1321	CCC	CAGCAGCGCGGTGTGTGCCCGGAGAAAGCCCCAGGCTGTGTGCGGCCCGAGG	1380
QY	1381	AG	GAGACACAGACCCCGTGCCTGTGACGTGCTCCGACAGACAGACGACCCCTGGC	1440
Db	1381	AG	GAGAGACACAGACCCCGTGCCTGTGACGTGCTCCGACAGACAGACGACCCCTGGC	1440
QY	1441	AG	GTACGCGTTCTGTGCGGCGCTGCCTGCGCGCGCTGGTCCCCAGGCTTGGGCT	1500
Db	1441	AG	GTACGCGTTCTGTGTGCGGCGCTGCCTGCGCGCGCTGGTCCCCAGGCTTGGGCT	1500
QY	1501	CC	AGCACAAAGACGCGCTTCTCAGGAACACCAAGATTATCTCCCTGGGAAGC	1560
Db	1501	CC	AGCACAAAGACGCGCTTCTCAGGAACACCAAGATTATCTCCCTGGGAAGC	1560
QY	1561	AT	GCAAGCTCTGCTGAGGAGTGAAGTGAAGATGACGCTGCGGACTGCGCTTGGC	1620
Db	1561	AT	GCAAGCTCTGCTGAGGAGTGAAGTGAAGATGACGCTGCGGACTGCGCTTGGC	1620
QY	1621	TG	CGCAGAGCGCCAGGGGTTGGCTGTGTTCCGCGCAGAGCACCGTGTGCTGAGAGA	1680
Db	1621	TG	CGCAGAGCGCCAGGGGTTGGCTGTGTTCCGCGCAGAGCACCGTGTGCTGAGAGA	1680
QY	1681	TC	CTGCGCAAGTCTCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGCTT	1740
Db	1681	TC	CTGCGCAAGTCTCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGCTT	1740
QY	1741	TC	TTTATGTCACGGAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGTG	1800

Db	1741	TCTTTATGTCA	CGGAGACCACGTTTCA	AAAAGACAGGCTCTTTTCTAC	CGGAGAGTG	1800
QY	1801	TCTGGAGCAAGT	TGCAAGCATTTGAATCAGACACA	CTTGAAGAGG	GTGCAGTGC	1860
Db	1801	TCTGGAGCAAGT	TGCAAGCATTTGAATCAGACACA	CTTGAAGAGG	GTGCAGTGC	1860
QY	1861	AGCTGTGGAA	GAGAGGTTCAGGCAGCATCGG	GAAGCCAGG	CCCCCTGTGTGAC	1920
Db	1861	AGCTGTGGAA	GAGAGGTTCAGGCAGCATCGG	GAAGCCAGG	CCCCCTGTGTGAC	1920
QY	1921	GACTCCGCTT	CAATCCCCAAGCCTGACGGG	CTGCGCCGATTTGTGA	CACTGACTACGTCG	1980
Db	1921	GACTCCGCTT	CAATCCCCAAGCCTGACGGG	CTGCGCCGATTTGTGA	CACTGACTACGTCG	1980
QY	1981	TGGGAGCCAGA	ACGTTCCGCAAGAAAAAGAGG	CCGAGCGTCTACCTCGAGG	GTGAAG	2040
Db	1981	TGGGAGCCAGA	ACGTTCCGCAAGAAAAAGAGG	CCGAGCGTCTACCTCGAGG	GTGAAG	2040
QY	2041	CACTGTTACG	CGTGTCTCACTACGAGCGGG	CGCGGCGCCCCCGGCTCTG	GGGCGCTCTG	2100
Db	2041	CACTGTTACG	CGTGTCTCACTACGAGCGGG	CGCGGCGCCCCCGGCTCTG	GGGCGCTCTG	2100
QY	2101	TGCTGGGCTT	GACGATATCCACAGGGCCTG	CGGCACTTCGTGCTGCGT	GTGCGGGCCC	2160
Db	2101	TGCTGGGCTT	GACGATATCCACAGGGCCTG	CGGCACTTCGTGCTGCGT	GTGCGGGCCC	2160
QY	2161	AGGACCCGCG	CGCTGAGCTGTACTTTGTCAAG	GTGATGTGACGGGCGCGTA	CGACACCA	2220
Db	2161	AGGACCCGCG	CGCTGAGCTGTACTTTGTCAAG	GTGATGTGACGGGCGCGTA	CGACACCA	2220
QY	2221	TCCCCAGAGA	CAGGCTCACGGAGTCA	TCGCGCAGCATCATCAAA	CCCCAGAACAGTACT	2280
Db	2221	TCCCCAGAGA	CAGGCTCACGGAGTCA	TCGCGCAGCATCATCAAA	CCCCAGAACAGTACT	2280
QY	2281	GCGTGCCTG	GTATGCGGTGTGCCAGAA	GCGCGCCCATGGGCACGT	CCGCAAGCCTTCA	2340
Db	2281	GCGTGCCTG	GTATGCGGTGTGCCAGAA	GCGCGCCCATGGGCACGT	CCGCAAGCCTTCA	2340
QY	2341	AGAGCCACGT	CTCTAACCCTTGACAGAC	CTCCAGCCGTACATGCGAC	AGTTCGTGGCTCAC	2400
Db	2341	AGAGCCACGT	CTCTAACCCTTGACAGAC	CTCCAGCCGTACATGCGAC	AGTTCGTGGCTCAC	2400
QY	2401	TGCAGGAGA	CCAGACCCCGCTGAGG	AGATGCCCTGCTCATTCGAG	CAGAGCTCCTCCCTGA	2460
Db	2401	TGCAGGAGA	CCAGACCCCGCTGAGG	AGATGCCCTGCTCATTCGAG	CAGAGCTCCTCCCTGA	2460
QY	2461	AGGCCAGCA	GTGCGCTCTTCGACGTCT	TCCTACGCTTCACTCATGT	GCCACCA	2520
Db	2461	AGGCCAGCA	GTGCGCTCTCTTCGACGTCT	TCCTACGCTTCACTCATGT	GCCACCA	2520
QY	2521	TCAGGGGCA	AGTTCCTACGTCCAGT	GCCAGGGGATCCCGCAGG	GGCTCCATCTCTCCAC	2580
Db	2521	TCAGGGGCA	AGTTCCTACGTCCAGT	GCCAGGGGATCCCGCAGG	GGCTCCATCTCTCCAC	2580
QY	2581	TGCTCTGCA	GCTGTGTACGGCGCACAT	GAACAACAAGCTGTTG	CGGGGGAATTCGGCGGG	2640
Db	2581	TGCTCTGCA	GCTGTGTGTACGGCGCACAT	GAACAACAAGCTGTTG	CGGGGGAATTCGGCGGG	2640
QY	2641	ACGGGCTG	CTCTGCGTTTGTGTGA	TAATTTCTGTGTGTGAC	ACCTCACTCA	2700
Db	2641	ACGGGCTG	CTCTGCGTTTGTGTGA	TAATTTCTGTGTGTGAC	ACCTCACTCA	2700
QY	2701	CGAAAACTT	CTCAGGACCCCTG	GTCCAGAGTGTCCCTG	AGTATGCGTGTGTA	2760
Db	2701	CGAAAACTT	CTCAGGACCCCTG	GTCCAGAGTGTCCCTG	AGTATGCGTGTGTA	2760
QY	2761	TGCGGAAGA	CAGTGTGAACCTTCC	TGTAGAAGACGAGG	CCCTGGGTGGCA	2820
Db	2761	TGCGGAAGA	CAGTGTGAACCTTCC	TGTAGAAGACGAGG	CCCTGGGTGGCA	2820
QY	2821	TTCAGATG	CGCGCCACGCGCCTAT	TCCCTGTGTGCGCCTG	CTGTGTGAATAC	2880
Db	2821	TTCAGATG	CGCGCCACGCGCCTAT	TCCCTGTGTGCGCCTG	CTGTGTGAATAC	2880

Db 2821 TTCAGATGCGGCCCAAGCGCTATTCCTGTGTGCGGCTGTGCTGTGATACCCGGAACC 2880
QY 2881 TGGAGTGCAGAGCACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACT 2940
Db 2881 TGGAGTGCAGAGCACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACT 2940
QY 2941 TCAACCGCGCTTCAAGGCTGGAGGACATGCGTCAAACTCTTTGGGCTTTGGGCGC 3000
Db 2941 TCAACCGCGCTTCAAGGCTGGAGGACATGCGTCAAACTCTTTGGGCTTTGGGCGC 3000
QY 3001 TGAAGTGCAGAGCTGTCTGTGATTTGAGTGAACAGAGCTCCAGACGCTGTGACCA 3060
Db 3001 TGAAGTGCAGAGCTGTCTGTGATTTGAGTGAACAGAGCTCCAGACGCTGTGACCA 3060
QY 3061 ACATCTACAAGATCTCTGCTGCTGAGGCTACAGGTTTACGATGTGTGCTGAGCTCC 3120
Db 3061 ACATCTACAAGATCTCTGCTGCTGAGGCTACAGGTTTACGATGTGTGCTGAGCTCC 3120
QY 3121 CATTTCAAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGG 3180
Db 3121 CATTTCAAGCAAGTTTGAAGAACCCACATTTTCTGCGGCTCATCTGTGACAGG 3180
QY 3181 CCTCCCTGTCTACTCCATCTCTGAAGCCAGAGGATGT-----GACAG 3230
Db 3181 CCTCCCTGTCTACTCCATCTCTGAAGCCAGAGGATGTCTGCTGGGCGCCAGG 3240
QY 3231 TGCCTGCGCTCAGTGGCAGCAGTGCCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGT 3290
Db 3241 GCGCGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
QY 3291 GAATCTGGGCTTGAAGATCTTACCTTTTTCGATCAGAGGATGTTTAAACCA 3350
Db 3301 TCAAGCTGACTGCAGACCGCTGTCACTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3360
QY 3351 CTGTGAGCTGT 3410
Db 3361 AGACGCACTGAGTGGAGGCTTCCGCGGAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGT 3420
QY 3411 GGAGCTGT 3449
Db 3421 ACCCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480
QY 3450 --GCTGTGGGAGCGCTGGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3507
Db 3481 AGCGCGAGAGAGACACAGCAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3540
QY 3508 GGGCGTGGCTGT 3567
Db 3541 GGGCGCGCAGACCGCGCGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3600
QY 3568 TAGGCGCTGT 3622
Db 3601 AGCGCTGATGT 3660
QY 3623 ACCCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3682
Db 3661 AAGGCTGATGT 3719
QY 3683 CTGCTTCCAGTCAAGCTGT 3742
Db 3720 CCACCGCGGCGAGCTTGT 3779
QY 3743 GATCGCTGTGAATTTCAAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3802
Db 3780 GTCCATCCCGAGATTTGCGCATTTGTCAACCTC-----GCCCTGCCCTCTTGTGCTT 3832
QY 3803 TGT 3862
Db 3833 CCACCGCGCAGCTCAGAGT 3892
QY 3863 GTGACCAAGGT 3922
Db 3893 GTGACCAAGGT 3952

QY 3923 GGGTCAATTTGGGGGAGGT 3982
Db 3953 GGGTCAATTTGGGGGAGGT 4012
QY 3983 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4012
Db 4013 TTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4042

RESULT 4
US-09-582-246-2

; Sequence 2, Application US/09582246
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; APPLICANT: Hagen, Gustav
; APPLICANT: Wick, Maresa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Regulatory DNA Sequences of the Gene for the Human Catalytic Tel
; TITLE OF INVENTION: Subunit, and their Diagnostic and Therapeutic Use
; FILE REFERENCE: Lea 32 805
; CURRENT APPLICATION NUMBER: US/09/582,246
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: PCT/EP98/08216
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: DE19757984.1
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent version 3.1
; SEQ ID NO 2
; LENGTH: 4042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-582-246-2

Query Match 83.1%; Score 3333.6; DB 24; Length 4042;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3645; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 1 GTTTCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
Db 1 GTTTCAGGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
QY 61 CGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 CGATGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
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QY 241 GGGAGCGACG 300
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US-08-974-549-343
Sequence 343, Application US/08974549
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note="refined sequence of hTERT cDNA"
US-08-974-549-343

Query Match 82.8%; Score 3320.2; DB 13; Length 4037;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3638; Conservative 3; Mismatches 356; Indels 46; Gaps 6;

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DB 2941 CGGCTTCAAGGCTGGGAGGAAACATGCGTGCAGAACTCTTTGGGGTCTTGGCGCTGAAGTG 3000
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QY 3068 CAAGATCCTCTGCTGACGCGGTACAGGTTTACAGCATGTGTGCTGACGCTCCATTCA 3127
DB 3061 CAAGATCCTCTGCTGACGCGGTACAGGTTTACAGCATGTGTGCTGACGCTCCATTCA 3120
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QY 3188 CTGCTACTCCATCTGAAAGCCAGAACAGCAGATGT-----GAGGTGCTGG 3237
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DB 3481 GAGCAGACACCAAGAGCCTGTCAAGCGCGGCTCTACGTCACAGGAGGAGGCGCGCC 3540
QY 3515 GCCTCTCTGTTTGGCGCTGTGTTGGATTGGGCTGTCTCCGTCATGAGCACTTAGGGCC 3574
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DB 3661 GAGTGTCCAGACACACTGCGCTCT-TCACTTCCCAAGAGCTGCGCTCCAGCCACCC 3719
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DB 3780 CCCAGATTC-GCCATGTTCACCCYTCGCCCTGCTT-----CCTTGGCTTCCACCCC 3832
QY 3810 TTTCTGTGTGTGAGAGCCTGAGAGGAGCCCTGGAGCTCTGGGAATTTGAGTGAACCA 3869
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QY 3870 AAGGTGCGCTGTACAGAGCGAGAGACCTGACACTGATGGGGTTCCTGTGGTCAA 3929

QY	908	CACCTCTTTTGAGAGGTGCGCTCTCTTGGAACGCCCACTCCCAACCAATCCGTGGGCGGCCA	967
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QY	968	GCACCAACGCCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACAACGCTTGTCC	1027
Db	961	GCACCAACGCCGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACAACGCTTGTCC	1020
QY	1028	CCCCGTGTACGCCCGAGAACCAAGCACTTCTCTACTCTCAGGCGCAAGAGACAGCTGCG	1087
Db	1021	CCCCGTGTACGCCCGAGAACCAAGCACTTCTCTACTCTCAGGCGCAAGAGACAGCTGCG	1080
QY	1088	GCCCTCCTTCTCTACTCAGCTCTCTAGGCCCCAGCCTGACTGGCGCTCGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTCTACTCAGCTCTCTAGGCCCCAGCCTGACTGGCGCTCGAGGCTCGTGA	1140
QY	1148	GACCATCTTTCTGGGTTCCAGGCCCTGAGTCCAGGGACTCCCGAGGTTGCCCGGCTT	1207
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QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGCTGCTTGGGAACACGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGCTGCTTGGGAACACGCGCA	1260
QY	1268	GTCGCCCTTACGGGGTGCTCTCTAAGACGCACTGCCCGCTGCCAGCTGCCGTACCCCCAGC	1327
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QY	1328	AGCCGGTGTCTGTGCCCGGGAGAACCCCCAGGGCTCTGTGGCGCCCCCGAGAGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCGGGAGAACCCCCAGGGCTCTGTGGCGCCCCCGAGAGAGGA	1380
QY	1388	CACAGACCCCCCGTCGCTGTGTGACGTGCTCCGCCAGACACAGACCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCCGTCGCTGTGTGACGTGCTCCGCCAGACACAGACCCCCCTGGCAGGTGA	1440
QY	1448	CGGCTTCGTGCGGGGCTGCTCGCGCCGCGCTGTGCCCCCAGGCTCTGGGGCTCCAGGCA	1507
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QY	1508	CAACGAACGCCGCTTCTCTAGAGAACCAAGAAATTCTCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCCGCTTCTCTAGAGAACCAAGAAATTCTCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGGAGCTGACGTGAGAGATGAGCGTGCGGGACTGCGCTTGCTGCGCAG	1627
Db	1561	GCTCTCGCTGCAGGAGCTGACGTGAGAGATGAGCGTGCGGGACTGCGCTTGCTGCGCAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTGTTCGGCCGAGAGACCGTCTGCTGAGAGATCCTGGC	1687
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QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGGAGACCAAGTTTCAAAAGAACAGGCTTTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGGAGACCAAGTTTCAAAAGAACAGGCTTTTTTCTACCGCGGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAGCATTTGGAATCAGACGACTTGAAGAGGTGACGTGCGGAGCTGTTC	1867
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QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCTGTGACGTCCAGACTCCG	1927
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QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGAGTACGTCTGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTAACATGAGTACGTCTGTGGAGC	1980
QY	1988	CAGAAGCTCCGCAAGAAAAGAGGGCCGAGCCTCTACCTCGAGGTTGAAGGCACTGTT	2047

Db	1981	CAGAACGTTCCGCAGAGAAAAGAGGGCCCGAGCGCTTCACCTCGAGGGTGAAAGGCACTGTT	2040
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QY	2168	GCCGCCGTAGCTGTACTTTTGTCAAGGTGATGTGACGGGGCGCGTACGACACCATCCCCCA	2227
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QY	2228	GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2287
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QY	2288	TGCGTATGCCGTGTGTCCAGAAAGGCCGCCCATGGGCACTCCGCAAGGCTTCAAGAGCCA	2347
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Db	2341	CGTCTCTACCTTGAAGACCTCCAGCCGTACATGCGACAGTTGCGTGTCTCACTTGACAGA	2400
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QY	2468	CAGTGGCCTCTTGCAGCTCTTCTACGCTTCAATGTGCCACCAAGCCGTGGCGATCAGGGG	2527
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QY	2588	CAGCCTGTGCTACGCGGCACATGGAGAACAGCTGTTTGGGGGATTCCGGCGGACCGGCT	2647
Db	2581	CAGCCTGTGCTACGCGGCACATGGAGAACAGCTGTTTGGGGGATTCCGGCGGACCGGCT	2640
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QY	3455	GGGAAGCGCTGGGGGCGCTGTCTCTCTGTTTGCCCCATGTTGGGATTTGGGGGCGCTG	3514
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RESULT 7
US-09-721-477-343
; Sequence 343, Application US/09721477
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim

```

1      Nakamura, Toru
2      Chapman, Karen B.
3      Morin, Gregg B.
4      Harley, Calvin B.
5      Andrews, William H.
6      TITLE OF INVENTION: Human Telomerase Catalytic Subunit
7      NUMBER OF SEQUENCES: 727
8      CORRESPONDENCE ADDRESS:
9      ADDRESSEE: Townsend and Townsend and Crew LLP
10     STREET: Two Embarcadero Center, Eighth Floor
11     CITY: San Francisco
12     STATE: California
13     COUNTRY: USA
14     ZIP: 94111-3834
15     COMPUTER READABLE FORM:
16     MEDIUM TYPE: Floppy disk
17     COMPUTER: IBM PC compatible
18     OPERATING SYSTEM: PC-DOS/MS-DOS
19     SOFTWARE: PatentIn Release #1.0, Version #1.30
20     CURRENT APPLICATION DATA:
21     APPLICATION NUMBER: US/09/721,477
22     FILING DATE: 22-NOV-2000
23     CLASSIFICATION: <Unknown>
24     PRIOR APPLICATION DATA:
25     APPLICATION NUMBER: 08/974,549
26     FILING DATE: <Unknown>
27     APPLICATION NUMBER: US 08/844,419
28     FILING DATE: 18-APR-1997
29     APPLICATION NUMBER: US 08/846,017
30     FILING DATE: 25-APR-1997
31     APPLICATION NUMBER: US 08/851,843
32     FILING DATE: 06-MAY-1997
33     APPLICATION NUMBER: US 08/854,050
34     FILING DATE: 09-MAY-1997
35     APPLICATION NUMBER: US 08/911,312
36     FILING DATE: 14-AUG-1997
37     APPLICATION NUMBER: US 08/912,951
38     FILING DATE: 14-AUG-1997
39     APPLICATION NUMBER: US 08/915,503
40     FILING DATE: 14-AUG-1997
41     APPLICATION NUMBER: WO PCT/US97/17618
42     FILING DATE: 01-OCT-1997
43     APPLICATION NUMBER: WO PCT/US97/17885
44     FILING DATE: 01-OCT-1997
45     ATTORNEY/AGENT INFORMATION:
46     NAME: Apple, Randolph Ted
47     REGISTRATION NUMBER: 36,429
48     REFERENCE/DOCKET NUMBER: 015389-002610US
49     TELECOMMUNICATION INFORMATION:
50     TELEPHONE: (415) 576-0200
51     TELEFAX: (415) 576-0300
52     INFORMATION FOR SEQ ID NO: 343:
53     SEQUENCE CHARACTERISTICS:
54     LENGTH: 4037 base pairs
55     TYPE: nucleic acid
56     STRANDEDNESS: single
57     TOPOLOGY: linear
58     MOLECULE TYPE: cDNA
59     FEATURE:
60     NAME/KEY: CDS
61     LOCATION: 56..3454
62     OTHER INFORMATION: /note="refined sequence of hTERT cDNA"
63     SEQUENCE DESCRIPTION: SEQ ID NO: 343:
64     US-09-721-477-343
65
66     Query Match      82.8%; Score 3320.2; DB 31; Length 4037;
67     Best Local Similarity 90.0%; Pred. No. 0;
68     Matches 3638; Conservative 3; Mismatches 356; Indels 46; Gaps 6;
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70     8 GCAGCGCTGCTCTGCTGCGCACGTCGGAAGCCCTGAGCCCGGCGCACACCCCGCGATGCC 67
71     |||||
72     1 GCAGCGCTGCTCTGCTGCGCACGTCGGAAGCCCTGAGCCCGGCGCACACCCCGCGATGCC 60

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Query Match	82.8%;	Score 3320.2;	DB 31;	Length 4037;
Best Local Similarity	90.0%;	Pred. No. 0;		
Matches 3638;	Conservative	3;	Mismatches 356;	Indels 46;
				Gaps 6;

QY 8 GCAGCGCTGCGTCTCTGCTGCGCACGTTGGAAAGCCCTGGCCCCGGCCACCCCGCGATGCC 67
DB 1 GCAGCGCTGCGTCTCTGCTGCGCACGTTGGAAAGCCCTGGCCCCGGCCACCCCGCGATGCC 60

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Db 61 GCGGCTCCCGCTGCGAGCCGTGCGCTCCCTGTGCGCAGCCACTACCGGAGGTGCT 120
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QY 788 TGCGGCTGAGCG 847
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Db 2161 GCGGCGCTGAGTGTACTTTGTCAAGGTGATGTGACGCGCGCGCGCGCGCGCGCGCG 2220
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[illegible]

QY	3358	GCTCGTCTGCCCGCCCTCTCGTGGGTGACAGACACCTGATGAAGGACAGAGCTG	3417
Db	3361	GCTGAGTGGAACTCCCGGGGACGACGCTGACTGCTGAGGCGCAGCCAACCCGGC	3420
QY	3418	TCTGGAGCTGCCATCCCTTCCACCTTGCTCT-----GCTCG	3454
Db	3421	ACTGCCCTCAGACTTCAAGACCATCCTGCACTGATGCCACCCGCCACAGCAGGCCGA	3480
QY	3455	GGGAAGCGCTGGGGGCGCTGCTCTCTCCTGTTGCCCATGTGSGATTGGGGGCGCTG	3514
Db	3481	GAGCAGACACCAAGACCGCTGTACACGCCGGGCTTACGTCCAGGGAGGGGGGCGCC	3540
QY	3515	GCCTCTCCTGTTGCCCTGTGTGGATTGGGCTGTCTCCCGTCCATGGCACTTAGGGCC	3574
Db	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCTGAGTAGTGTTTGGCCGAGGCTG	3600
QY	3575	CTTGTGCMAAACCCAGGCCAAG----GGCTTAGAGGAGGCCAGGCCAGGCTACCCCAAC	3629
Db	3601	CATGTCGGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3630	CCCTCTCAGAGACGAGGCGCGGTATCACCAAGACAGAGCCCGCGCGCTCTGCTTC	3689
Db	3661	GAGTGTCCAGCACACTGCGGTCT-TCACTTCCCAACAGGCTGCGCTCCACCCC	3719
QY	3690	CCAGTCACCGTCTCTGCCCCCTGACACATTGTCCAGCATCAGGAGGTTTCTGATCCGT	3749
Db	3720	AGGGCCAGCTTTTCYTCAACAGAGAGCCGGCTTCACTCCCAATAGAAATGTCATC	3779
QY	3750	CTGAATTCAGCCATGTGCAACCTGCGGTCTGAGCTTAACAGCTTCTTCTGTTTC	3809
Db	3780	CCCAGATTG--GCCATTGTTCAACCCYTGCCCTGCCYT----CCTTGCTTCCACCCC	3832
QY	3810	TTTCTGTTGTGGAGACCCCTGAGAAGAACCTTGGAGCTCTGGAATTGAGTGACCA	3869
Db	3833	CACCATCCAGTGGAGAGACCCCTGAGAAGAACCTTGGAGCTCTGGAATTGAGTGACCA	3892
QY	3870	AAGGTGTGCCCTGTACACAGCGAGAGACCCCTGCACCTGATGGGGGTCCCTGTGGCTCA	3929
Db	3893	AAGGTGTGCCCTGTACACAGCGAGAGACCCCTGCACCTGATGGGGGTCCCTGTGGCTCA	3952
QY	3930	ATTGGGGGAGGTGCTGTGGAGTAATACTGAATATATGAGTTTTCAGTTTGAATA	3989
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QY	3990	AAAAAAAAAAAAAAAAAAAAA 4012	
Db	4013	AAAAAAAAAAAAAAAAAAAAA 4035	

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RESULT 8
US-09-721-506-343
; Sequence 343, Application US/09721506
; GENERAL INFORMATION:
;
; APPLICANT: Cech, Thomas R.
;           Lingner, Joachim
;           Nakamura, Toru
;           Chapman, Karen B.
;           Morin, Gregg B.
;           Harley, Calvin B.
;           Andrews, William H.
;
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
;
; NUMBER OF SEQUENCES: 727
;
; CORRESPONDENCE ADDRESS:
;
;   ADDRESSEE: Townsend and Crew LLP
;   STREET: Two Embarcadero Center, Fifth Floor
;   CITY: San Francisco
;   STATE: California
;   COUNTRY: USA
;
;   ZIP: 94111-3834
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,506
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610USE

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

SEQUENCE CHARACTERISTICS:

LENGTH: 4037 base pairs

TYPE: nucleic acid

STRANDEDNESS: 81ngle

JOELOG: LINE
SITE TYPE: CDNA

URH..

NAME/KEY: CDS

LOCATION: 56.

OTHER INFORMATION:

DESCRIPTION: SEQ ID NO: 343:

343

Query Match	82.8%;	Score 3320.2;	DB 31;	length 4037;
Best Local Similarity	90.0%;	Pred. No. 0;		
Matches 3638; Conservative	3;	Mismatches 356;	Indels 46;	Gaps 6

QY	8	GCAGCGCTGCGTCTGTGTCGGCACGTGGGAAGCCCTTGAGCCCCGGGCCACCCCCGGATGCC	67
Db	1	GCAGCGCTGCGTCTGTGTCGGCACGTGGGAAGCCCTTGAGCCCCGGGCCACCCCCGGATGCC	60
QY	68	GCGCGCTCCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCCACTACCGCGAGGTGCT	127
Db	61	GCGCGCTCCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCCACTACCGCGAGGTGCT	120
QY	128	GCCGCTGGCCACGTTGCTGCGGGCGCCTGGGGCCCCCAGGGGCTGGCGGCTGGTGACGCGGG	187
Db	121	GCCGCTGGCCACGTTGCTGCGGGCGCCTGGGGCCCCCAGGGGCTGGCGGCTGGTGACGCGGG	180
QY	188	GGACCCGGGCGGCTTTTCCGGCGCGCTGGTGAGCCACAGTGCCTGGTGTGGTGCCCTTGGGACGC	247
Db	181	GGACCCGGGCGGCTTTTCCGGCGCGCTGGTGAGCCACAGTGCCTGGTGTGGTGCCCTTGGGACGC	240
QY	248	ACGGCCGCCCCCGCGCGCCCCCTCTCTTCCGGCAGGTGTCTGCTGAAAGAGCTGGTGCC	307
Db	241	ACGGCCGCCCCCGCGCGCCCCCTCTCTTCCGGCAGGTGTCTGCTGAAAGAGCTGGTGCC	300
QY	308	CCGAGTGTCTGCAGAGAGCTGTGTCGAGCGCGCGCGGAAGAACGTGCTGGACCTTGGGCTTGGC	367

Db	301	CCGAGTGTCTGACAGGCTGTGCGAGCGCGCGCGAGACGTGTGCTTGGCTTCGC	360
QY	368	GCTGTGACCGGGCCCCGGGGGGCCCCCCCCGAGGCTTCAACCAAGCGTGGCAGCTA	427
Db	361	GCTGTGACCGGGCCCCGGGGGGCCCCCCCCGAGGCTTCAACCAAGCGTGGCAGCTA	420
QY	428	CCTGCCCAACACGCTGACCGCAGCACTGCGGGGAGCGGGCGCTGGGGGCTGCTGCG	487
Db	421	CCTGCCCAACACGCTGACCGCAGCACTGCGGGGAGCGGGCGCTGGGGGCTGCTGCG	480
QY	488	CCGCGTGGGCGACGACGTGCTGTTCACTGTGSGACGCTGCGCGCTCTTGTGCTGT	547
Db	481	CCGCGTGGGCGACGACGTGCTGTTCACTGTGSGACGCTGCGCGCTCTTGTGCTGT	540
QY	548	GGCTCCCGAGCTGCGCCTACCGAGTGTGCGGGCGCGCGCTGTACCAGCTCGGCGTGCAC	607
Db	541	GGCTCCCGAGCTGCGCCTACCGAGTGTGCGGGCGCGCGCTGTACCAGCTCGGCGTGCAC	600
QY	608	TCAGGCCCCGCCCCCGCCACACGCTAGTGAACCCCGAAGGCGTCTGGATGCAACGGG	667
Db	601	TCAGGCCCCGCCCCCGCCACACGCTAGTGAACCCCGAAGGCGTCTGGATGCAACGGG	660
QY	668	CTGAACCATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTGCGAGCCCGGGTGCAG	727
Db	661	CTGAACCATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTGCGAGCCCGGGTGCAG	720
QY	728	GAGCGCGGGGCGAGTGCCAGCCGGAAGTCTGCCGTTGCCAAGAGGCCAGCGTGCGC	787
Db	721	GAGCGCGGGGCGAGTGCCAGCCGGAAGTCTGCCGTTGCCAAGAGGCCAGCGTGCGC	780
QY	788	TGCCCCGTGAGCCCGGAGCGGACGCCCGTTGGGCAAGGGTCTGGGCCACCCGGGCAAGAC	847
Db	781	TGCCCCGTGAGCCCGGAGCGGACGCCCGTTGGGCAAGGGTCTGGGCCACCCGGGCAAGAC	840
QY	848	GCGTGAACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCGCAAGCCCGCGAAGAC	907
Db	841	GCGTGAACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCGCAAGCCCGCGAAGAC	900
QY	908	CACCTCTTTTGAAGGGTGCGCTCTCTGGCAAGCGCACTCCCAACCATCCGTGGCGCGCA	967
Db	901	CACCTCTTTTGAAGGGTGCGCTCTCTGGCAAGCGCACTCCCAACCATCCGTGGCGCGCA	960
QY	968	GCACCAACGCGGGCCCCCATTCACATCGCGGCCAACACGTCCCTGGGACACGCTTGTCC	1027
Db	961	GCACCAACGCGGGCCCCCATTCACATCGCGGCCAACACGTCCCTGGGACACGCTTGTCC	1020
QY	1028	CCCGGTGTACGCGCGAGAACCAAGCACTTCTCTACTCTCTCAAGCGACAAGAGCAGCTGCG	1087
Db	1021	CCCGGTGTACGCGCGAGAACCAAGCACTTCTCTACTCTCTCAAGCGACAAGAGCAGCTGCG	1080
QY	1088	GCCCTCTTCTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTCGGAGGCTGTGA	1147
Db	1081	GCCCTCTTCTCTACTCAGCTCTCTGAGGCCAGCTGACTGGCGCTCGGAGGCTGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCCCCGTGATGCCAGGACTCCCCGAGGTTGCCCGCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCCCCGTGATGCCAGGACTCCCCGAGGTTGCCCGCT	1200
QY	1208	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAGCTGTGGGAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAGCTGTGGGAACCAAGCGCA	1260
QY	1268	GTCGCCCTACGGGGTGCTCCTCAAGAGCACTGCCGCTGCGAGCTGCGGTCAACCCAGC	1327
Db	1261	GTCGCCCTACGGGGTGCTCCTCAAGAGCACTGCCGCTGCGAGCTGCGGTCAACCCAGC	1320
QY	1328	AGCGGTTGTGTGCCCCGGAGAAAGCCCAAGGGCTTGTGGCGCCCCCGAGAGAGGA	1387
Db	1321	AGCGGTTGTGTGCCCCGGAGAAAGCCCAAGGGCTTGTGGCGCCCCCGAGAGAGGA	1380
QY	1388	CACAGACCCCCGTGCGCTGTGACGCTGTCCGCAAGACAGACGCCCTGGCAGGTGTA	1447

Db	1381	CACAGACCCCCCGTCGCGCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCCTTGCGAGGTGTA	1440
QY	1448	CGGCTTCGTGCGGGGCGCTGCGCTGCGCGGCGCTGCTGTGCCCGCCAGGCGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCGTGCGGGGCGCTGCGCTGCGCGGCGCTGCTGTGCCCGCCAGGCGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAAACGCCCGCTTCCTCAGGAAACACCAAGAATTCACTCTCCCTGGGGAAAGCATGCGAA	1567
Db	1501	CAACGAAACGCCCGCTTCCTCAGGAAACACCAAGAATTCACTCTCCCTGGGGAAAGCATGCGAA	1560
QY	1568	GCTCTCCCTGCAGGAGCTGACGTGGAAAGATGAGCGTGCGGGAACTCGCTTGGCTGCAG	1627
Db	1561	GCTCTCCCTGCAGGAGCTGACGTGGAAAGATGAGCGTGCGGGAACTCGCTTGGCTGCAG	1620
QY	1628	GAGCCCAAGGGGTTGGCTGTGTTCGCGCCGCGAGAGCACCGCTCTGCGTAGAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCGCGCCGCGAGAGCACCGCTCTGCGTAGAGAGATCTGGC	1680
QY	1688	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGTCCTTCTTTA	1747
Db	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGTCCTTCTTTA	1740
QY	1748	TGTCAACGAGAACCAAGTTTCAAAGAACAAGGCTCTTTTCTAACGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCAACGAGAACCAAGTTTCAAAGAACAAGGCTCTTTTCTAACGGAAGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAAGCATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACCGGGCTCGCGCCGATTGTGAACATGGACTACGTCGTGGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACCGGGCTCGCGCCGATTGTGAACATGGACTACGTCGTGGGAGC	1980
QY	1988	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGCTTCACTTCGAGGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCGAGAGAAAGAGGGCCGAGCGCTTCACTTCGAGGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCAACTACGAGCGGGCGCGGCGCCCGGCGCTCTGGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCAACTACGAGCGGGCGCGGCGCCCGGCGCTCTGGGCGCTCTGTGCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCGCTGGCGCACTTCGTGCTGCGTGTGCGGGCCAGAGACC	2167
Db	2101	CCTGACGATATCCACAGGGCGCTGGCGCACTTCGTGCTGCGTGTGCGGGCCAGAGACC	2160
QY	2168	GCCGCGTAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTAGACACCATCCCCCA	2227
Db	2161	GCCGCGTAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTAGACACCATCCCCCA	2220
QY	2228	GGAACAGGCTACGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2287
Db	2221	GGAACAGGCTACGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2280
QY	2288	TCCGTATGCCGTGTTCAGAAAGCGCCCATGGGACGTCCGCAAGGCTTCAAGAGCCA	2347
Db	2281	TCCGTATGCCGTGTTCAGAAAGCGCCCATGGGACGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTTACTTTGACAGACTCCAGCCGTACATGCGACAGTTGCTGCTTCACTGACAGA	2407
Db	2341	CGTCTTACTTTGACAGACTCCAGCCGTACATGCGACAGTTGCTGCTTCACTGACAGA	2400
QY	2408	GACCAGCCCGCTGAGGGATGCCGTGTCATGAGCAGAGAGCTCCTCCTGAATGAGGCCAG	2467
Db	2401	GACCAGCCCGCTGAGGGATGCCGTGTCATGAGCAGAGAGCTCCTCCTGAATGAGGCCAG	2460
QY	2468	CAGTGGCCTCTCGACGTCTTCTACGCTTCAATGTGCCACCAAGCCGCTGCGCATCAGGGG	2527
Db	2461	CAGTGGCCTCTCGACGTCTTCTACGCTTCAATGTGCCACCAAGCCGCTGCGCATCAGGGG	2520

QY	2528	CAAGTCCACGTCACAGTGCACAGGGGATCCCGCAGGCGTCCATTCCTCTCCACGCTGCTCTG	2587
Db	2521	CAAGTCCACGTCACAGTGCACAGGGGATCCCGCAGGCGTCCATTCCTCTCCACGCTGCTCTG	2580
QY	2588	CAGCCTGTGTACTACGGCGACATGAGGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT	2647
Db	2581	CAGCCTGTGTACTACGGCGACATGAGGAACAAGCTGTTTGCGGGGATTCGGCGGGACGGGCT	2640
QY	2648	GCTCCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACTCACCCACGGCAAAAC	2707
Db	2641	GCTCCTGCGTTTGGTGATGATTTCTGTGTGTGACACCTCACTCACCCACGGCAAAAC	2700
QY	2708	CTTCTCAAGAACCCCTGTCGCCAGGTGTCCCTGAGTATGGCTGCTGTTGAACCTTGGCGAA	2767
Db	2701	CTTCTCAAGAACCCCTGTCGCCAGGTGTCCCTGAGTATGGCTGCTGTTGAACCTTGGCGAA	2760
QY	2768	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACCGGCTTTGTTCAGAT	2827
Db	2761	GACAGTGTGAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACCGGCTTTGTTCAGAT	2820
QY	2828	GCCGGCCCCACGGCCTATTTCCCTGTGTGCGGCTGCTGTGTGATACCCGGACCTTGAGGT	2887
Db	2821	GCCGGCCCCACGGCCTATTTCCCTGTGTGCGGCTGCTGTGTGATACCCGGACCTTGAGGT	2880
QY	2888	GCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2947
Db	2881	GCAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACTTCAACCG	2940
QY	2948	CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTGGGGCTTGGCGGTGAAGTG	3007
Db	2941	CGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTCTTGGGGCTTGGCGGTGAAGTG	3000
QY	3008	TCAACAGCCTGTTTCTGATTGTGACGTTGACAGCTTCCAGACGGTGTGACCAACATCTA	3067
Db	3001	TCAACAGCCTGTTTCTGATTGTGACGTTGACAGCTTCCAGACGGTGTGACCAACATCTA	3060
QY	3068	CAAGATCCTCCTGCTGACAGGCGTACAGGTTTACGCATGTGTGCTGACGTCCCATTTCA	3127
Db	3061	CAAGATCCTCCTGCTGACAGGCGTACAGGTTTACGCATGTGTGCTGACGTCCCATTTCA	3120
QY	3128	TCAGCAAGTTTGAAGAACCCCAATTTCCTGCGGCTCATCTCTGACAGGCTCCCT	3187
Db	3121	TCAGCAAGTTTGAAGAACCCCAATTTCCTGCGGCTCATCTCTGACAGGCTCCCT	3180
QY	3188	CTGCTACTCCATCCTGAAGCCCAAGAACGACGATGT-----GCAAGTGCCTGG	3237
Db	3181	CTGCTACTCCATCCTGAAGCCCAAGAACGACGATGT-----GCAAGTGCCTGG	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTAGTGTGTCAGAGACTGATGATCTG	3297
Db	3241	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT	3300
QY	3298	GGCTTAGGAAGTCTTACCCCTTTTCGATCAGGAAGTGTTTAACCCAACCACTGTCAAG	3357
Db	3301	GACTCGACACCGTGTCACTACGTGACACTCTGGGGTCACTCAGGACAGCCACAGCA	3360
QY	3358	GCTCGTGTGCCGCCCTCTGCTGGGTGAGCAGACCACTGATGGAAGGACAGAGCTG	3417
Db	3361	GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAAGCCGCAACCCGGC	3420
QY	3418	TCTGGAGCTGCATCCTTCCACCTTGTCT-----GCCTG	3454
Db	3421	ACTGCCCTCAGACTTCAAGACCATCCTGCACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3455	GGGAAGCGCTGGGGGGCTGTCTCTCTGTTTGCCCATGTGGGATTTGGGGGGCTG	3514
Db	3481	GAGCAGACACGACGACCCCTGTCAACGCGGGGCTTACGTCCCAAGGAGGAGGGGGCGGCC	3540
QY	3515	GCCTCTCCTGTTTCCCTGTGTGTGGGATTTGGGCTGTCTCCCTCATGGCACTTAGGGCC	3574
Db	3541	CACACCCAGGCCCGCACCGCTGGGAGTCTGAGGCCCTGAGTGAATGTTTGGCCGAGGCTTG	3600

QY 3575 CTGTGCAAAACCCAGGCCAAG-----GCTTAGAGAGAGGCCAGGCCAGGCTACCCAC 3629
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Db 3601 CATGTCCGGGTGAAGGCTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAGGCT 3660
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QY 3630 CCCTCTCAGAGCAGAGGCGCGGTATCACCAGACAGAGCCCGCGCGCTCTGCTTC 3689
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QY 3690 CCAATCAGCGTCTCTGCGCGCTGAGACTTTGTCAGAGCAGGAGGTTCTGATCCGT 3749
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Db 3720 AGGCGCAGCTTTCTCTACACAGAGCGCGCTTCCACTCCACATAGGAATAGTCATC 3779
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QY 3750 CTGAATTCAGCCATGTGGAACCTGCGGCTCTGAGCTTAACAGCTTCTACTTCTGTC 3809
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Db 3780 CCCAGATTC--GCCATGTTCACCCCTGCGCGCTGCGCT-----CCTTGCCTTCCAGCC 3832
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QY 3810 TTTCTGTGTGTGAGAGACCCCTGAGAGAGACCCCTGAGAGCTGTGGAATTTGAGTACCA 3869
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Db 3833 CACCATCCAGGTGAGAGACCCCTGAGAGAGACCCCTGAGAGCTGTGGAATTTGAGTACCA 3892
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QY 3870 AAGGTGTGCTGTACACAGGCGAGACCCCTGACCTGGAATGGGGTCCCTGTGGCTCA 3929
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Db 3893 AAGGTGTGCTGTACACAGGCGAGACCCCTGACCTGGAATGGGGTCCCTGTGGCTCA 3952
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QY 3930 ATTGGGGGAGGTGCTGTGAGAGTAATACTGAATATATGAGTTTTCAGTTTGA 3989
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QY 3990 AAAAAAAAAAAAAAAAAAAAAA 4012
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Db 4013 AAAAAAAAAAAAAAAAAAAAAA 4035
| | | | |

RESULT 9
US-10-325-810-343Sequence 343, Application US/10325810
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/325,810

FILING DATE: 20-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181

FILING DATE: 29-Sep-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-Oct-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-Apr-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-Apr-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-May-1997

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 343:
SEQUENCE CHARACTERISTICS:
LENGTH: 4037 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /note="refined sequence of hTERT cDNA"
US-10-325-810-343

Query Match 82.8%; Score 3320.2; DB 49; Length 4037;
Best Local Similarity 90.0%; Pred. No. 0;
Matches 3638; Conservative 3; Mismatches 356; Indels 46; Gaps 6;

QY 8 GCAGCGTGCCTGCTGCTGCGCAGTGGAGAGCCCTGCGCCCGCCAGCCCGGATGCC 67
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Db 1 GCAGCGTGCCTGCTGCTGCGCAGTGGAGAGCCCTGCGCCCGCCAGCCCGGATGCC 60
| | | | |
QY 68 GCGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGC 127
| | | | |
Db 61 GCGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGC 120
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QY 128 GCGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGC 187
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Db 121 GCGCGTCCCGCTGCGCAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGC 180
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QY 188 GGAACCGCGCGCTTCCGCGCGCTGCTGCGCAGTGCCTGCTGCTGCTGCTGCTGCTG 247
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Db 181 GGAACCGCGCGCTTCCGCGCGCTGCTGCGCAGTGCCTGCTGCTGCTGCTGCTGCTG 240
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QY 248 ACGCGCGCGCGCGCGCGCGCGCTTCCGCGCGCTGCTGCGCAGTGCCTGCTGCTGCTG 307
| | | | |
Db 241 ACGCGCGCGCGCGCGCGCGCGCTTCCGCGCGCTGCTGCGCAGTGCCTGCTGCTGCTG 300
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QY 308 CCGAGTGTGAGAGGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
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Db 301 CCGAGTGTGAGAGGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
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QY 368 GCTGTGAGCG 427
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Db 361 GCTGTGAGCG 420
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| | | | |
Db 421 CTTGCCAACAACGCTGACGACGCACTGCGGGGAGCGGGGCGTGGGGGCTGCTGCG 480
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QY 488 CCGGCTGGGCGAGCAGCGTGTGCTTCACTGCTGCGAGCGCTGCGCGCTTGTGCTGT 547
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| | | | |
QY 548 GGTCCAGCTGCGCTACAGTGTGCGGGCGCGCGCTGTACCAAGCTGCGCGCTGCCAC 607
| | | | |

Db	541	GGCTCCACAGCTGCGCCTACCAAGTGTGCGGGCCGCCGCTGTACAGACTCGGCGTGCCAC	600
QY	608	TCAGGCCCCGGCCCCCGCCACACAGCTAGTGGAACCCCGAAGCGCTCTGGGATGCGAACGGGC	667
Db	601	TCAGGCCCCGGCCCCCGCCACACAGCTAGTGGAACCCCGAAGCGCTCTGGGATGCGAACGGGC	660
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Db	661	CTGGAACCATAGCGTCAGGGAGGCGCGGGTCCCCCTGGGCTGCCAGCCCCGGGTGCCAG	720
QY	728	GAAGCGCGGGGGCAGTGCCAGCCGGAAGTCTGCCGTTGCCAAAGAGCCCAAGCGTGCGC	787
Db	721	GAAGCGCGGGGGCAGTGCCAGCCGGAAGTCTGCCGTTGCCAAAGAGCCCAAGCGTGCGC	780
QY	788	TGCCCCCTGAGCCGGAGCGGACGCCGTTGGGCAGGGGTCTCTGGGCCCAACCCGGCAGAC	847
Db	781	TGCCCCCTGAGCCGGAGCGGACGCCGTTGGGCAGGGGTCTCTGGGCCCAACCCGGCAGAC	840
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Db	841	GCGTGGAACCGAGTGACCGGTGTTCTGTGTGTGTCACTGCGCAGACCCCGCGAAGAGC	900
QY	908	CACCTCTTTGGAGGGTGCGCTCTCTGGCAACCGGCCACTCCCAACCAATCCGTGGCGCCA	967
Db	901	CACCTCTTTGGAGGGTGCGCTCTCTGGCAACCGGCCACTCCCAACCAATCCGTGGCGCCA	960
QY	968	GCAACCAAGCGGGCCCCCATCCACATCGCGGCCAACCAAGTCCCTGGGAACAAGCTTGTCC	1027
Db	961	GCAACCAAGCGGGCCCCCATCCACATCGCGGCCAACCAAGTCCCTGGGAACAAGCTTGTCC	1020
QY	1028	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCCTCAGGGCACAAGAGCAGTGC	1087
Db	1021	CCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCCTCAGGGCACAAGAGCAGTGC	1080
QY	1088	GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCCTGACTGCGCTCGGAGGCTCGTGA	1147
Db	1081	GCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCCTGACTGCGCTCGGAGGCTCGTGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGGCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCGCAGGTTGCCCGGCT	1200
QY	1208	GCCCCAGCGCTACTGCAAAATGCGGCCCTGTGTTCTGAGAGTGTGGAAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGCAAAATGCGGCCCTGTGTTCTGAGAGTGTGGAAACCAAGCGCA	1260
QY	1268	GTGCCCCCTACGGGTGCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTACCCCCAGC	1327
Db	1261	GTGCCCCCTACGGGTGCTCCTCAAGACGACTGCCCGCTGCGAGCTGCGGTACCCCCAGC	1320
QY	1328	AGCCGCTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGGCCCCCGAGAGGAGA	1387
Db	1321	AGCCGCTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGGCCCCCGAGAGGAGA	1380
QY	1388	CACAGACCCCCCGTCCGCTGATGACGCTGCTCCGCCAGCAGACAGCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCCGTCCGCTGATGACGCTGCTCCGCCAGCAGACAGCCCCCTGGCAGGTGA	1440
QY	1448	CGGCTTCTGTGCGGGCCTGCTGCGCCGGCTGTGTGCCCCCAAGGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTCTGTGCGGGCCTGCTGCGCCGGCTGTGTGCCCCCAAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCCGCTTCCCTCAGGAACACCAAGAAGTTCAATTCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCCGCTTCCCTCAGGAACACCAAGAAGTTCAATTCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTCCGGGACTGCCCTTGGCTGCCAG	1627
Db	1561	GCTCTCGCTGCAAGAGCTGACGTGGAAGATGAGCGTCCGGGACTGCCCTTGGCTGCCAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCCGGCCGCAAGACACCGTCTGCGTGAGGAAGATCCTGGC	1687
Db	1621	GAGCCCAAGGGGTGGCTGTGTTCCGGCCGCAAGACACCGTCTGCGTGAGGAAGATCCTGGC	1680

QY	1688	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACCTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGGAG	1807
Db	1741	TGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTCTACCGGCGGAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGAGCTGTCTC	1867
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGAGCTGTCTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGCAATTGTGAACATGACTACGTGTGGAGC	1987
Db	1921	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGCAATTGTGAACATGACTACGTGTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2047
Db	1981	CAGAACGTTCCGACAGAAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGCACTGTT	2040
QY	2048	CAGCGTGTCAACTACGACGGGGCGCGGCCCGCCCTCCTGGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCAACTACGACGGGGCGCGGCCCGCCCTCCTGGGCGCTCTGTGCTGGG	2100
QY	2108	CCTGAGCATATCCACAGGGCCTGCGCACTTCTGTGCTGCTGTGCGGGCCAGAACCC	2167
Db	2101	CCTGAGCATATCCACAGGGCCTGCGCACTTCTGTGCTGCTGTGCGGGCCAGAACCC	2160
QY	2168	GCCGCTGAGCTGACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA	2227
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Db	2281	TCCGTATGCCGTGTCCAGAAGGCCGCCCATGGGCACTCCGCAAGGCTTCAAGAGCCA	2340
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QY	2408	GACCAAGCCCGCTGAGGGGATGCCGTGCTCATGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2467
Db	2401	GACCAAGCCCGCTGAGGGGATGCCGTGCTCATGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2468	CAGTGGCCTCTTGAACGTCCTCTACGCTTCATGTGCCACCAAGCCGTGCGCATCAGGGG	2527
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Db	2521	CAAGTCTTACGTCAAGTGCACAGGGGATCCCGCAGGGGCTCCATCTCTCCACGCTGCTTG	2580
QY	2588	CAGCCTGTGCTACGGCGCACATGAGAAACAAGCTGTTTGGCGGGGATTCGGCGGGAAGGGCT	2647
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QY	2888	GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCACTTCAACCG	2947
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Db	2941	CGGCTTCAAGGCTGGAGGAACATGCGTCGAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
QY	3008	TCACAGCCTGTTTCTGATTTGCAAGTGAACAGCCCTCAGACGGTGTGCAACCAACATCTA	3067
Db	3001	TCACAGCCTGTTTCTGATTTGCAAGTGAACAGCCCTCAGACGGTGTGCAACCAACATCTA	3060
QY	3068	CAAGATCCTCCTGCTGCAGAGCGTACAGTTTCAACGATGTGTGTCAGACTCCCATTTCA	3127
Db	3061	CAAGATCCTCCTGCTGCAGAGCGTACAGTTTCAACGATGTGTGTCAGACTCCCATTTCA	3120
QY	3128	TCAGCAAGTTTGAAGAACCCCAATTTTTCCTGCGCTCATCTTGACACGGCCTCCCT	3187
Db	3121	TCAGCAAGTTTGAAGAACCCCAATTTTTCCTGCGCTCATCTTGACACGGCCTCCCT	3180
QY	3188	CTGCTACTCCATCCTGAAAGCCAGAACGACAGTATGT-----GCAGGTGCTGG	3237
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QY	3298	GGCTTGAAGAGTTCTTACCCCTTTTCGCATCAGGAAGTGTGTTAACCAACCACTGTCAAG	3357
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QY	3358	GCTGCTGTGCCCCGCTCTGCTGGGGGTGAGCAGAGCACTGATGGAAGGACAGAGACTG	3417
Db	3361	GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCTGGAGCCGACGCCAACCCGGC	3420
QY	3418	TCTGGAGCTGCCATCCTTCCCACTTGTCT-----GCCTG	3454
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QY	3455	GCGAAGCGCTGGGGGCGCTGATCTCTCCTGTTTGCCCATGATGGGAATTTGGGGGCGCTG	3514
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QY	3575	CTTGTGCAAAACCAGGCCAAG-----GGCTTAGAGAGAGGCCAGGCCAGGCTACCCCAAC	3629
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QY	3630	CCCTCTCAGAGCAGAGCGCCGCTATCACCAAGACAGACAGAGCCCGCGCCGCTCCTGTCTTC	3689
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Db 4013 AAAAAAAAAAAAAAAAAAAAAA 4035

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RESULT 10
US-08-974-524E-117
: Sequence 117, Application US/08974524E
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
:           Lingner, Joachim
:           Nakamura, Toru
:           Chapman, Karen B.
:           Morin, Gregg B.
:           Harley, Calvin B.
:           Andrews, William H.
: TITLE OF INVENTION: Telomerase Reverse Transcriptase
: NUMBER OF SEQUENCES: 477
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/974,524E
: FILING DATE: 19-Nov-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/724,643
: FILING DATE: 01-OCT-1996
: APPLICATION NUMBER: US 08/844,419
: FILING DATE: 18-APR-1997
: APPLICATION NUMBER: US 08/846,017
: FILING DATE: 25-APR-1997
: APPLICATION NUMBER: US 08/851,843
: FILING DATE: 06-MAY-1997
: APPLICATION NUMBER: US 08/854,050
: FILING DATE: 09-MAY-1997
: APPLICATION NUMBER: US 08/911,312
: FILING DATE: 14-AUG-1997
: APPLICATION NUMBER: US 08/912,951
: FILING DATE: 14-AUG-1997
: APPLICATION NUMBER: US 08/915,503
: FILING DATE: 14-AUG-1997
: APPLICATION NUMBER: WO PCT/US97/17618
: FILING DATE: 01-OCT-1997
: APPLICATION NUMBER: WO PCT/US97/17885
: FILING DATE: 01-OCT-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Elmhorn, Gregory P.
: REGISTRATION NUMBER: 38,440
: REFERENCE/DOCKET NUMBER: 015389-002950US
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QY 1928 CTTATCCCAAGCCTGACGGGCTGCGCGATTGTGAACATGACTACGTCGTGGAGC 1987
Db 1921 CTTATCCCAAGCCTGACGGGCTGCGCGATTGTGAACATGACTACGTCGTGGAGC 1980
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Db 1981 CAGACGTTCCGAGAGAAAAGAGGCGGAGCGCTCTCACTCGAGGGTGAAGCACTGTT 2040
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RESULT 11

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DB 1741 TGTACGAGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGAAGTGTCTGAG 1800
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DB 1801 CAAGTTCAAAGCATTGGAATCAGACGACTTGAAGAGGTGACGTGCGGAGCTGTC 1860
QY 1868 GGAAGCAGAGTCAAGCAGCATGCGGAAGCCAGGCCCTGCTGACGTCCAGACTCCG 1927
DB 1861 GGAAGCAGAGTCAAGCAGCATGCGGAAGCCAGGCCCTGCTGACGTCCAGACTCCG 1920
QY 1928 CTTCAATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTGCGGAGC 1987
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QY 1988 CAGAAGCTTCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGTTGAAGCACTGTT 2047
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DB 2041 CAGCGTCTCACTACGAGCGGGCGGGCGGCCCTCTGCGGCTCTGTGCTGGG 2100
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QY 2168 GCCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGCGTACGACACCATCCCCA 2227

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DB 2761 GACAGTGTGACTTCCCTGTGAGAGACGAGGCGCTGGGTGGACCGGCTTTGTTCAGAT 2820
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Db      3241 CGGCCCTCTGCCCCTCCGAGGCGGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCT 3300
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QY      3418 TCTGGAGCTGCCATCTTCCCACTTGTCTCT-----GCCTG 3454
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QY      3630 CCCTCTCAGAGCAGAGCGCCGCTATACCAACGACAGAGCCCCGCGCTCCTGTGCTTC 3689
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QY      3690 CCAGTACCCGCTCCTCTGCCCTGGAACACTTTGTCCAGCATCAGGAGGTTCTGATCCGT 3749
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QY      3750 CTGAAATTCAGCCCATGTCCGAACCTGCGGCTCTGAGCTTAAACAAGCTTCTACTTCTGTTG 3809
Db      3780 CCCAGATTG--GCCATTGTTCAACCCYTCGCCCTGCCYT-----CCTTGCCCTTCCACCCC 3832
QY      3810 TTTCGTGTGTGTGAGAACCCCTGAGAGGAGACCCCTGGAGCTCTGGGAATTTGAGTGACCA 3869
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Db      3953 ATTGGGGGGAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGRA AA 4012
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Db      4013 AAAAAAAAAAAAAAAAAAAAAA 4035

RESULT 12
US-09-126-981-35
; Sequence 35, Application US/09026981
; GENERAL INFORMATION:
; APPLICANT: Couter, Christopher M.
; APPLICANT: Meyerson, Matthew
; APPLICANT: Weinberg, Robert A.
; TITLE OF INVENTION: Telomerase Catalytic Subunit Gene and
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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1 COMPUTER: IBM PC compatible
2 OPERATING SYSTEM: PC-DOS/MS-DOS
3 SOFTWARE: PatentIn Release #1.0, Version #1.30
4 CURRENT APPLICATION DATA:
5 APPLICATION NUMBER: US/09/026,981
6 FILING DATE: 20-FEB-1998
7 CLASSIFICATION: 435
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER: US 60/064,322
10 FILING DATE: 30-OCT-1997
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 60/055,762
13 FILING DATE: 14-AUG-1997
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 60/054,549
16 FILING DATE: 01-AUG-1997
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 60/047,151
19 FILING DATE: 20-MAY-1997
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 60/038,750
22 FILING DATE: 20-FEB-1997
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Granahan, Patricia
25 REGISTRATION NUMBER: 32,227
26 REFERENCE/DOCKET NUMBER: WHI97-11p4AM
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 781-861-6240
29 TELEFAX: 781-861-9540
30 INFORMATION FOR SEQ ID NO: 35:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 4023 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36
37 US-09-026-981-35

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Query Match	82.5%	Score 3311.4	DB 14	Length 4023
Best Local Similarity	89.9%	Pred. No. 0		
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QY	65	GCCGCGCGCTCCCCCGCTGCGGAGCCGTGGGCTCCCTGCTGGCGCAGCCACTACCGGAGGT	124	
Db	61	GCCGCGCGCTCCCCCGCTGCGGAGCCGTGGGCTCCCTGCTGGCGCAGCCACTACCGGAGGT	120	
QY	125	GCTGCCGCTGGCCACGTTCTGTGCGCGCCTGGGGCCCCAGGGCTGCGCGCTGTGCAAGCG	184	
Db	121	GCTGCCGCTGGCCACGTTCTGTGCGCGCCTGGGGCCCCAGGGCTGCGCGCTGTGCAAGCG	180	
QY	185	CGGGGACCCGCGCGGCTTTCGCGCGCTGTGGCCAGTGCTGTGTGCGTGCCTTGGA	244	
Db	181	CGGGGACCCGCGCGGCTTTCGCGCGCTGTGGCCAGTGCTGTGTGCGTGCCTTGGA	240	
QY	245	CGCACGCGCGCCCCCGCGCGCCCTCTCTCCGCCAGGTGTCTGCTGAAGAGCTGCT	304	
Db	241	CGCACGCGCGCCCCCGCGCGCCCTCTCTCCGCCAGGTGTCTGCTGAAGAGCTGCT	300	
QY	305	GCGCCGAGTGTGTGAGAGGCTGTGCGAGCGCGCGCGGAAGACGTGTGCTTGGCTT	364	
Db	301	GCGCCGAGTGTGTGAGAGGCTGTGCGAGCGCGCGGAAGACGTGTGCTTGGCTT	360	
QY	365	CGCGTCTGTGACGCGGCGCGCGCGCCCCCGGAGGCTTCAACCAACAGCGTGGCAG	424	
Db	361	CGCGTCTGTGACGCGGCGCGCGCGCCCCCGGAGGCTTCAACCAACAGCGTGGCAG	420	
QY	425	CTACTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGCGTGGGGCTGTGCT	484	
Db	421	CTACTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGCGTGGGGCTGTGCTT	480	

QY 485 GCGCCGCTGGGCGACGACGCTGCTGCTCACTGCTGCGACGCTGCGGCTCTTTGTGCT 544
Db 481 GCGCCGCTGGGCGACGACGCTGCTGCTCACTGCTGCGACGCTGCGGCTCTTTGTGCT 540
QY 545 GGTGGCTCCAGCTGCGCTTACAGGTGTGCGGCGCGGCTGTACAGCTCGGCGTGC 604
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QY 605 CACTCAGGCG 664
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Db 661 GGCCTGGAACCATAGCGTCAAGGAGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY 725 GAGAGCG 784
Db 721 GAGAGCG 780
QY 785 CGCTGCGCTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 844
Db 781 CGCTGCGCTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
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Db 841 GACGCGTGAACCGAGTGAACCGGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
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QY 965 CCAGACCAACG 1024
Db 961 CCAGACCAACG 1020
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Db 1021 TCCCGCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCTCTCTCTCTCTCTCT 1080
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QY 1865 GTCCGAGCAAGAGTCAAGGAGCATCGGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1924
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QY 3927 CAAATTGGGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGA 3986
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QY 3987 AAAAAAAAAA 3997
Db 4013 AAAAAAAAAA 4023

RESULT 13
US-08-911-312-1
; Sequence 1, Application US/08911312
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Telomerase Reverse Transcriptase
; NUMBER OF SEQUENCES: 170
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,312
; FILING DATE: 14-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; ATTORNEY/AGENT INFORMATION:

NAME: Einhorn, Gregory P.
REGISTRATION NUMBER: 38,440
REFERENCE/DOCKET NUMBER: 015389-002500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 782..4177
OTHER INFORMATION: /product= "human telomerase reverse
OTHER INFORMATION: transcriptase (hTRT)"
OTHER INFORMATION: /note= "cDNA contained in plasmid
US-08-911-312-1"

Query Match 82.4%; Score 3307; DB 13; Length 7029;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3619; Conservative 0; Mismatches 360; Indels 46; Gaps 5;

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DB 785 CCGCGCGCTCCCGCTGCGCAGCCGCTGCGTCCCTGCTGCGCAGCCACTACCGGAGGTG 844
QY 126 CTGCGCGTGGCCACGTTGCTGCGCGCGCTGCGGCCCCCAGGGCTGGCGGCTGTGACGCG 185
DB 845 CTGCGCGTGGCCACGTTGCTGCGCGCGCTGCGGCCCCCAGGGCTGGCGGCTGTGACGCG 904
QY 186 GGGGACCCCGCGGCTTCCCGCGCGCTGCTGCGCCAGTGCCTGTGTGCGTCCCTGGGAC 245
DB 905 GGGGACCCCGCGGCTTCCCGCGCGCTGCTGCGCCAGTGCCTGTGTGCGTCCCTGGGAC 964
QY 246 GCAAGCG 305
DB 965 GCAAGCG 1024
QY 306 GCGCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 365
DB 1025 GCGCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1084
QY 366 GCGCTGTGAGCGGGCG 425
DB 1085 GCGCTGTGAGCGGGCG 1144
QY 426 TACCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGTG 485
DB 1145 TACCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTGCTGTG 1204
QY 486 CGCGCGGTGGCGAGCAGTGTGTTCACTGCTGCAAGCGCGCTCTTGTGTGCTG 545
DB 1205 CGCGCGGTGGCGAGCAGTGTGTTCACTGCTGCAAGCGCGCTCTTGTGTGCTG 1264
QY 546 GTGGCTCCAGCTGCGCTTACCAAGTGTGCGGGCGCGCGCTGTACCAAGTCCGCGCTGC 605
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DB 4325 CCCTGTGCAAAACCCAGGCGCGTGAAGTTCGGGCTGAGGCTGAGGAGTGTCCAGGCGAAG 4384
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RESULT 14
US-08-911-312A-1

/ Sequence 1, Application US/08911312A
/ GENERAL INFORMATION:

/ APPLICANT: Cech, Thomas R.
/ APPLICANT: Lingner, Joachim
/ APPLICANT: Nakamura, Toru
/ APPLICANT: Chapman, Karen B.
/ APPLICANT: Morin, Gregg B.
/ APPLICANT: Harley, Calvin B.
/ APPLICANT: Andrews, William
/ TITLE OF INVENTION: Telomerase Reverse Transcriptase
/ NUMBER OF SEQUENCES: 171
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834

COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/911,312A
/ FILING DATE: 14-AUG-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-OCT-1996

/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-APR-1997

/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-MAY-1997

/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-AUG-1997

ATTORNEY/AGENT INFORMATION:

/ NAME: Elmhorn, Gregory P.

/ REGISTRATION NUMBER: 38,440

/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200

/ TELEFAX: (415) 576-0300

/ INFORMATION FOR SEQ ID NO: 1:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 7029 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: cDNA

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: 782..4177
/ OTHER INFORMATION: /product= "human telomerase reverse
/ OTHER INFORMATION: transcriptase (hTRT)"
/ OTHER INFORMATION: /note= "cDNA contained in plasmid
/ OTHER INFORMATION: pGRN121"
US-08-911-312A-1

Query Match 82.4%; Score 3307; DB 13; Length 7029;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3619; Conservative 0; Mismatches 360; Indels 46; Gaps 5;

QY 6 AGGACAGCTGCGTCTGCTGCGACGTGGAGAGCCCTGGCCACCCCGCGCATG 65
Db 725 ACGACAGCTGCGTCTGCTGCGACGTGGAGAGCCCTGGCCACCCCGCGCATG 784
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Db 3425 ACCTTCTCAGACCTGCTCCGAGGTGCTGATGATGCTGCTGCTGCTGCTGCTGCTG 3484
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Db 3485 AAGACAGTGTGAATTTCCCTGTAGAAGAGAGCCCTGGGTGCAAGGCTTTTGTGAG 3544
QY 2826 ATGCCGCGCCAGCGCTATTCCCTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2885
Db 3545 ATGCCGCGCCAGCGCTATTCCCTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3604
QY 2886 GTGACAGGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCACTCTCACTTCAAC 2945
Db 3605 GTGACAGGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCACTCTCACTTCAAC 3664
QY 2946 CCGGCTTCAAGGCTGGAGAGACATGCGTCCAACTCTTTGGGGCTTGGCGTGAAG 3005
Db 3665 CCGGCTTCAAGGCTGGAGAGACATGCGTCCAACTCTTTGGGGCTTGGCGTGAAG 3724
QY 3006 TGTCAAGGCTGTTTCTGATTTGCAAGTGAACAGCTCCAGAGGCTGCAACCAATC 3065
Db 3725 TGTCAAGGCTGTTTCTGATTTGCAAGTGAACAGCTCCAGAGGCTGCAACCAATC 3784
QY 3066 TACAGATCTCTCTGCTGCAAGGCTGACAGGTTTCAAGCATGTGCTGCAAGTCTCCATTT 3125
Db 3785 TACAGATCTCTCTGCTGCAAGGCTGACAGGTTTCAAGCATGTGCTGCAAGTCTCCATTT 3844

QY 3126 CATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACAGGCTCC 3185
DB 3845 CATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCACTCTGACACAGGCTCC 3904
QY 3186 CTCTGCTACTCCATCTCTGAAGCCCAAGACGATATGT-----GCAGTGGCT 3235
DB 3905 CTCTGCTACTCCATCTCTGAAGCCCAAGACGATATGTCTGCGCGTCACTCTGACACAGGCTCC 3964
QY 3236 GGCCTCAGTGGCAGCAGTGCCTGCTGCTGTGTAGTGTGACAGAGACTGATGATC 3295
DB 3965 GCGCGCTCTGCGCTCCGAGCGCTGAGTGTGCTGACCAAGCATTCCTGCTCAG 4024
QY 3296 TGGCTTAGAAGTCTTACCCCTTTTCCGATCAGAGAGTGTGTTAACCAACACTGTC 3355
DB 4025 CTGACTGACACCGTGTCACTACGTGCACTCTGCGTCACTCAGGACAGCCCAAGC 4084
QY 3356 AGGCTGCTGCGCGCTCTCTGCGGTGAGCAGAGCACCCTGATGGAAGGACAGAGC 3415
DB 4085 CAGCTGAGTCGGAAGCTCCCGGAGCAGAGCTGACTGCGCTGAGGCGCGACCAACCG 4144
QY 3416 TGTCTGGAGCTGCCATCTCTCCACCTTGTCT-----GCC 3452
DB 4145 GCACTGCCCTCAGACTTCAAGACCATCTGACTGATGCGCACCCGCCACAGCCAGGCC 4204
QY 3453 TGGGGAAGCGCTGGGGGGCTGCTCTCTCTGTTTGGCCCATGCTGGGATTTGGGGGCC 3512
DB 4205 GAGAGCAGACACCCAGCAGCCCTGTCTACCGCGGGCTTACGTCACAGGAGGAGGGGGCG 4264
QY 3513 TGGCTCTCTCTGTTTGGCTGTGTGGATTTGGGCTGTCTCCGCTCATGACCTTAAGG 3572
DB 4265 CCCACACCCAGCGCGCGCACCGCTGGAGTGTGAGCGCTGAGTGTGTTGGCGAGGCC 4324
QY 3573 CCCTGTGCAAAACCCAGCGCAAG-----GCTTAGAGAGGCGCAGCGCTACCC 3627
DB 4325 TGCATGTCCGCTGAAGGCTGAGTGTCCGCTGAGGCGCTGAGCGATGTCAGCCAGGG 4384
QY 3628 ACCCTCTCAGAGCAGAGCGCGCTGATCAACGACAGAGCGCGCGCTCTGCT 3687
DB 4385 CTGAGTGTCCAGACACCTGCGCTT-TCATTTCCACAGGCTGCGCTCGCTCCAC 4443
QY 3688 TCCAGTCAACCTGCTCTGCGCTGACACTTTGTCAGCATCAGGAGTTTCTGATCC 3747
DB 4444 CCAGGCGCAGCTTTCTCTCAGCAGAGCGCGCTTCCACTCCCAATAGGAATAGTCCA 4503
QY 3748 GTCTGAATTCAGCCATGTCGAACCTGCGCTGAGCTTAAAGCTTCTACTTCTGT 3807
DB 4504 TCCCGAGATTGCGCATGTGTCACCCCT-----CGCCCTGCGCTCTTGCCTTCCAC 4556
QY 3808 TCTTCTGTGTGTGAGAGCCCTGAGAGGAGCCCTGGAGCTCTGGAATTGAGTAC 3867
DB 4557 CCCACCATCAGGTGAGAGCCCTGAGAGGAGCCCTGGAGCTCTGGAATTGAGTAC 4616
QY 3868 CAAAGGTGTGCTGTACACAGGCGAGGACCTGACCTGATGGGGTCCCTGTGGTC 3927
DB 4617 CAAAGGTGTGCTGTACACAGGCGAGGACCTGACCTGATGGGGTCCCTGTGGTC 4676
QY 3928 AAATTGGGGGAGGTGTGTGGAGTAATACTGAATATATGAGTTTTCAGTTTGA 3987
DB 4677 AAATTGGGGGAGGTGTGTGGAGTAATACTGAATATATGAGTTTTCAGTTTGA 4736
QY 3988 AAAA 3992
DB 4737 AAAA 4741

RESULT 15
PCT-US01-15774-3
; Sequence 3, Application PC/TUS0115774
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier

; APPLICANT: Edward V. Wanciewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0568
; CURRENT APPLICATION NUMBER: PCT/US01/15774
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 3
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56) ... (3454)
PCT-US01-15774-3

Query Match 82.4%; Score 3306.6; DB 1; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 8 GCAGCGTGGCTCTGCTGCGCAGCTGGAAGCCCTGGGCGCCGCGGATGCC 67
DB 1 GCAGCGTGGCTCTGCTGCGCAGCTGGAAGCCCTGGGCGCCGCGGATGCC 60
QY 68 GCGGCTCCCGCTGCGAGCGCTGCTCTGCTGCGCAGCTGCGGATGCC 127
DB 61 GCGGCTCCCGCTGCGAGCGCTGCTCTGCTGCGCAGCTGCGGATGCC 120
QY 128 GCGGCTGCGCAGCTGCTGCGCAGCTGCGGCGCCGCGGCTGCGGATGCC 187
DB 121 GCGGCTGCGCAGCTGCTGCGCAGCTGCGGCGCCGCGGCTGCGGATGCC 180
QY 188 GGAACCGCGGCTTTCCGCGCTGCTGCGCAGCTGCTGCTGCGGATGCC 247
DB 181 GGAACCGCGGCTTTCCGCGCTGCTGCGCAGCTGCTGCTGCGGATGCC 240
QY 248 ACGGCG 307
DB 241 ACGGCG 300
QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGAGAGAGCTGCTGCG 367
DB 301 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGAGAGAGCTGCTGCG 360
QY 368 GCTGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
DB 361 GCTGCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 428 CCTGCCAACAACGAGTACCGAGCTGCGGAGAGCGGCGCGCGCTGCTGCG 487
DB 421 CCTGCCAACAACGAGTACCGAGCTGCGGAGAGCGGCGCGCGCTGCTGCG 480
QY 488 CCGGCTGAGCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
DB 481 CCGGCTGAGCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 548 GGTCCAGCTGCGCTTACAGGTGTGCGGCGCGCGCGCTGCTGCTGCTG 607
DB 541 GGTCCAGCTGCGCTTACAGGTGTGCGGCGCGCGCGCTGCTGCTGCTG 600
QY 608 TCAGGCG 667
DB 601 TCAGGCG 660
QY 668 CTGAACCATAGCTCAGGAGGCGCGGCTCCCTGCGCGCTGCGGATGCCAG 727
DB 661 CTGAACCATAGCTCAGGAGGCGCGGCTCCCTGCGCGCTGCGGATGCCAG 720
QY 728 GAGCG 787
DB 721 GAGCG 780

QY	788	TGCCCCCTGAGCCCGGAGCGCGCCGTTGGGCAGGGGCTCTGGCCACCCGGGACAGAC	847
Db	781	TGCCCCCTGAGCCCGGAGCGCGCCGTTGGGCAGGGGCTCTGGCCACCCGGGACAGAC	840
QY	848	GCGTGACCCGAGTGAACCGTGGTTCTGTGTGTATCACTGACAGACCCGCCGAAGAAGC	907
Db	841	GCGTGACCCGAGTGAACCGTGGTTCTGTGTGTATCACTGACAGACCCGCCGAAGAAGC	900
QY	908	CACCTCTTTGGAGGGTGCCTCTGGCACCGGCACTCCCAACCATCCGTGGGCCCA	967
Db	901	CACCTCTTTGGAGGGTGCCTCTGGCACCGGCACTCCCAACCATCCGTGGGCCCA	960
QY	968	GCAACCAAGCGGGCCCCCATCCACATGCGGCGCCACCAAGTCCCTGGGACAAGCCTTGTCC	1027
Db	961	GCAACCAAGCGGGCCCCCATCCACATGCGGCGCCACCAAGTCCCTGGGACAAGCCTTGTCC	1020
QY	1028	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAGAGCAGCTGCG	1087
Db	1021	CCCCGTGTACGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAGAGCAGCTGCG	1080
QY	1088	GCCCTCTCTCTACTACTAGCTCTCTGAGGCCAGCCTGACTGCGCTCGGAAGCTCGTGA	1147
Db	1081	GCCCTCTCTCTACTACTAGCTCTCTGAGGCCAGCCTGACTGCGCTCGGAAGCTCGTGA	1140
QY	1148	GACCATCTTTCTGGGTTCAGAGCCCTGGAATGCCAGGGACTCCCCGAGGTTGCCCGCCT	1207
Db	1141	GACCATCTTTCTGGGTTCAGAGCCCTGGAATGCCAGGGACTCCCCGAGGTTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAAATGCGCCCTGTTTCTGAGCTGCTTGGAAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAAATGCGCCCTGTTTCTGAGCTGCTTGGAAACCAAGCGCA	1260
QY	1268	GTGCCCCCTACGGGGTGTCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTACCCACGC	1327
Db	1261	GTGCCCCCTACGGGGTGTCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTACCCACGC	1320
QY	1328	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGGCCCCCGAGAGAGAGA	1387
Db	1321	AGCCGGTGTCTGTGCCCCGGGAGAAAGCCCCAGGGCTCTGTGCGGCCCCCGAGAGAGAGA	1380
QY	1388	CACAGACCCCCGCTGCGCTGTGTGACGTGCTCCGCACGACAGCAGCCCCCTGGCAGGTGA	1447
Db	1381	CACAGACCCCCGCTGCGCTGTGTGACGTGCTCCGCACGACAGCAGCCCCCTGGCAGGTGA	1440
QY	1448	CGGCTTGTGCGGGGCTGCTGCGCCGGCTGTGTGCCCCCAGGCTCTGGGGCTCCAGGCA	1507
Db	1441	CGGCTTGTGCGGGGCTGCTGCGCCGGCTGTGTGCCCCCAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCTTCTCTCAGGAACAACCAAGAAATCATCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCTTCTCTCAGGAACAACCAAGAAATCATCTCCCTGGGGAAGCATGCCAA	1560
QY	1568	GCTCTGCTGACGAGAGCTGAAGTGAAGATGAGCGTGGGGAAGCTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTGCTGACGAGAGCTGAAGTGAAGATGAGCGTGGGGAAGCTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCCCAGGGGTTGGCTGTGTTCCGGCCGACAGCAACCGTCTGCGTGAAGAGATCCTGGC	1687
Db	1621	GAGCCCCAGGGGTTGGCTGTGTTCCGGCCGACAGCAACCGTCTGCGTGAAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTGCTGAGCTGCTCAGGCTCTTCTTTTA	1740
QY	1748	TGTCACGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1807
Db	1741	TGTCACGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1800
QY	1808	CAAGTTGCAAGCATTTGGAATCAGACAGCACTGAAAGAGGCTGACCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAGCATTTGGAATCAGACAGCACTGAAAGAGGCTGACCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCGAGCATCGGAAAGCCAGGCCCGCCTGTGACGTCCAGACTTCG	1927

Db	1861	GGAAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCAAGCCTGACGGGCTGCGGCCGATGTGAACATGGAATACTACGTGCTGGAGC	1987
Db	1921	CTTCATCCCAAGCCTGACGGGCTGCGGCCGATGTGAACATGGAATACTACGTGCTGGAGC	1980
QY	1988	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTTCGAGGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACTTCGAGGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGTCTAACTACGAGCGGGGCGCGGCCCGCCGCTCTCTGGGCGCTCTGTGCTGGG	2107
Db	2041	CAGCGTGTCTAACTACGAGCGGGGCGCGGCCCGCCGCTCTCTGGGCGCTCTGTGCTGGG	2100
QY	2108	CCTGAGCGATATCCACAGGGGCTGGCGCACTTCGTGCTGCTGTGCGGGCCAGAACCC	2167
Db	2101	CCTGAGCGATATCCACAGGGGCTGGCGCACTTCGTGCTGCTGTGCGGGCCAGAACCC	2160
QY	2168	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTACGGGGCGGTACGACACCATCCCCCA	2227
Db	2161	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTACGGGGCGGTACGACACCATCCCCCA	2220
QY	2228	GGACAGGCTCACGGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2287
Db	2221	GGACAGGCTCACGGAGGTATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2280
QY	2288	TGCGTATGCCGTGTTCAGAAAGGCCGCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2347
Db	2281	TGCGTATGCCGTGTTCAGAAAGGCCGCCATGGGCAAGTCCGCAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTCTACCTTGAAGACCTCCAGCGGTATGCGACAGATTGCTGCTCACTGCAAGGA	2407
Db	2341	CGTCTCTACCTTGAAGACCTCCAGCGGTATGCGACAGATTGCTGCTCACTGCAAGGA	2400
QY	2408	GAACCAAGCCGCTGAGGGAATGCCGTGCTCATTCGACAGAGAGTCTCTCCGTAATGAGCCAG	2467
Db	2401	GAACCAAGCCGCTGAGGGAATGCCGTGCTCATTCGACAGAGAGTCTCTCCGTAATGAGCCAG	2460
QY	2468	CAGTGGCCTCTTGCAGCTCTTCCCTACGCTTCAATGTGCCACCAAGCCGTGCGCATCAGGG	2527
Db	2461	CAGTGGCCTCTTGCAGCTCTTCCCTACGCTTCAATGTGCCACCAAGCCGTGCGCATCAGGG	2520
QY	2528	CAAGTCTACGTTCAGTGGCCAGGGGATCCCGAGGGCTCCATCTCTCCAGCGTGTCTG	2587
Db	2521	CAAGTCTACGTTCAGTGGCCAGGGGATCCCGAGGGCTCCATCTCTCCAGCGTGTCTG	2580
QY	2588	CAGCCTGTGCTACGGCGCATGTGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCT	2647
Db	2581	CAGCCTGTGCTACGGCGCATGTGAGAACAAAGCTGTTTGGGGGATTCGGCGGAGCGGCT	2640
QY	2648	GCTCCTGCGTTTGTGTGATGATTTCTGTTGTGACACTCACTCAACCCAGCGGAAAAC	2707
Db	2641	GCTCCTGCGTTTGTGTGATGATTTCTGTTGTGACACTCACTCAACCCAGCGGAAAAC	2700
QY	2708	CTTCTCTAGGACCCCTGTGCCAGGTGTCCTGAGTATGAGTGTGCTGTGAACCTTGCAGAA	2767
Db	2701	CTTCTCTAGGACCCCTGTGCCAGGTGTCCTGAGTATGAGTGTGCTGTGAACCTTGCAGAA	2760
QY	2768	GACAGTGTGAACTTCCCTGTGAAGAAGAGGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2827
Db	2761	GACAGTGTGAACTTCCCTGTGAAGAAGAGGAGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2820
QY	2828	GCCGCGCCACGGCCTATTCCTCTGTGTGCGGCTGTGCTGTGATACCGGACCTTGAGGT	2887
Db	2821	GCCGCGCCACGGCCTATTCCTCTGTGTGCGGCTGTGCTGTGATACCGGACCTTGAGGT	2880
QY	2888	GCAGAGCGAATACTCAGCTATGCCGGAACCTCATCAGAGCCAGTTCACCTTCAACCG	2947
Db	2881	GCAGAGCGAATACTCAGCTATGCCGGAACCTCATCAGAGCCAGTTCACCTTCAACCG	2940
QY	2948	CGGCTTCAAGGCTGGGAGGAACATGCTGCAAACTCTTGGGGTCTTGGCGCTGAAGTG	3007


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Search completed: March 1, 2004, 22:58:46
Job time : 8185.61 secs
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Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGCTCGAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
QY	3008	TCACAGCCTGTTTCTGATTTGGAGGTGAACAGCCTCCAGACGGGTGTGCACCAACATCTA	3067
Db	3001	TCACAGCCTGTTTCTGATTTGGAGGTGAACAGCCTCCAGACGGGTGTGCACCAACATCTA	3060
QY	3068	CAAGATCCTCTCTGCTGCAGGCGGTACAGGTTTCAACGCAATGTGTGCAGCTCCCAATTCA	3127
Db	3061	CAAGATCCTCTCTGCTGCAGGCGGTACAGGTTTCAACGCAATGTGTGCAGCTCCCAATTCA	3120
QY	3128	TCAGCAAGTTTGAAGAACCCTCATTTTTCCTGCGCGTCACTCTGACACAGGCTCCCT	3187
Db	3121	TCAGCAAGTTTGAAGAACCCTCATTTTTCCTGCGCGTCACTCTGACACAGGCTCCCT	3180
QY	3188	CTGCTACTCCATCCTGAAAGCCAAGAACGACAGTATGT-----GCAGGTGCTGG	3237
Db	3181	CTGCTACTCCATCCTGAAAGCCAAGAACGACAGTATGTCTGCGGCGCAAGGCGCGCC	3240
QY	3238	CCTCAATGGCAGCAGTGCCTGCTGCTGTGTGTAGTGTGTACAGAGACTGAGTGAATCTG	3297
Db	3241	CGGCGCTTGCCCTCCGAGGCGCGTGCAGTGTGTGTGCACCAAGCATTCCTGCTCAAGCT	3300
QY	3298	GGCTTAGGAAGTTCTTACCCTTTTTCGCATCAGGAAGTGTGTTAACCAACCACTGTCAAG	3357
Db	3301	GACTCGACACCGTGTACACTACGTGCCACTCCTGGGGTCACTCAGACAGCCCCAGACGA	3360
QY	3358	GCTCGTCTGCCCGCCCTCTCGTGGGGGTGACAGACGACCTGATGGAAGGACAGAGACTG	3417
Db	3361	GCTGAGTGGGAAGCTCCCGGGGACGACGCTGACTGCTCCCTGGAAGCCGACCAACCCGGC	3420
QY	3418	TCTGGAGCTGCCATCCTTCCCACTTGTCT-----GCCTG	3454
Db	3421	ACTGCCCTCAGACTTCAAGACCATCTTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3455	GGGAAGCGCTGGGGGCGCTGTCTCTCTGTGTTGCCCATGTGTGGATTGGGGGCGCTG	3514
Db	3481	GAGCAGACACCAAGCAGCCCTGTCAAGCCGGGCTTACGTGCCAGGAGGGAGGGCGGCC	3540
QY	3515	GCCTCTCCTGTTTGGCCCTGTGTGGGATTGGGCTGTCTCCCGTCCATGGCACATTAGGCC	3574
Db	3541	CACACCCAGGCCCCGACCGCTGGGAGTCTGAGGCTGAGTGAAGTGTGTCGCGAGCCTG	3600
QY	3575	CTGTGCAAAACCCAGGCCAAG-----GGCTTAGGAGGAGGCCAGGCCAGGCTAACCCAC	3629
Db	3601	CATGTCCGGCTGAAGGTGAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3630	CCCTCTCAGGACAGAGCGCGCTATACACCAAGACAGACCCCGCGCGCTCTGTCTTC	3689
Db	3661	GAGTGTCCAGCACACCTGCGTCT-TCACTTCCCCACAGGCTGGCGTCCGCTCCACCCC	3719
QY	3690	CCAGTCACCGTCTCTGCCCCCTGACACTTTGTCCAGCATCAGGAGGTTTCTGATCCGT	3749
Db	3720	AGGCGCAGCTTTTCTCAACAGAGACCCCGCTTCACTCCCAATAGAAATGTCATC	3779
QY	3750	CTGAATTCAGCCATGTGCAACCTGCGTCTGAGCTTAACAGCTTCTACTTCTGTTC	3809
Db	3780	CCCAGATTCGCCATTGTTCACCCCT-----CGCCCTGCCCTCCTTGCCTTCCACCCC	3832
QY	3810	TTTCTGTGTGTGGAACCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTTGAGTGACCA	3869
Db	3833	CACCATTCAGGTGGAACCCCTGAGAAGGACCCCTGGAGCTCTGGGAATTTGAGTGACCA	3892
QY	3870	AAGGTGTGCCCTGTACACAGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAA	3929
Db	3893	AAGGTGTGCCCTGTACACAGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAA	3952
QY	3930	ATTGGGGGAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAATA	3989
Db	3953	ATTGGGGGAGGTGCTGTGGGAGTAAATATCTGAATATATGAGTTTTCAGTTTGAATA	4012
QY	3990	AAA 3992	
Db	4013	AAA 4015	

QY	168	TGGCGGCTGGTGGACGGCGGGGACCCCGGGGCTTTCGGCGCGCTGTGGCCCAGTGCTTG	227
Db	126	TGGCGCTCGACCCCGTCGGCGCGCCCTTGCTCCGCGGCCCTCGCTCGCCCGCGCGG	185
QY	228	GTGTGCGTGGCCCTGGGACGCACGCGCGCCCCCGCGCCCTTCCTTCCGCCAGTGTTC	287
Db	186	CGCGGGCAGCGCCGCGCCCCCAACGCGGCGCTTCGCGGCCCCCCCCCGCCCTGCGCGCA	245
QY	288	TGCCTGAAGAGACTGTGTGGCCCCGAGTGTTCAGAGGCTGTGTCCAGCGCGGCGGAAGAC	347
Db	246	CCCCGCGCGCCCGGCCACTTCCGCTGCGCGCCCCGCTTCGCCCGCGGCAACGCGCGC	305
QY	348	GTGCTGCGCTTCCGCTTCCGCGCTGTGCAACGGGGCCCCCGGGGGCCCCCGAGGCTTC	407
Db	306	TGTCCGGGCTGC-GCGCCCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAC	364
QY	408	ACCACCAAGCGTGGCGCAGCTACCTGCCCAACACGCTGACCGACGCACTGCGGGGAGCGGG	467
Db	365	CTCGCCCTTGGGCGCGTGTCCCTCTCTCGGCGGGCGCACAGCGGCGCTCCCGGCACTTC	424
QY	468	GCGTAGGGGCTGCTGTGCGCGCGCGCGTGGGCGACGACGTGTGGTTCACTGTGGCAACG	527
Db	425	CCCTGCGCGTCGACGCGCGGCGCCCCCGCGTCCCCCGCGCGCGCGCGCGCGCGCGCGCTCGCCAC	484
QY	528	TGCGCGCTTTGTGCTGTGTGCTCCCACTGCGCTACC	567
Db	485	TCCGCGCTCCCTGGAGGAGGGCGTCCCTCGCGCGCGCGCGCTCC	524

RESULT 5
US-10-767-471-10913/C
; Sequence 10913, Application US/10767471

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: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CL001505
: CURRENT APPLICATION NUMBER: US/10/767,471
: CURRENT FILING DATE: 2004-01-30
: NUMBER OF SEQ ID NOS: 50231
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10913
: LENGTH: 40000
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)..(40000)
: OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tab1
US-10-767-471-10913

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Query Match	1.48;	Score 56.8;	DB 6;	Length 40000;	.
Best Local Similarity	48.28;	Pred. No. 0.0042;			
Matches 160;	Conservative	0;	Mismatches 172;	Indels 0;	Gaps 0;

QY 1 GTTTCAGGCAGCGCTGCGTCTCTGTCGCGACGTGGGAAGCCCTGCGCCCGGCCACCCCCG 60

Db 24768 GTGCCGGCCGCGCCGCGCGACCTGTCGCGTCCCCCGCGCCCGCGCGCCGCTTTCGCCC 24709

QY 61 CGATGCCGCGCGCTCCCGGCTGCGCGAAGCCGTGCGTCCCTGTGTCGAGCCACTACCGCG 120

Db 24708 CGGCTTGGAGAGCCCGCGCGGCTCCGGCTGAGCCCCCACCGCGCGCCCGCCCGCC 24649

QY 121 AGGTGCTGCCGCGCTGGCCACGTTGTCGCGCGCCCTGGGGCCCCAGAGGCTGGCGGTGTGC 180

Db 24648 GCGCGCGCGCGCCCGCGCGTGCCTCGGCGCGCGCGCGGCGGAACTGCTCGCGCGGTGCAGC 24589

QY 181 AGCGCGGGGAACCCGCGGCTTTCCGCGCGCTGTGTGGCCAGTGCCTGTGTGCGTGCCCT 240

Db 24588 CCTTCACTTCGCGCGCCCGCGCGCCCTCTGTGCACCGGGGGCGCTGCGCGGGCGCGAGCCTT 24529

QY 241 GGGACGCACGCGCGCGCCCGCGCGCGCCCTCTCTCCGCCAGGTGTCTGCTGAAGAGC 300

Db 24528 CGCGGGCTTTTGCCGCGCGCCCGCCCTTTTGCGGCGCGCCCGCCGCTGTGGGGGAGA 24469

QY 301 TGGTGCGCCGAGTCTGTGACAGGCTGTGCGAG 332

Db 24468 CGCGGGCTTTGGGGGGGAGAGGCGCGCGTG 24437

RESULT 6
US-10-767-701-4866

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; Sequence 4866, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4866
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS92278_1
US-10-767-701-4866

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Query Match	1.4%;	Score 54.6;	DB 6;	Length 666;
Best Local Similarity	46.8%;	Pred. No. 0.0025;		
Matches 240;	Conservative 0;	Mismatches 269;	Indels 4;	Gaps 2;

QY 228 GTGTGCGTGGCCCTGGGACGCAAGGCGGGCCCCCCCCCGGCGGCCCCCTCTTCCGCGCAGGTGCC 287
 Db 38 GCGCGCCTGCAGGCTTCCACTCGGCGCGCTCCGACGCGGTCAAGCCGGTCCGCGCGCGGGCAG 97
 QY 288 TGCCTGAAGGAGCTGTGTGCCCCGAGTGTCTGCAGAGAGCTGTGCCAGCGCGGCGCGAAGAAC 347
 Db 98 GGGCGGGCACCCCGGTGCACAGCGCCGGGCCCGACGCGGCGCGGCCCGCGCGCGGGGGCG 157
 QY 348 GTGCTGGACCTTCGGGCTTCGCGCTGCTGTGACCGGGGCGCGCGGGGGCCCCCGGAGGCTTC 407
 Db 158 GCGGCCCAAGTCGCGCGCGCGCGGCTGTGCGCGCGGCTGCACCGTCCCGCGCTTGC 217
 QY 408 ACCACCAAGCGGTGCGCAGCTACCTGCCCCAACACGCGTGACCGACGCACTGCGGGGAGCGGG 467
 Db 218 TCCCTCCCGCCCTCCGCGCCCTCCCGCCCC--TCCGCGGCCCCCTCACTCGGCGAG 274
 QY 468 GCGTGGGGGCTGTGCTGCGCGCGCGCTGGGCGAAGACGTGCTGTTCACCTGTGACAGC 527
 Db 275 CCGCGCCGCTCTACAGCGCGCGCGCCCTCGTGAAGCGCTCCTCATGTCTGGGGGCG 334
 QY 528 TCGCGCCTTTGTGTGTGTGGCTCCAGCTCGCCTTACAGAGTGTGCGGCGCGCGCTG 587
 Db 335 GTGCGCCCGCTGTCAAGCTGTCCCCCGCGCGGTTCAGCGGCTGCGCGCGCGCCAGC 394
 QY 588 TACCAGCTGCGCGCTGCCACTCAGGCCCGGCGCGCGCCACACAGCTAGTGACCCCGAAG 647
 Db 395 TCCGCGGCGCGCGC--GCGGCGGCGCGCCCTGCGCGCGCGCGCGCGCGGCTCCTCC 453
 QY 648 CGTCTGGGATGCGACGCGGCTTGAACCATAGCTCAGGAGGCCGCGGTCCTCCCTGGGC 707
 Db 454 CCCCCCGCGCGCGCGCGCGCTGTGTGCGCGCGGATGCCCTCGGTGGCTGCGCGCGGGC 513
 QY 708 CTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGC 740
 Db 514 CCGGGCGCTCCGCGAGGCTGGGGCGCGGGCGC 546

```

RESULT 7
US-10-767-701-4186
; Sequence 4186, Application US/1076770D
: GENERAL INFORMATION:

```

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4186
LENGTH: 584
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS73536_1
US-10-767-701-4186

Query Match 1.4%; Score 54.2; DB 6; Length 584;
Best Local Similarity 45.7%; Pred. No. 0.0029;
Matches 188; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

QY 20 CCTGCTGCGACGTGGGAAGCCCTGGCCCCGGCCACACCCCGGATGCGCGCTCCCG 79
DB 144 CCCCCCG 203
QY 80 CTGCGGAGCGCTGCGCTCTCTGCTGCGGAGCCACTACCGCGAGGTGCTGCGCGCAC 139
DB 204 CCGCTGC 263
QY 140 GTTCGTGCGCGCGCTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 199
DB 264 GCG 323
QY 200 TTTCGCGCGCGCTGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 259
DB 324 CG 383
QY 260 CGCGCGCGCGCTCTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 319
DB 384 GCTCCCGCGCGCTCG 443
QY 320 GAGGCTGTGCGAGCG 379
DB 444 CCGCGAGGCGCTCCACTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 503
QY 380 GGCG 430
DB 504 CGACCG 554

RESULT 8
US-10-767-701-2473/c

Sequence 2473, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 2473
LENGTH: 570
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(570)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41826_1

US-10-767-701-2473

Query Match 1.3%; Score 53.4; DB 6; Length 570;
Best Local Similarity 52.9%; Pred. No. 0.0042;
Matches 137; Conservative 0; Mismatches 121; Indels 1; Gaps 1;

QY 574 GCGGCGCGCGCTGTACAGCTCGCGCGCTGCCACTCAGGCGCGCGCGCGCGCGCGCG 633
DB 260 GCGGCG 201
QY 634 GTG-GACCGGAGGCGCTGTGGATGCGAAGCGCGCGCTGGAACCATAGCTCAGGAGGCC 692
DB 200 GTGCGCGCGCGGAGGAGCGCGCGCGCGGAGCTGCGCGCGCGGAGCGCGCGCGCGCG 141
QY 693 GGGTCCCGCTGGGCTGCG 752
DB 140 GGGGCG 81
QY 753 AGTCTGCGCGTTGCCAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 812
DB 80 CCG 21
QY 813 GTTGGGAGGCGGTCTGCG 831
DB 20 CCGGCG 2

RESULT 9

US-10-767-701-4466

Sequence 4466, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 4466
LENGTH: 580
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS80039_1
US-10-767-701-4466

Query Match 1.3%; Score 53.4; DB 6; Length 580;
Best Local Similarity 52.3%; Pred. No. 0.0043;
Matches 147; Conservative 0; Mismatches 126; Indels 8; Gaps 1;

QY 12 CGTGCCTCTGCTGCGACGTGGGAAGCCCTGGCCCCGGCCACACCCCGGATGCGCGC 71
DB 125 CG 184
QY 72 GCTCCCGCTGCGAGCGCGCTGCGCTCTGCTGCGAGCACTACCGGAGGTGCTGCG 131
DB 185 CG 244
QY 132 CTGCGCACTTGTGCGCGCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 191
DB 245 GGGGCG 304
QY 192 CCGGCGCTTTCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 251
DB 305 CTTGCT 356
QY 252 CCG 292
DB 357 CTCCCG 397

RESULT 10
US-10-767-701-9739
; Sequence 9739, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 9739
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS33367_1
US-10-767-701-9739

Query Match 1.3%; Score 53.4; DB 6; Length 1092;
Best Local Similarity 45.0%; Pred. No. 0.0055;
Matches 201; Conservative 0; Mismatches 246; Indels 0; Gaps 0;

QY 39 GCCCTGCCCCCGCCACCCCGCATGCGCGCGCTCCCGCTGCCAGCGCTGCGCTCC 98
DB 177 GGCCCTGGCGCGCGCGCTCCACCCCTCCCGCGCGCGCTCCCGCTCCCGCTCC 236
QY 99 CTGCTGCGACGACTACCGGAGGTGCTGCGCTGCGCACTGCTGCGCGCGCTGCGG 158
DB 237 CGCCCCCGCGCGCGCGCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 296
QY 159 CCCCAGGCGTGGCGCGCTGCTGACGCGCGCGGAGACCGCGCGCTTCCGCGCGCTGCGC 218
DB 297 CCGC 356
QY 219 CAGTGCCTGCTGCTGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGC 278
DB 357 CGC 416
QY 279 CAGTGTCTGCTGCTGCTGAGGAGGTGCTGCGCGCGCGCGCGCGCGCTGCGAGCGCGC 338
DB 417 CCGC 476
QY 339 GCGAAGACGCTGCTGCGCTTCCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGC 398
DB 477 GTCGTCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 536
QY 399 GAGGCTTTCACCAACGAGCGTGGCGAGTACCTGCCCAACAGGTGACCGGACGCTGCGG 458
DB 537 CCGCTCCCGCTGC 596
QY 459 GCGAGCGCGCGCTGCGCGCTGCTGCTG 485
DB 597 GC 623

RESULT 11
US-10-767-701-30024
; Sequence 30024, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30024
; LENGTH: 522

TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 9848339
US-10-767-701-30024

Query Match 1.3%; Score 53.2; DB 6; Length 522;
Best Local Similarity 49.4%; Pred. No. 0.0045;
Matches 167; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

QY 122 GGTGCTGCGCGTGGCCACGTTCTGTCGCGCGCGCTGGGCGCCAGGCGTGGCGCTGCA 181
DB 56 GAGCGCGGTGCTGCGCGCTGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCGCGC 115
QY 182 CCGCGCGGACCGCGCG--GCTTCCCGCGCGCTGTCGCGCGCGCGCGCGCGCGC 238
DB 116 GC 175
QY 239 CTGGACGACGC 298
DB 176 GCTGCTGCTGC 235
QY 299 GCTGTGC 358
DB 236 CATGC 295
QY 359 CGGCTTCCGC 418
DB 296 CGACCTCGC 355
QY 419 GCGGACGCTGC 456
DB 356 GCTGTGAGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 393

RESULT 12
US-10-767-701-8805
; Sequence 8805, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8805
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56975_1
US-10-767-701-8805

Query Match 1.3%; Score 53.2; DB 6; Length 667;
Best Local Similarity 45.0%; Pred. No. 0.005;
Matches 199; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

QY 126 CTGCGCGTGGCCACGTTCTGTCGCGCGCGCTGGGCGCCAGGCGTGGCGCTGCGC 185
DB 23 CTCTCTGTATGC 82
QY 186 GCGGACCGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 245
DB 83 CACCAACCGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 142
QY 246 GCGGC 305
DB 143 GCGTGGC 202
QY 306 GCGGAGTGTGCGAGGCGTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGC 365

Db 203 CCCCCCCCCCCCCCTCCCCCCCCCGGCGCCCTCCCCCCCCCCCCCCCCCGCGCCG 262
QY 366 GCGCTGTGAGAGGG 425
Db 263 GCG 322
QY 426 TACCTGCCAACAAGGTGACCGACGCTGCGGGGAGCGGGGCGTGGGGGCTGTGCTG 485
Db 323 GCG 382
QY 486 GCG 545
Db 383 GCG 442
QY 546 GTGGCTCCCACTGCGCTACC 567
Db 443 CTCCCGTGGCGGG 464

RESULT 13

US-10-767-701-4420
; Sequence 4420, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535) B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4420
; LENGTH: 697
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS78455_1
US-10-767-701-4420

Query Match 1.3%; Score 52.6; DB 6; Length 697;
Best Local Similarity 44.8%; Pred. No. 0.0069;
Matches 246; Conservative 0; Mismatches 299; Indels 4; Gaps 1;

QY 40 CCGTGGCG 99
Db 14 CCG 73
QY 100 TGTGCGGAGCACTACCGCGAGGTGCTGCGGTGCGCAAGTTCGCGCGCGCGCGCGCG 159
Db 74 CCG 133
QY 160 CCGAGGGGTGCG 219
Db 134 CTGCG 193
QY 220 AGTGCCTGTGTGCTGCG 279
Db 194 CGCGTGGCG 253
QY 280 AGGTGTCTGCTGAGAGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 339
Db 254 CG 313
QY 340 CGAAGAGCTGTGCG 395
Db 314 CG 373
QY 396 CCGGAGGCTTACCAACGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 455
Db 374 CCAAGCGCGGTGGTCCCGCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 433

QY 456 CCGGAGAGCG 515
Db 434 CCGGTGAGAGCG 493
QY 516 CTGCTGGAGAGCTGCG 575
Db 494 CTCCCTTTTCCCAAGGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 553
QY 576 GGGCGCGCG 584
Db 554 GTGTGGCGG 562

RESULT 14

US-10-767-471-195/c
; Sequence 195, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 14800
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-195

Query Match 1.3%; Score 52.2; DB 6; Length 14800;
Best Local Similarity 45.8%; Pred. No. 0.029;
Matches 324; Conservative 3; Mismatches 366; Indels 14; Gaps 4;

QY 8 GCAGCGCTGCTCTGCTGCGAGCGTGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 67
Db 6139 GCGGTGCGCGCTCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6080
QY 68 GCGCGTCCCG 127
Db 6079 GCGCGCGTCTCTCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6020
QY 128 GCGGTGCG 187
Db 6019 CTTGTGCGCGAGCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5960
QY 188 GAGCG 247
Db 5959 CCGCGTGGCAAGCG 5900
QY 248 ACG 307
Db 5899 CTTGCG 5840
QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Db 5839 CCGAGTGTGCGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5780
QY 368 GCTGTGAGAGCG 427
Db 5779 GCT 5728
QY 428 CTTGCGCGCAACAGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Db 5727 GCGGTGTCT 5669
QY 488 CCGCGTGGGCGAGCGAGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 547
Db 5668 TGGCTCTGCGCGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5609
QY 548 GGTCTCCAGCTGCGCTTACAGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607

Db 5608 GCGCCGCTCTTCTCCGAGCTG---CCGCTGCCCTTGCCCTCTCCGACAGGCAC 5552
QY 608 TCAGGC--CCGCCCCCGCCACACGCTAGTGAACCCGAGAGCGTCTGGATGCGACGG 665
Db 5551 GCAGCGGGCGCTCTCTCGCCAGCTCGCGGAAACCGCCGCTCGGCTCCAGCTCT 5492
QY 666 GCCTGGAACCATAGCTCAGGAGCGCGGCTCCCTGGGCTGCC 712
Db 5491 GCTTGACTTCTCGCTGTGAGCGGAGCTCTCTCAGCCCTYGCC 5445

RESULT 15

US-10-767-471-603/c
; Sequence 603, Application US/10767471
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001505
; CURRENT APPLICATION NUMBER: US/10/767,471
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 50231
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 11409
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-603

Query Match 1.3%; Score 52; DB 6; Length 11409;
Best Local Similarity 44.2%; Pred. No. 0.028;
Matches 184; Conservative 6; Mismatches 226; Indels 0; Gaps 0;

QY 17 CGTCTGCTGCGCAGTGGAGACCCCTGGCCCCCGCCACCCCGGATGCCGCGCTCC 76
Db 1943 CCTCCTCAGCAGCTGCCGCTGTCTCCCTCTGCTCCGCTCGGCCGAGCCGATCA 1884
QY 77 CCGTCCGAGCCGCTGCGCTCCCTGCTGCGACCACTACCCGAGGTGCTGCCGCTGGC 136
Db 1883 ACTCCTGCTCCGCGGCCAGGCGCTGCTGCGCGCTTCCGCCAGCTGCCGCTGCTTCT 1824
QY 137 CACGTCGTGCGGCGCTGGGCGCCAGAGGCTGGCGCTGTGACGCGGGGACCCGCGC 196
Db 1823 CCACTCTTGTTCAGCCAGCTCCCGCTRCCGGAAGCGGCTGTCTCCGCTTGCCGCGC 1764
QY 197 GCGTTCCGCGCGCTGTGGCCAGTGTGCTGTGCGTGGAGCGACGCGCGCC 256
Db 1763 GCGCGCGCTGCGCTCGGCTCTCTCTGCTTCTCAGCTCGGCTGCGCAGGCTCT 1704
QY 257 CCGCGCGCGCGCT 316
Db 1703 TCTGCTGCRGCACT 1644
QY 317 GCAGAGGCTGTGCGAGCGCGCGGCAAGACGTGTGCTGCTTGGCTTGGCGCTGGA 376
Db 1643 GCCAGCGCTCCAGCTSCCGCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1584
QY 377 CCGCGCGCGCGCGCGCGCGCGCGCGCGCTTACCAACAGCGTGGAGCTACTGC 432
Db 1583 GTGCCGCGCGCTCAGCT 1528

Search completed: March 1, 2004, 23:56:49
Job time : 60.9188 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 17:50:03 ; Search time 6357.7 Seconds
(without alignments)
18844.394 Million cell updates/sec

Title: US-09-424-686F-12
Perfect score: 4012
Sequence: 1 gtttcagcagcgcgtgcgtc.....aaaaaaaaaaaaaaaaaaaa 4012

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1346.4	33.6	1826	29 AY407349	AY407349 Homo sapi
2	1308.6	32.6	1584	29 AY407350	AY407350 Pan trogl
3	810.2	20.2	1835	29 AY407351	AY407351 Mus muscu
4	806	20.1	925	12 BM453198	BM453198 AGENCOURT

C	5	706	17.6	813	12	BG198331	BG198331 RST17589
	6	500.2	12.5	851	13	BU702370	BU702370 UI-M-FIO-
	7	445	11.1	492	12	BM824748	BM824748 K-EST0096
	8	385.8	9.6	389	9	AA281296	AA281296 zt0802.r
	9	355.8	8.9	851	12	BG917907	BG917907 602820830
	10	346.2	8.6	688	14	CF531121	CF531121 UI-M-FYO-
	11	340.4	8.5	649	14	CF531069	CF531069 UI-M-FYO-
	12	322	8.0	599	10	BB618671	BB618671 BB618671
	13	317.8	7.9	664	13	BQ258274	BQ258274 NISC_kp11
	14	290.8	7.2	614	10	BB651920	BB651920 BB651920
	15	287.4	7.2	303	9	AA299878	AA299878 EST12462
	16	267	6.7	866	10	BE371943	BE371943 601217728
	17	252.2	6.3	715	10	BE396925	BE396925 601290610
	18	249.6	6.2	409	9	AA311750	AA311750 EST182469
	19	248.8	6.2	679	10	BE396606	BE396606 601289077
	20	243.2	6.1	649	10	BE514070	BE514070 601316575
	21	243	6.1	610	10	BE514188	BE514188 601316376
	22	214	5.3	344	14	CF531258	CF531258 UI-M-FYO-
	23	208.6	5.2	779	10	BE268183	BE268183 601125261
	24	203.8	5.1	336	13	BY775178	BY775178 BY775178
	25	203.2	5.1	343	13	BY783093	BY783093 BY783093
	26	200.6	5.0	338	13	BY784804	BY784804 BY784804
	27	192.2	4.8	326	13	BY149368	BY149368 BY149368
	28	182.6	4.6	347	10	AW244516	AW244516 BR_END06B
	29	173	4.3	315	9	AA748707	AA748707 ny02e05.s
	30	172	4.3	340	9	AA811084	AA811084 oa85c05.s
	31	168	4.2	468	10	AW270031	AW270031 xv57e03.x
	32	167.6	4.2	775	12	BI388013	BI388013 BFL26_002
	33	167	4.2	416	10	AW276315	AW276315 xrl0b12.x
	34	154.8	3.9	696	13	BU139751	BU139751 603134527
	35	151.4	3.8	880	13	BU377259	BU377259 603811228
	36	150.4	3.7	668	14	CA380121	CA380121 659344 NC
	37	148	3.7	148	9	AI824948	AI824948 wb04c01.x
	38	132	3.3	641	28	AZ972318	AZ972318 2M0246F07
	39	128.8	3.2	875	13	BU122597	BU122597 603148441
	40	126.2	3.1	753	13	BU452535	BU452535 603767927
	41	116.8	2.9	632	14	CA353864	CA353864 625469 NC
	42	115.8	2.9	732	13	BX889962	BX889962 BX889962
	43	107.4	2.7	366	10	BF511837	BF511837 UI-H-BI4-
	44	107.4	2.7	519	10	BF802688	BF802688 PM4-CIT007
	45	107	2.7	1610	28	BZ569386	BZ569386 pac82-164

ALIGNMENTS

RESULT 1	AY407349	1826 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY407349				
DEFINITION	Homo sapiens TERT gene, VIRTUAL TRANSCRIPT, partial sequence.				
ACCESSION	AY407349				
VERSION	AY407349.1	GI:39763320			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
AUTHORS	1 (bases 1 to 1826)				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1826)				
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source 1.1826
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="TERT"
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Query Match 33.6%; Score 1346.4; DB 29; Length 1826;
Best Local Similarity 84.7%; Pred. No. 8e-159;
Matches 1347; Conservative 0; Mismatches 243; Indels 0; Gaps 0;
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Db 61 TGCACTGGCTGATGATGTGTGATGCTGCTGAGCTGCTCAGGCTTTCTTTATGTCAGG 120
QY 1756 AGACCACTTTCAAGAACAGAGCTCTTTTCTACCGAAGATGCTGAGCAAGTTC 1815
Db 121 AGACCACTTTCAAGAACAGAGCTCTTTTCTACCGAAGATGCTGAGCAAGTTC 180
QY 1816 AAAGCATTGGAATCAGACAGCACTTGAAGAGGTGACAGCTGCGGAGCTGTGGAAGAG 1875
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QY 1876 AGGTCAAGCAGATCGGGAAGCCAGGCGCCCTGCTGACGTCAGACTCCGCTTATCC 1935
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QY 1936 CCAAGCTGACGGGCTGCGGCGGATGTAATGATGACTACGTCGTGGAGCCAGAACGT 1995
Db 301 CCAAGCTGACGGGCTGCGGCGGATGTAATGATGACTACGTCGTGGAGCCAGAACGT 360
QY 1996 TCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGCTGAAGGCACTGTTCAGCGTGC 2055
Db 361 TCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGCTGAAGGCACTGTTCAGCGTGC 420
QY 2056 TCACTACGAGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2115
Db 421 TCACTACGAGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
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QY 2176 AGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2235
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QY 2296 CCGTGTCCAGAGGCCGCCCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2355
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QY 2356 CCTTGACAGACCTCCAGCCGTACATGCGAGAGTTCGTGGCTCACCTGACAGAGACAGCC 2415
Db 721 CCTTGACAGACCTCCAGCCGTACATGCGAGAGTTCGTGGCTCACCTGACAGAGACAGCC 780
QY 2416 CGCTGAGGATGCGGCTGCTCATGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCC 2475
Db 781 CGCTGAGGATGCGGCTGCTCATGAGCAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 840

QY 2476 TCTTGACGCTCTTCTACGCTTCATGTGCAACACGCGGCTGCGCATCAGGGGCAAGTCT 2535
Db 841 NNN 900
QY 2536 ACGTCCAGTGCAGAGGGATTCGCCAGAGGCTCCATCTCTCCACGCTGCTGACGCTGT 2595
Db 901 ACGTCCAGTGCAGAGGGATTCGCCAGAGGCTCCATCTCTCCACGCTGCTGACGCTGT 960
QY 2596 GCTACGGCGCATGAGAACAGAGCTGTTGCGGGGATTCGGCGGAGCGGCTGCTCTGC 2655
Db 961 GCTACGGCGCATGAGAACAGAGCTGTTGCGGGGATTCGGCGGAGCGGCTGCTCTGC 1020
QY 2656 GTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAACCTTCTCTCA 2715
Db 1021 GTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAGCGGAAACCTTCTCTCA 1080
QY 2716 GGAACCTGTGCGAGGCTGTCCTGAGTATGCTGCGGTGCTGTAAGTTCGGAAGACAGTGG 2775
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QY 2836 ACGGCTATTTCCCTGTGTCGGGCTGCTGCTGATACCCGAGCCTGAGGTGACAGCG 2895
Db 1201 ACGGCTATTTCCCTGTGTCGGGCTGCTGCTGATACCCGAGCCTGAGGTGACAGCG 1260
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Db 1261 ACTACTCCAGCTATGCGCGGAGCTCCATCAGAGCCAGTCTCACTTCAACCGCGGCTTCA 1320
QY 2956 AGGCTGGAGGAACATGCGTGGCAACTCTTTGGGCTTTGGCGTGAAGTGTACAGCG 3015
Db 1321 AGGCTGGAGGAACATGCGTGGCAACTCTTTGGGCTTTGGCGTGAAGTGTACAGCG 1380
QY 3016 TGTTCCTGATTTGACAGGTGAAACAGCCTCCAGACGCGTGTGACCAACATCTCAAGATCC 3075
Db 1381 TGTTCCTGATTTGACAGGTGAAACAGCCTCCAGACGCGTGTGACCAACATCTCAAGATCC 1440
QY 3076 TCCTGCTGACGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTTATCAGCAAG 3135
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QY 3136 TTTGGAAGAACCCCATTTTCTGCGGCTCATCTCTGACACGCGCTCCCTGCTACT 3195
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Db 1561 CCATCCTGAAGCCAAAGACGAGATGT 1590

RESULT 2
AY407350 1584 bp DNA linear GSS 15-DEC-2003
LOCUS
DEFINITION Pan troglodytes TERT gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
VERSION AY407350
KEYWORDS
SOURCE
ORGANISM
GSS.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
AUTHORS
1 (bases 1 to 1584)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

[illegible]

QY	2356	CCCTTGACAGACCTCCAGCCGTA	CATGCGACAGTTTCGTGCTCACCTG	CAGAGACCAAGCC	2415
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QY	2416	CGCTGAGGGGATGCCGTCGT	CATCGAGCAGAGCTCTCCCTGA	ATGAGGCCAGAGTGCC	2475
Db	781	CACTGAGGGATGCCGTCAT	CATCGAGCAGAGCTCTCCCTGA	ATGAGGCCAGAGTGCC	840
QY	2476	TCCTCGACGCTTCTCAAGCT	CATGTGCCACCAAGCCGCTGCG	CATCAGGGCAAGTCT	2535
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QY	2536	ACGTCCAGTGCAGGGGATCCG	CAGGCTCCACTCTCCACGCTG	CTGACGCTGT	2595
Db	901	ACGTCCAGTGCAGGGGATCCG	CAGGCTCCACTCTCTCCACGCTG	CTGACGCTGT	960
QY	2596	GCTACGGCGACATGAGAA	CAAGCTGTTTGCGGGATTCGG	CGGGGACGGGCTCTCTGC	2655
Db	961	GCTACGGCGACATGAGAA	CAAGCTGTTTGCGGGATTCGG	CGGGGACGGGCTCTCTGC	1020
QY	2656	GTTTGTGATGATTTCTTGT	TGTGTGACACCTCACTCA	CCCAAGGAAACCTTCTCA	2715
Db	1021	GTTTGTGATGATTTCTTGT	TGTGTGACACCTCACTCA	CCCAAGGAAACCTTCTCA	1080
QY	2716	GGAACCTGTGTCGAGGTGTC	CCCTGAGTATGGCTGCTGTA	ACTTGCGGAGACAGTGG	2775
Db	1081	NGAACCTGTGTCGAGGTGTC	CCCTGAGTATGGCTGCTGTA	ACTTGCGGAGACAGTGG	1140
QY	2776	TGAACCTCCCTGTAGAA	AGAGGCCCTGGGTGGCA	CGGCTTTGTTCAGATGCCG	2835
Db	1141	TGAACCTCCCTGTAGAA	AGAGGCCCTGGGTGGCA	CGGCTTTGTTCAGATGCCG	1200
QY	2836	ACGGCCTATTCCCTGTGTC	GCGGCTGCTGTGATACCCG	AGCCCTGAGGTGCAGAGCG	2895
Db	1201	ACGGCCTATTCCCTGTGTC	GCGGCTGCTGTGATACCCG	AGCCCTGAGGTGCAGAGCG	1260
QY	2896	ACTACTCCAGCTATGCCCC	GGACCTCCATCAGACCA	AGTCTCACTTCAACCGCGGCTTCA	2955
Db	1261	ACTACTCCAGCTATGCCCC	GGACCTCCATCAGACCA	AGTCTCACTTCAACCGCGGCTTCA	1320
QY	2956	AGGCTGGAGGAAACATGCG	TGCGAAACTCTTTGGGGCTT	GCGGCTGAAGTGTCA	3015
Db	1321	AGGCTGGAGGAAACATGCG	TGCGAAACTCTTTGGGGCTT	GCGGCTGAAGTGTCA	1380
QY	3016	TGTTCTTGATTTGACG	TGTAACAGCCTCCAGACG	GTGTGACCAACATCTACA	3075
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QY	3076	TCCTGCTGACGCGTACAG	GTTCACGCATGTGTGCA	AGCTCCCATTTTCATCAG	3135
Db	1441	TCCTGCTGACGCGTACAG	GTTCACGCATGTGTGCA	AGCTCCCATTTTCATCAG	1500
QY	3136	TTTGGAAGAACCCCA	CATTTTCTGCGGCTCATCT	TGACACGGGCTCCCTGCTACT	3195
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RESULT 3	AY407351	1835 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	AY407351				
DEFINITION	Mus musculus TERT gene, genomic survey sequence.			VIRTUAL TRANSCRIPT, partial sequence,	
ACCESSION	AY407351				
VERSION	AY407351.1	GI:39763322			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

REFERENCE 1 (bases 1 to 1835)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1835)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 64.5%; Pred. No. 6.7e-92;
Matches 1028; Conservative 0; Mismatches 560; Indels 7; Gaps 2;
QY 1636 GGGTGGTGTGTTCGGCCGAGACACCGCTGCGTGAGAGATCCTGCGCAATTC 1695
Db 1 GGAAGGACCGTGTCCCGCTGACAGACCGCTGTGAGGAGAGATCCTGCGTACGTTCC 60
QY 1696 TGCACCTGGCTGATGAGTGTACGTCGTCGAGCTGCTCAGGCTTTCTTTATGTCACGG 1755
Db 61 TGTTCGTGCTGATGACACATACGTGTGTAACAGCTGCTTACGTTCTTTTACATCACAG 120
QY 1756 AGACCACGTTTCAAAAGAACAGGCTCTTTTCTTACCGGAAGAGTGTCTGAGCAAGTGC 1815
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QY 1816 AAAGCATTGGAATCAGACAGCACTTTGAAGAGGGTGACGTCGGGAGAGCTGTGGAAGCAG 1875
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Db 241 AGGTACGACATCACGAGACACCTGCTGAGCATGCCCCATCTGACAGACTGCGCTTCATCC 300
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QY 1996 TCCGCAAG-AGAAAAGAGGGCGGAGGCTCTACCTGAGGAGTGAAGGCACTGTTACGCTG 2054
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QY 2055 CTCAACTACGAGCGGGCGCGGCGCGCCCTCTGCGGCGCTCTGTGCTGGGCGCTGAGC 2114
Db 421 CTCAACTATGAGCGGACAAAACATCTTCACTTATGCGGTCTTGTACTGGGTATGAAT 480
QY 2115 GATATCCAGAGGGCTGCGCACCTTCTGTGCTGCGTGTGCGGCGCCAGAGACCGCGCT 2174
Db 481 GACATCTACAGGACCTGCGGCGCTTGTGTGCTGCGTGTGCTGTGAGACCAAGACACC 540
QY 2175 GAGCTGTACTTTGTCAAGGTGATGACGGGCGCGTACGACACCATCCCGCAGACAGG 2234
Db 541 AGGATGTACTTTGTTAAGNN 600

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QY 2409 ACCAGCCGCTGAGGATGCGCTGTCATGACAGAGCTCTCCCTGAATGAGGCGAGC 2468
Db 781 GCCAGTGAAGTGAAGAACTCCGTTGTCTATGACAGAGNNNNNNNNNNNNNNNNNN 840
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Db 841 NNN 900
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QY 2589 AGCCTGTGTAAGCGGACATGAGAAACAAGCTGTTTGGCGGAGTTGCGGCGAGCGGCTG 2648
Db 961 AGTGTGTGTTTCGAGACATGAGAAACAAGCTGTTTGTGAGGTGACGCGGAGTGTG 1020
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Db 1561 TGCTACTCATCTCTGAAGCAAGAACGAGTAT 1595
RESULT 4
BM453198
LOCUS BM453198 925 bp mRNA linear EST 05-FEB-2002

DEFINITION	AGENCOCURT_6387556 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5529840 5', mRNA sequence.									
ACCESSION	EM453198									
VERSION	EM453198.1 GI:18502238									
KEYWORDS	EST.									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.									
AUTHORS	NIH-MGC http://mgs.nci.nih.gov/.									
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)									
JOURNAL	Unpublished (1999)									
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: L1AM12208 row: p column: 01 High quality sequence stop: 646.									
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	/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.									
	Average insert size 2.1 kb.									
ORIGIN										
Query Match	20.1%; Score 806; DB 12; Length 925;									
Best Local Similarity	99.2%; Pred. No. 2.7e-91;									
Matches	821; Conservative 0; Mismatches 5; Indels 2; Gaps 1;									
QY	2156	GGCCAGGACCCGCGCTGAGCTGTA	CTTTGTCAAGGTGATGTACGGGCGGTACGA	2215						
DB	2	GGCCAGGACCCGCGCTGAGCTGTA	CTTTGTCAAGGTGATGTACGGGCGGTACGA	61						
QY	2216	CACCATCCCCCAGACAGGCTCA	CGGAGTCAATCGCCAGCATCAAA	2275						
DB	62	CACCATCCCCCAGACAGGCTCA	CGGAGTCAATCGCCAGCATCAAA	121						
QY	2276	GTA	CTGCGTGGTATGCGCGTGTCC	AGAGGCGCCCATGGGCA	2335					
DB	122	GTA	CTGCGTGGTATGCGCGTGTCC	AGAGGCGCCCATGGGCA	181					
QY	2336	CTTCA	GAGCCACGCTCTTACCTTGA	CAGACCTCCAGCCGTACATG	CGACAGTTGCTGGC	2395				
DB	182	CTTCA	GAGCCACGCTCTTACCTTGA	CAGACCTCCAGCCGTACATG	CGACAGTTGCTGGC	241				
QY	2396	TCAC	CTGCAGAGACCAAGCCCGCTG	AGGGATGCCGTGTCATCGA	CGAGAGCTCCTCCT	2455				
DB	242	TCAC	CTGCAGAGACCAAGCCCGCTG	AGGGATGCCGTGTCATCGA	CGAGAGCTCCTCCT	301				
QY	2456	GAAT	GAGGCCACAGTGGCTCTTGA	CGCTCTTCTTACGCTTCA	TGTGCAACCA	2515				
DB	302	GAAT	GAGGCCACAGTGGCTCTTGA	CGCTCTTCTTACGCTTCA	TGTGCAACCA	361				
QY	2516	GCGC	ATCAGGGGCAAGTCTTACG	TCCAGTGCACAGGGGAT	CCCGCAGGGCTCCATCCT	2575				
DB	362	GCGC	ATCAGGGGCAAGTCTTACG	TCCAGTGCACAGGGGAT	CCCGCAGGGCTCCATCCT	421				
QY	2576	CACG	CTGCTCTGCAAGCTGTGCTA	CGGCGACATGGAGAA	CAAGCTGTTGCGGGGATTCG	2635				
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Query Match	Best Local Similarity	Score	DB	Length	813;
Matches 723;	Conservative	0;	Mismatches	12;	Indels 1; Gaps 1;

QY 3090 TACAGGTTTACGCGATGTGTGCTGAGCTCCCATTTTCATCAGCAAGTTGGAAGAACCC 3149
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Db 749 TTCAGGTTTACGCGATGTGTGCTGAGCTCCCATTTTCATCAGCAAGTTGGAAGAACCC 690
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QY 3150 ACATTTTCTGCGCGTATCTCTGACACGGCTCCCTCTGCTACTCCATCTGAAAGCC 3209
| | | | |
Db 689 ACATTTTCTGCGCGTATCTCTGACACGGCTCCCTCTGCTACTCCATCTGAAAGCC 630
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QY 3210 AAGAAGCGAGTATGTGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3269
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QY 3270 TAGTGTGTGAGGAGTATGTGAGTATGTGAGTATGTGAGTATGTGAGTATGTGAGTAT 3329
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Db 569 TAGTGTGTGAGGAGTATGTGAGTATGTGAGTATGTGAGTATGTGAGTATGTGAGTAT 510
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QY 3390 GAGCACTGATGAAAGGACAGAGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 3449
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Db 449 GAGCACTGATGAAAGGACAGAGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAG 390
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QY 3450 GCGTGGGAGAGCGTGGGGGGGCGCTGTCTCTCTGTTTGGCCCATGTTGGGATTTGGGG 3509
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Db 389 GCGTGGGAGAGCGTGGGGGGGCGCTGTCTCTCTGTTTGGCCCATGTTGGGATTTGGGG 330
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QY 3510 GCCTGGCT 3569
| | | | |
Db 329 GCCTGGCT 270
| | | | |
QY 3570 GGGCCCTTGTGCAACCAAGGCGGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 3629
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Db 269 GGGCCCTTGTGCAACCAAGGCGGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 210
| | | | |
QY 3630 CCCTCTCAGAGAGAGGCGCGCTATCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3689
| | | | |
Db 209 CCCTCTCAGAGAGAGGCGCGCTATCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 150
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QY 3690 CCACTCACCGTCTCTGCCCCCTGACACTTTTCTCAGCATCAGGAGGAGTTTCTGATCC 3749
| | | | |
Db 149 CCACTCACCGTCTCTGCCCCCTGACACTTTTCTCAGCATCAGGAGGAGTTTCTGATCC 90
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QY 3750 CTGAATTCAGCCATGTGCAACCTGCGGTCTGAGCTTAACAGCTTTCTACTTCTGTC 3809
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Db 89 CTGAATTCAGCCATGTGCAACCTGCGGTCTGAGCTTAACAGCTTTCTACTTCTGTC 30
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QY 3810 TT-TCTGTGTGTGA 3824
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Db 29 TTAAGTGTGTGTGA 14
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RESULT 6
BU702370 851 bp mRNA linear EST 15-JUL-2003
LOCUS UI-M-F10-Dyx-f-12-0-UI.r1 NIH_BMAP_F10 Mus musculus cDNA clone
DEFINITION IMAGE:6400523 5', mRNA sequence.
ACCESSION BU702370
VERSION BU702370.1 GI:23627105
KEYWORDS EST,
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIN at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5,
Location/Qualifiers
1. .851
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6400523"
/tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F10"
/note="Organ: Brain; Vector: pyx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CAGCCACGAC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Query Match 12.5%; Score 500.2; DB 13; Length 851;
Best Local Similarity 75.1%; Pred. No. 4.1e-53;
Matches 638; Conservative 0; Mismatches 206; Indels 6; Gaps 1;
QY 2269 AGAAGCTACTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 2328
| | | | |
Db 1 AGCGCAGTACTGTATCCGCCAGTATGAGTGTGCTCCGAGAGATAGCCAAAGGCCAAGTCC 60
| | | | |
QY 2329 GCAAGGCTTCAAGAGCCAGCTCTTACCTTGAACAGACTCCAGCGGTACATGCGACAGT 2388
| | | | |
Db 61 ACAAGTCTTTAGAGAGACAGGTCAACCCCTCTTGAACCTCCAGCCATACATGAGCCAGT 120
| | | | |
QY 2389 TCGTGGCTCACTGAG-----GAGACAGAGCCCGCTGAGGAGTGGCTGTCATGAGC 2442
| | | | |
Db 121 TCCTTAAGCATGTGAGGAGTTCAGATGCGAGTCACTGAGGAGTCCGTTGTCATGAGC 180
| | | | |
QY 2443 AGAGCTCTCTCTGAATGAGGCGCAGAGGCTCTTGAAGCTTTCTTCAAGCTTCATGT 2502
| | | | |
Db 181 AGAGCATCTTATGATGAGAGCAGCAGAGCTGTTGACTTCTTCTGCACTTCTGCTGC 240
| | | | |
QY 2503 GCCACCAAGCGGTGCGCATCAGGGGCAAGTCTTACGTCAGTGCAGGAGGAGTCCCGCAGG 2562
| | | | |
Db 241 GTACAGTGTGTAAGATTGGTACAGGTGCTATACGACAGTGCAGGAGGAGTCCCGCAGG 300
| | | | |
QY 2563 GCTCCATCTCTTCCAGCGCTGCTGAGCGCTGTGCTACGGCGAGATGAGAACAAAGCTGT 2622
| | | | |
Db 301 GCTCCAGCTTATCCACCCTGCTCTGAGTCTGTGTTTCCGAGACATGAGAACAAAGCTGT 360
| | | | |
QY 2623 TTGGGGGATTCGGCGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2682
| | | | |
Db 361 TTGCTGAGGTGAGCGGAGTGGTGTCTTTACGTTTGTGATGACTTCTGTGTGTGA 420
| | | | |
QY 2683 CACCTCACCTCAACCCAGCGAAACCTTCTCAGGAGCCCTGCTGAGGAGTGTCCCTGAGT 2742
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Db 421 CGCCTCACTTGAGCAAGCAAAACCTTCTCAGCAGCCCTGCTGATGAGGCTTCTGAGT 480
| | | | |

QY 2743 ATGGCTGCGTGTGAACCTTGGGAGAGACAGTGTGAACCTTCCCTGTAGAGACGAGGCC 2802
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Db 481 ATGGGTGATGATTAACCTTGACAGAGACAGTGTGAACCTTCCCTGTAGAGCCGTGTACC 540
QY 2803 TGGGTGACAGCGCTTTTGTTCAGATGCCGCCACCGCCTATTCCCTGTGTGGCGCTGC 2862
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Db 541 TGGGTGTGACAGCTTCATACACAGCTGCCTGTCTCACTGCTTCCCTGTGTGTGCCTGC 600
QY 2863 TGCTGATACCCGACCCCTGAGGTGACAGGCACTACTCCAGCTATGCCCGGACCTCCA 2922
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Db 601 TGCTGACACTCAGACTTTGAGAGGTGTCTGTGACTACTCAGGTATGCCAGACCTCAA 660
QY 2923 TCAGAGCCAGTCTCACTTCAACCGCGCTTCAAGGCTGGAGAGACATGCCGTCCAAAC 2982
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Db 661 TTAAGACGAGCCTCACTTCCAGAGTGTCTTANAGCTGGAGAGACCATGCCGGAACANGC 720
QY 2983 TCTTTGGGCTTTCGCGCTGAAGTGTCAACAGCTGTTTCTGATTTGAGAGGTGAACAGCC 3042
|||||
Db 721 TCCTGTGCTTTCGCGGTGAAGTGTCAACGCTTATTTCTAGACTTGCAGAGTGAACAGCC 780
QY 3043 TCCAGACGCTGTGCACCAACATCTACAGAGTCTCTGCTGACAGGCGTACAGGTTTCAAG 3102
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Db 781 TCCAGACAGTCTGCTCATATATATACAGAGTCTCTGCTTCAAGGCTACAGGTTTCCATG 840
QY 3103 CATGTGTGCT 3112
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Db 841 CATGTGTGAT 850

RESULT 7
BM824748 492 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0096335 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-99-E07
DEFINITION 5', mRNA sequence.
ACCESSION BM824748
VERSION BM824748.1 GI:19181161
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 492)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 99 row: B column: 07
High quality sequence stop: 492.
Location/Qualifiers
1. 492

FEATURES
Source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-99-E07"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/clone_id="S22SNU16n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The S22SNU16 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldio, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested

cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

Query Match 11.1%; Score 445; DB 12; Length 492;
Best Local Similarity 100.0%; Pred. No. 3.7e-46;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
QY 2775 GTGAACCTCCCTGTAGAGACGAGGCCCTGGGTGGCAAGGCTTTGTTCAGATGCCGCC 2834
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Db 1 GTGAACCTCCCTGTAGAGACGAGGCCCTGGGTGGCAAGGCTTTGTTCAGATGCCGCC 60
QY 2835 CACGGCTATTCCCTGTGTGCGGCTGCTGTGATACCCCGGACCTGTGAGGTGACAGAGC 2894
|||||
Db 61 CACGGCTATTCCCTGTGTGCGGCTGCTGTGATACCCCGGACCTGTGAGGTGACAGAGC 120
QY 2895 GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCGCTTC 2954
|||||
Db 121 GACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACTTCAACCGCGCTTC 180
QY 2955 AAGGCTGGAGAACATGCGTGCMAACTCTTTGGGCTTTCGCGCTGAGTGTACAGAGC 3014
|||||
Db 181 AAGGCTGGAGAACATGCGTGCMAACTCTTTGGGCTTTCGCGCTGAGTGTACAGAGC 240
QY 3015 CTGTTTCTGATTTGAGGTGAACAGAGCTCCAGAGCGGTGTGACCAACATCTACAAGATC 3074
|||||
Db 241 CTGTTTCTGATTTGAGGTGAACAGAGCTCCAGAGCGGTGTGACCAACATCTACAAGATC 300
QY 3075 CTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGACAGCTCCATTTCATCAGCAA 3134
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Db 301 CTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGACAGCTCCATTTCATCAGCAA 360
QY 3135 GTTGAAGAACCCCAATTTTCTGCGGCGTCACTCTGACACAGGCTCCCTGTGCTAC 3194
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Db 361 GTTGAAGAACCCCAATTTTCTGCGGCGTCACTCTGACACAGGCTCCCTGTGCTAC 420
QY 3195 TCCATCTCTGAAGCCAGAACGAGCAG 3219
|||||
Db 421 TCCATCTCTGAAGCCAGAACGAGCAG 445

RESULT 8
AA281296 389 bp mRNA linear EST 14-AUG-1997
LOCUS zt08g02.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',
DEFINITION mRNA sequence.
ACCESSION AA281296
VERSION AA281296.1 GI:1924194
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 389)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
This clone is available royalty-free through LIND; contact the
IMAGE Consortium (info@image.lind.gov) for further information.
Insert Length: 2187 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 385.
Location/Qualifiers
1. 389

FEATURES
Source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:712562"

tissue_type="germinal center B cell"
/lab_host="DH10B"
/clone_lib="NCI CGAP GCBI1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
15'-TGTTACCAATCGAAGTGGAGCGCCGCTCATTTTTTTTTTTT-3'
}. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match	9.6%	Score 385.8;	DB 9;	Length 389;
Best Local Similarity	99.5%;	Pred. No. 9.8e-39;		
Matches 387; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Best local Similarity 99.5%; Pred. No. 9.8e-39;
Matches 387; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 387; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1686	GCCAAAGTTCCTGCAC	TGGCTGATGAGTGTGTACGT	CGTCAGACTGCTCAGGCTCTTCTT	1745
Db	1	GCCAAGTTCCTGCAC	TGGCTGATGAGTGTGTACGT	CGTCAGACTGCTCAGGCTCTTCTT	60
QY	1746	TATGTACCGGAGAGACC	ACGCTTTCAAAAGAACAGAGGCTCTTTTCTACCCGGAAAGATGTCTGG	1805	
Db	61	TATGTACCGGAGAGACC	ACGCTTTCAAAAGAACAGAGGCTCTTTTCTACCCGGAAAGATGTCTGG	120	
QY	1806	AGCAAGTTGCCAAAGCAT	TGGAAATCAGACAGCACTTGAAGAGGGTGACGCTGCGGAGCTG	1865	
Db	121	AGCAAGTTGCCAAAGCAT	TGGAAATCAGACAGCACTTGAAGAGGGTGACGCTGCGGAGCTG	180	
QY	1866	TCGGAAGCAGAGGTCA	GCGCAGCATCGGGAAGCCAGGCCCTGCTGACGTCCAGACTC	1925	
Db	181	TCGGAAGCAGAGGTCA	GCGCAGCATCGGGAAGCCAGGCCCTGCTGACGTCCAGACTC	240	
QY	1926	CGCTTCATCCCCCAAG	CGCTGACGGGCTCGGCCGATTTGTGAACATGAGTACGTGCTGGGA	1985	
Db	241	CGCTTCATCCCCCAAG	CGCTGACGGGCTCGGCCGATTTGTGAACATGAGTACGTGCTGGGA	300	
QY	1986	GCCAGAAGCTTCGCG	CAGAGAAAAGAGGGCCGAGCGCTTCACCTCGAGGGTGAAAGGCACTG	2045	
Db	301	GCCAGAAGCTTCGCG	CAGAGAAAAGAGGGCCGAGCGCTTCACCTCGAGGGTGAAAGGCACTG	360	
QY	2046	TTCAGCGTGTCAACT	ATACGAGCGGGCGCG	2074	
Db	361	TTCAGCGTGTCAACT	ATACGAGCGGGCGCG	389	

RESULT 9	LOCUS	DEFINITION
BG917907	851 bp	mRNA
602820830F1	NCI_CGAP_Mam6	Mus musculus cDNA clone
IMAGE:4949887	5',	EST 05-JUN-2001
mRNA sequence.		

ACCESSION	BG917907
VERSION	BG917907.1
KEYWORDS	GI:14298383
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 851)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
DNA Sequencing by: Incyte Genomics, Inc.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.

ACCESSION CF531121
VERSION CF531121.1 GI:34583085
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 688)
NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: PYX-5.
Location/Qualifiers
1..688
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355988"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: PYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 8.6%; Score 346.2; DB 14; Length 688;
Best Local Similarity 73.9%; Pred. No. 7.3e-34;
Matches 438; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
QY 47 CCGGGCCACCCCGGATGCGCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTCGC 106
DB 63 CCGGGCTTGAGCACATGACCCGCGCTCCTGCTTGCCCCCGGCGCTCTGCTGCG 122
QY 107 CAGCCACTACCGCGAGGTGCTGCGCTGCCACGTTGCTGCGCGCGCTGGGGCCCGAGGG 166
DB 123 CAGCCGATACCGGAGGTGCTGCGCGCTGCGCACTTTGTGCGCGCGCTGGGGCCCGAGGG 182
QY 167 CTGGCGGCTGTGTCAGCGCGGGGAGACCCGGCGCTTCCGCGCGCTGGTGGCCAGTGCTT 226
DB 183 CAGCGGCTGTGTCACACCGGGGAGACCCGAAGATCTACCGCACTTGGTTGCCCAATGCTT 242
QY 227 GGTGTGCGTGGCTGGGACGACAGCGCGCGCGCGCGCGCGCGCTCTTCCGCGAGGTGTC 286
DB 243 AGTGTGATGCACTGGGGCTCAACGCTTCCAGCTGCGGACCTTCTTCCACCAAGTGTTC 302
QY 287 CTGCTGAAGAGAGCTGTGGTGGCGGAGTGTCTGAGAGGCTGTGCGAGCGCGCGGAGAGAA 346
DB 303 ATCCCTGAAGAGAGCTGTGGTGGCGGAGGTTGTGCAAGAGACTCTGCGAGCGCAACGAGAGAA 362

QY 347 CGTGTGCGCTTGGCTTGGCGCTGCTGACGGGGCCCGGGGGCCCCCGAGGCTT 406
DB 363 CGTGTGCGCTTGGCTTGGAGCTGCTTAACAGAGCCAGAGCGGGGCTCCATGGCTT 422
QY 407 CACCACAGCGTGGCGAGCTACTGCCCCAACAGCGGTGACCGACGCACTGGGGGAGCGG 466
DB 423 CACTAGTAGCGTGGCTAGCTACTGCCCCAACAGCTGTATTAGAGACCCGTGCTGAGTG 482
QY 467 GCGGTGGGGCTGCTGCTGCGCGCGCGGTGGGCGACGCTGCTGTCACTGCTGGCAGC 526
DB 483 TGCATGATGCTACTGTTGAGCCGAGTGGGCGACGACCTGCTGTACTGCTGGCACA 542
QY 527 CTGCGCGCTCTTGTGTGTGTGCTGCTGCCAGCTGGCGCTTACCAGGTGTGCGGGCCGCT 586
DB 543 CTGTGCTCTTATCTTCTGTGTGCTGCGCGCGCGCGCGCTTACCAGGGAGATGGCCAGAGC 602
QY 587 GTACCAAGCTCGCGCTGCCACTCAGGCGCGCGCGCGCGCGCGCGCTTACGTAGTGAC 639
DB 603 GTCTAAACCCCTATCTCTACTCAGCANCCTCCAGCCTTACTTACTGCTGGGCGC 655

RESULT 11
CF531069 649 bp mRNA linear EST 12-SEP-2003
LOCUS
DEFINITION UI-M-FY0-cgp-c-19-0-UI.r1 NIH_BMAP_FY0 Mus musculus CDNA clone
IMAGE:30355746 5', mRNA sequence.
ACCESSION CF531069
VERSION CF531069.1 GI:34583033
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 649)
NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: PYX-5.

Location/Qualifiers

1..649
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30355746"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: PYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National

QY 189 GACCCGCGGCTTTCCGCGGCTGTGGCCAGTGCCCTGTGTGCTGCCCTGGAGCGCA 248
DB 241 GACCCGAAGATCTACCGCACTTTGGTGCCCAATGCCCTAGTGTGATGCACTGGGGCTCA 300
QY 249 CGCCCGCCCCCGCCCGCCCTCCCTCCGCGCAGGTGTCTCTGTGAAGAGAGCTGTGCGC 308
DB 301 CAGCCTCCACTGCGCCAGCTTCTCTCCACCAAGGTGTCTATCCCTGAAGAGAGCTGTGCGC 360
QY 309 CGAGTGTCTGAGAGGCTGTGCGAGCGCGCGCGGAAGAACGTGTGCTGCTTGGCTTGGCG 368
DB 361 AGGTTGTGAGAGACTCTGCGAGCGCAACGAGAAACGTGTGCTGCTTGGCTTGGAG 420
QY 369 CTGCTGACCGGGGCG 428
DB 421 CTGCTTAACGAGCGCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 429 CTGCCCCAACACGCTGACCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 488
DB 481 TTGCCCAACACTGTATTAGAGACCGCTGCGGTGTGATGTGATGATGATGATGATGATG 540
QY 489 CGCGTGGGCGACGACGCTGTGTCTACCTGCTGTGCGACGCGCGCGCGCGCGCGCGCG 546
DB 541 CGAGTGGGCGACGACCTGTGTCTACCTGCTGTGCGACGCGCGCGCGCGCGCGCGCG 598

RESULT 13
LOCUS BQ258274 664 bp mRNA linear EST 06-MAY-2002
DEFINITION NISC_kp11904.q3 Baker mouse embryo e7.5 Mus musculus cDNA clone
IMAGE:5409222, mRNA sequence.
BQ258274
BQ258274.1 GI:20459030
EST.

KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
CDNA Library Preparation: J. Baker (Stanford University)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
info@image.llnl.gov
MG1:1845958

FEATURES
Seq primer: Sp6 primer.
Location/Qualifiers
1..664
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:5409222"
/tissue_type="embryo, late gastrula"
/dev_stage="embryo, 7.5 dpc"
/lab_host="XLI-Blue"
/clone_lib="Baker mouse embryo e7.5"
/note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA
made by oligo-dT priming. Directionally cloned into
SalI/NotI sites using the following 5' adaptor:
5'-TCGACCCACGCGTCCG-3'. Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
University)."

ORIGIN

Query Match 7.9%; Score 317.8; DB 13; Length 664;
Best Local Similarity 68.3%; Pred. No. 2.6e-30;
Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;
QY 1115 GCCCAGCCTGACTGGCGCTCGAGGCTGTGAGACCATCTTCTGGGTTCCAGGCCCTG 1174
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QY 1235 CCTGTTCTGAGCTGCTTGGGAACACGCGCAGTGCGCGCTTACCGGCTCTCTCAAGAC 1294
DB 129 CCTGTTCCACAGCTGCTGTGAAACATGACAGAGTGCCAATATGTCAAGACTCTCAGGT 188
QY 1295 GCACTGCGCGCTGCGAGCTGCGGTCAACCCAGCAGCGCGGTGTGTGCGCGGAGAGCC 1354
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QY 1355 CCAGGCTGTGTGCG 1414
DB 233 -----TGAACACCAAGCCACCGACCTCATGATTT 263
QY 1415 GCTCCGCGACACAGCAGCGCCCTGCGAGGTGTACGGCTTGTGCGCGCGCTGCGCGCG 1474
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QY 1475 GCTGTGCGCGCGCGCGCGCTTGGGCTCCAGGACACAGCGCGCTTCTCAGAGAAC 1534
DB 324 GGT 383
QY 1535 CAAGAAGTTTCATCTCCCTGGGGAAGCATGCCAAGCTCTGCTGACAGAGCTGACGTGAA 1594
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QY 1595 GATGAGCGTGGCGGAGTGGCTTGGCTGCGCAGAGAGCGCGGTTGGCTGTGTCCGCG 1654
DB 444 GATGAAGTAGAGAGATTGCCACTGCTCCGCAAGAGCGCGGAGAGAGAGAGAGAGAG 503
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LOCUS BB651920 614 bp mRNA linear EST 26-OCT-2001
DEFINITION BB651920 RIKEN full-length enriched, ES cells Mus musculus cDNA
clone C330020G14 5', mRNA sequence.
BB651920
BB651920.1 GI:16486058
EST.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 614)
JOURNAL Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okita, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shitaki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,

TITLE Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
JOURNAL RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
COMMENT Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
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Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES
Location/Qualifiers
1. 614
/organism="Mus musculus"
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCC 3']."

ORIGIN
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Matches 378; Conservative 0; Mismatches 127; Indels 1; Gaps 1;

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Db 421 CTGCTTACGAGGCGCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTAC 480
QY 429 CTGCCCAACACGCTGACCGACGACGCTGCGGGGAGCGGGCGGTGGGGCTGTGCTGCGG 488
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RESULT 15
AA299878
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DEFINITION EST12462 Uterus tumor I Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION AA299878
VERSION AA299878.1 GI:1952209
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 303)
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulder, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstein, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitch, W.M., Fritchman, J.L., Geoghegan, N.S.,
Giodak, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.B., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Yi, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungtun, J., Li, H., Weissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

TITLE JOURNAL MEDLINE PUBMED
NATURE 377 (6547 Suppl), 3-174 (1995)
96026280
7566098
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 7.2%; Score 287.4; DB 9; Length 303;
Best Local Similarity 98.7%; Pred. No. 2e-26;
Matches 299; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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QY	3575	CTTGTGCMAAACCCAGGCCAAG----GGCTTAGAGAGAGGCCAGGCCAGGCTTACCCAC		3629
Db	3601	CATGTCCGCTGAAGCGTGAAGTGTCCGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCT		3660
QY	3630	CCCTCTCAGAGCAGAGGCGCGGTATCACCAAGACAGAGCCCGCGCGTCTTGCTTC		3689
Db	3661	GAGTGTCCAGCACACCTGCGCTCT-TCACTTCCCAACAGGCTGCGCTGCCCTCACCCC		3719
QY	3690	CCAGTCACCGTCTCTGCCCCCTGAGCACATTGTTCAGCATCAGGAGGTTTCTGATCCGT		3749
Db	3720	AGGGCCAGCTTTTCTTCAACAGAGCCCGCTTCCACTCCACATAGAATAATTCATC		3779
QY	3750	CTGAATTCAGCCCATGTTCGAACCTGCGTCTGAGCTTAAACAGCTTCTACTTCTGTTG		3809
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QY	3810	TTTCTGTGTGTGGAGACCCTGAGAAGACCCCTGGAGCTCTGGAAATTTGAGTGACCA		3869
Db	3833	CACCATCCAGGTGAGAGACCCTGAGAAGACCCCTGGAGCTCTGGAAATTTGAGTGACCA		3892
QY	3870	AAGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGTCCCTGTGGGTCAA		3929
Db	3893	AAGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA		3952
QY	3930	ATTGGGGGAGGTGTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAA		3989
Db	3953	ATTGGGGGAGGTGTGTGGAGTAAATACTGAATATATGAGTTTTCAGTTTGAATAA		4012
QY	3990	AAA 3992		
Db	4013	AAA 4015		

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RESULT 2
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258C
; CURRENT APPLICATION NUMBER: US/09/990,080
; CURRENT FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1

Query Match      82.4%; Score 3306.6; DB 9; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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Db	2161	GGCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCCCCA	2220
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Db	2221	GGACAGGCTCACGGAGGTCAATGCCAGCATCATCAAAACCCAGAACAGTACTGCGTGG	2280
QY	2288	TGCGTATGCCGTGGTTCAGAAAGCCGCCCATGGGCACGTCCGCAGAGCCCTTCAAGAGCCA	2347
Db	2281	TGCGTATGCCGTGGTTCAGAAAGCCGCCCATGGGCACGTCCGCAGAGCCCTTCAAGAGCCA	2340
QY	2348	CGTCTTCACTTGAACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCAGGA	2407
Db	2341	CGTCTTCACTTGAACAGACCTCCAGCCGTACATGCGACAGTTGCTGGCTCACCTGCAGGA	2400
QY	2408	GACCAAGCCCGCTGAGGAGTACCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG	2467
Db	2401	GACCAAGCCCGCTGAGGAGTACCGTCATCGAGCAGAGCTCTCCCTGAATGAGGCCAG	2460
QY	2468	CAGTGGCCTCTTGCAGCTCTTCCATCGCTTCATGTGCCACCAAGCCGTGGCATCAGGGG	2527
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QY	2768	GACAGTGTGAACCTCCCTGTAGAAAGACGAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2827
Db	2761	GACAGTGTGAACCTCCCTGTAGAAAGACGAGGCCCTGGGTGGACAGGCTTTTGTTCAGAT	2820
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QY	2888	GCAAGCGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2947
Db	2881	GCAAGCGACTACTCCAGCTATCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCG	2940
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QY	3068	CAAGATCCTCCTGCTGCAGGCGTACAGGTTTCAACGCAATGTGTGCTGCAGCTCCCATTTCA	3127
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QY	3128	TCAGCAAGTTTGAAGAACCCCAATTCTTCTGCGGTCATCTGACACGGGCTCCCT	3187
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Db	3181	CTGCTACTCCATCCTGAAAGCCAAAGACGACAGTATGTCTGCGGCCAAAGGCGCCGC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGTGTGTTAGTGTGTACAGAGACTGAGTGAATCTG	3297

Db	3241	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGTCTCAAGCT	3300
QY	3298	GGCTTAGGAAGTCTTACCCTTTTGGCATCAGGAAGGTTTAAACCAACCACTGTCAAG	3357
Db	3301	GACTCGACACCGGTCTACCTAACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAAGCGCA	3360
QY	3358	GCTCGTCTGCCGCCCTCTTCGTGGGGTGAGCAGACCACTGATGGAAGGGACAGGAGCTG	3417
Db	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTCTGGAGGCCGAGCCAACTCCGC	3420
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QY	3575	CTTGTGCAAAACCCAGGCCAAG----GGCTTAGGAGGAGGCCAGGCCAGGCTAACCCAC	3629
Db	3601	CATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGCGCTGAGCGAGTGTCCAGCCAAAGGCT	3660
QY	3630	CCCTCTCAGAGCAGAGGCCCGGTATCAACCAAGACAGAGCCCGCGCTCTGTCTTC	3689
Db	3661	GAGTGTCCAGCACACCTGCCGTCT-TCACTTCCCAAGAGGCTGGCGCTCGGCTCCACCCC	3719
QY	3690	CCAGTCACCGTCTCTGCCCTGGACACTTGTCCAGCATCAGGAGGTTTCTGATCCGT	3749
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QY	3750	CTGAATTCAGGCCATGTCCGAACCTGGCGTCTGAGCTTAACAGCTTCTACTTCTGTTC	3809
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QY	3990	AAA 3992	
Db	4013	AAA 4015	

RESULT 3
 US-09-843-676-224
 ; Sequence 224, Application US/09843676
 ; Patent No. US20020164786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cecch, Thomas R.
 ; Lingner, Joachim
 ; Nakamura, Toru
 ; Chapman, Karen B.
 ; Morin, Gregg B.
 ; Harley, Calvin
 ; Andrews, William H.
 ; TITLE OF INVENTION: No. US20020164786A1el Telomerase
 ; NUMBER OF SEQUENCES: 225
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ;

```

STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTfT"
/note= "human telomerase reverse
transcriptase (hTfT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224

Query Match      82.4%; Score 3306.6; DB 9; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5,

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QY	368	GCTGCTGACGGGGCCCCGGGGGGCCCCCCCCCGAGGCTTACCAACCAAGCGTGGCAGCTA	427
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QY	428	CCTGCCCAACACGCTGACCGACGCACTGGGGGGAGCGGGGGCTGGGGCTGCTGCTGG	487
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QY	488	CCGCGTGGCGACGACGTGCTGTTCACTGCTGGCACGCTGCGGCTCTTGTGCTGCT	547
Db	481	CCGCGTGGCGACGACGTGCTGTTCACTGCTGGCACGCTGCGGCTCTTGTGCTGCT	540
QY	548	GGCTCCCAAGTGGCTTACAGGTGTGGGGCCCGCTGTACCACTGCGGCTCTTGTGCTGCT	607
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QY	608	TCAGCCCCGGCCCCCGCCACACGCTAGTGAACCCGAAGCGTCTGGATGCAACGGGC	667
Db	601	TCAGCCCCGGCCCCCGCCACACGCTAGTGAACCCGAAGCGTCTGGATGCAACGGGC	660
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Db	661	CTGAACCATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTTGCAGCCCCGGGTGGAG	720
QY	728	GAGCGCGGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAAGCGTGGCGC	787
Db	721	GAGCGCGGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAAGCGTGGCGC	780
QY	788	TGCCCCTGAGCCCGAGCGGACGCCCGTTGGGCAAGGGGTCTGGGGCCACCCGGGCAAGAC	847
Db	781	TGCCCCTGAGCCCGAGCGGACGCCCGTTGGGCAAGGGGTCTGGGGCCACCCGGGCAAGAC	840
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QY	908	CACCTCTTTGAGAGGTGCGCTCTCTGGCACCGGCCACTCCCAACCATCCGTGGGCGGCCA	967
Db	901	CACCTCTTTGAGAGGTGCGCTCTCTGGCACCGGCCACTCCCAACCATCCGTGGGCGGCCA	960
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QY	1088	GCCCTCCTTCTACTCAAGTCTCTGAGGCCCAAGCTGACTGGCGCTCGGAGGCTGTGGA	1147
Db	1081	GCCCTCCTTCTACTCAAGTCTCTGAGGCCCAAGCTGACTGGCGCTCGGAGGCTGTGGA	1140
QY	1148	GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGAACTCCCCGCAAGTTGCCCGCCT	1207
Db	1141	GACCATCTTCTGGGTTCCAGGGCCCTGGATGCCAGGAACTCCCCGCAAGTTGCCCGCCT	1200
QY	1208	GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGGAACCAAGCGCA	1260
QY	1268	GTCGCCCTACGGGGTCTCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTCAACCCAGC	1327
Db	1261	GTCGCCCTACGGGGTCTCTCAAGACGCACTGCCCCGTGCGAGCTGCGGTCAACCCAGC	1320
QY	1328	AGCCGGTGTCTGTGCCCCGGGAGAGCCCCCAAGGCTCTGTGGCGGGCCCCCGAGGAGAGGA	1387
Db	1321	AGCCGGTGTCTGTGCCCCGGGAGAGCCCCCAAGGCTCTGTGGCGGGCCCCCGAGGAGAGGA	1380
QY	1388	CACAGACCCCCCGTGGCTGTGTGACGCTGCTCCGCAAGCAAGCAAGCCCCCTGGCAGGTGA	1447
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QY	1448	CGGCTTCGTGGGGGCTGCTTGGCGCGGCTGTGCCCCCAAGGCTCTGGGGGCTTCAAGGA	1507

Dp	1441	CGGCTTCGTGCGGGCCTGCTGCGCCGCGGTGTGTCGCCCAAGGCTCTGGGGCTCCAGGCA	1500
QY	1508	CAACGAACGCGCTTCTCTCAGGAACACCAAGAATTCAATCTCCCTGGGAAAGCATGCCAA	1567
Dp	1501	CAACGAACGCGCTTCTCTCAGGAACACCAAGAATTCAATCTCCCTGGGAAAGCATGCCAA	1560
QY	1568	GCTCTCGCTGCAGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGCTGGCGAG	1627
Dp	1561	GCTCTCGCTGCAGAGCTGACGTGGAAGATGAGCGTGGGGACTGCGCTTGCTGGCGAG	1620
QY	1628	GAGCCCAAGGGGTGGCTGTGTTCGCGCCGACAGACACCGTCTGCGTGAAGAGATCCTGGC	1687
Dp	1621	GAGCCCAAGGGGTGGCTGTGTTCGCGCCGACAGACACCGTCTGCGTGAAGAGATCCTGGC	1680
QY	1688	CAAGTCTCTGCACCTGGCTGATGAGTGTGTACGTGCTGCACTGCTCAGGTCTTTCTTTTA	1747
Dp	1681	CAAGTCTCTGCACCTGGCTGATGAGTGTGTACGTGCTGCACTGCTCAGGTCTTTCTTTTA	1740
QY	1748	TGTCAACGGAGACCACGTTCAAAAGAACAGAGCTCTTTTCTAACCGGAAGATGTCTGGAG	1807
Dp	1741	TGTCAACGGAGACCACGTTCAAAAGAACAGAGCTCTTTTCTAACCGGAAGATGTCTGGAG	1800
QY	1808	CAAGTTGCAAAAGCATTGGAAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1867
Dp	1801	CAAGTTGCAAAAGCATTGGAAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG	1927
Dp	1861	GGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTCCG	1920
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Dp	1921	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGAATACTACGTGTTGGAGC	1980
QY	1988	CAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGTGAAGGCACTGTT	2047
Dp	1981	CAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTTCGAGGGTGAAGGCACTGTT	2040
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Dp	2101	CCTGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTGCGGGCCAGAGACC	2160
QY	2168	GCCGCCGTAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA	2227
Dp	2161	GCCGCCGTAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCCCCA	2220
QY	2228	GGAACAGGCTACCGAGGTCAATGCCACGATCATMAAATCCCAAGAACACGTACTGTGTCG	2287
Dp	2221	GGAACAGGCTACCGAGGTCAATGCCACGATCATMAAATCCCAAGAACACGTACTGTGTCG	2280
QY	2288	TCGGTATGCCGTGTCCAGAAAGGCCGCCCATGGGCACTTCGCAAGGCTTCAAGAGCCA	2347
Dp	2281	TCGGTATGCCGTGTCCAGAAAGGCCGCCCATGGGCACTTCGCAAGGCTTCAAGAGCCA	2340
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QY	2408	GACCAGCCCGCTGAGGAGTGCCTGCTCATCGACGAGAGCTCTCCCTGAATGAGGCCAG	2467
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QY	2468	CAGTGGCCTCTTGACGTCTTCTTAAGCTTCAAGCTTCAATGTCACACGCCGTGCGCATCAGGGG	2527
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Db	2521	CAAGTCCTACGTTCCAGTGGCCAGGGGATCCCGCAGGGGCTCCATTCCTCTCCACGCTGCTCTG	2580
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Db	3181	CTGCTACTCCATTCCTGAAAGCCCAAGACGCGATATGT-----GCAGTGTCTGG	3240
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QY	3358	GCTGCTGTGCCGCCCTCTCGTGGGGTGAAGCAGACACCTGATGGAAGGACAGAGAGCTG	3417
Db	3361	GCTGAGTCGGAAGCTCCCGGGAGACAGCTGACTGCCCTGGAGGCCGACCAACCGGC	3420
QY	3418	TCTGGAGCTGCATCCTTCCCACTGTCT-----GCCTG	3454
Db	3421	ACTGCCCTCAGACTTCAAGACCAATCTGGACTGATGGCCACCCGCCACAGCCAGGCGCA	3480
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Dp	3720	AGGCCAGCTTTTCCCTCACCAAGAAGCCGGCTTCCACTCCCCACATAGGAATAGTCCATC	3779
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QY	3810	TTTCTGTGTTGTGGAGACCCTGAGAAGAACCCCTGGAGCTCTGGAAATTTGGAGTGACCA	3869
Dp	3833	CACCATCCAGGTGGAGACCCTGAGAAGAACCCCTGGAGCTCTGGAAATTTGGAGTGACCA	3892
QY	3870	AAGGTGTGCCCCGTGTACACAGCGAAGAACCCCTGCACCTGATGGGGGTCCCTGTGGGTCAA	3929
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QY	3930	ATTGGGGGAGGTGCTGTGGAGTAAATACTGAATATATAGATTTTTCAGTTTGGAAA	3989
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Dp	4013	AAA 4015	

RESULT 4
US-09-953-052-1
Sequence 1, Application US/09953052
Patent No. US20020173476A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953, 052
FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052, 919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844, 419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846, 017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851, 843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854, 050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911, 312

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? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/912,951
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/915,503
? FILING DATE: 14-AUG-1997
? APPLICATION NUMBER: US 08/974,549
? FILING DATE: 19-NOV-1997
? APPLICATION NUMBER: US 08/974,584
? FILING DATE: 19-NOV-1997
? APPLICATION NUMBER: WO PCT/US97/17618
? FILING DATE: 01-OCT-1997
? APPLICATION NUMBER: WO PCT/US97/17885
? FILING DATE: 01-OCT-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Parent, Annette S.
? REGISTRATION NUMBER: 42,058
? REFERENCE/DOCKET NUMBER: 015389-003600US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4015 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 56..3454
? OTHER INFORMATION: /product= "human telomerase reverse
? transcriptase (hTRT)"
? SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1

Query Match      82.4%; Score 3306.6; DB 9; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

      8 GCAGCGCTGCGTCTCTGCTGCGCAGCAGTG3GAGAGCCCTGCGCCCGCCACCCCGCGATGCC 67
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      68 GCGCGCTCCCGCTGCGCGAGCCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCT 127
      61 GCGCGCTCCCGCTGCGCGAGCCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTGCT 120

      128 GCGCGTGCGCAGCTGCTGCGCGCGCCCTGCGGCCCGCCAGGGCTGCGGCTGTGTCAGCGCG 187
      121 GCGCGTGCGCAGCTGCTGCGCGCGCCCTGCGGCCCGCCAGGGCTGCGGCTGTGTCAGCGCG 180

      188 GGACCCGCGCGCTTTCGCGCGCGCTGTGTGCGCCCAAGTCTGTGTGCGTGCCTTGGAGCG 247
      181 GGACCCGCGCGCTTTCGCGCGCGCTGTGTGCGCCCAAGTCTGTGTGCGTGCCTTGGAGCG 240

      248 ACGCGCGCCCGCCCGCGCCCGCTCTCTCCGCCAAGTGTCTGCTGTAAGAGAGCTGTGCG 307
      241 ACGCGCGCCCGCCCGCGCCCGCTCTCTCCGCCAAGTGTCTGCTGTAAGAGAGCTGTGCG 300

      308 CCGAGTGTGTGCAAGGCTGTGCGAGCGCGCGCGCGAAGAACTGTGCTGGCTTGGCTTGGC 367
      301 CCGAGTGTGTGCAAGGCTGTGCGAGCGCGCGCGCGAAGAACTGTGCTGGCTTGGCTTGGC 360

      368 GCTGTGTGACGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 427
      361 GCTGTGTGACGGGGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420

      428 CCGCGCAACACGCTGACCGACGCACTGCGGGGGAGCGGGGGCTGTGGGGCTGTGCTGCG 487
      421 CCGCGCAACACGCTGACCGACGCACTGCGGGGGAGCGGGGGCTGTGGGGCTGTGCTGCG 480

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Db 541 GGGTCCCGAGCTGCGCTTACAGGTGTGCGGCGCGCTGTACAGCTGCGCTGCCAC 600
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Db 601 TCAGGCGCGCGCGCGCGCACAGCTAGTGAACCCGGAAGGCGTCTGGATGCCAAGCGGC 660
QY 668 CTGGAACCATAGCGTCAAGGAGGCGCGGCTCCCGCTGGGCTGCCAGCGCGCGGTGGAG 727
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Db 961 GCACCAAGCG 1020
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RESULT 5
US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cecch, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

Publication No. US20030044394A1
GENERAL INFORMATION:
APPLICANT: Gaeta, Federico C.A.
APPLICANT: Geron Corporation
TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
FILE REFERENCE: 015389-003500PC
CURRENT APPLICATION NUMBER: US/10/208,243
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/675,321
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/112,006
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: WO PCT/US99/06898
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
US-10-208-243-1

Query Match 82.4%; Score 3306.6; DB 14; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 8 GCAGCGCTGCGTCTGCTGCGCAGCAGTGGGAAGCCCTGCCCCCGCCACCCCGCGATGCC 67
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; Publication No. US20030059787A1			
GENERAL INFORMATION:			
APPLICANT: Cech, Thomas R.			
Lingner, Joachim			
Nakamura, Toru			
Chapman, Karen B.			
Morin, Gregg B.			
Harley, Calvin			
Andrews, William H.			
TITLE OF INVENTION: No. US20030059787A1e1 Telomerase			

1	NUMBER OF SEQUENCES:	225
2	CORRESPONDENCE ADDRESS:	
3	ADDRESSEE: Townsend and Townsend and Crew LLP	
4	STREET: Two Embarcadero Center, 8th Floor	
5	CITY: San Francisco	
6	STATE: California	
7	COUNTRY: United States of America	
8	ZIP: 94111	
9	COMPUTER READABLE FORM:	
10	MEDIUM TYPE: floppy disk	
11	COMPUTER: IBM PC compatible	
12	OPERATING SYSTEM: PC-DOS/MS-DOS	
13	SOFTWARE: Patentln Release #1.0, Version #1.30	
14	CURRENT APPLICATION DATA:	
15	APPLICATION NUMBER: US/10/054,611	
16	FILING DATE: 18-Jan-2002	
17	CLASSIFICATION: 536	
18	PRIOR APPLICATION DATA:	
19	APPLICATION NUMBER: 08/854,050	
20	FILING DATE: <Unknown>	
21	APPLICATION NUMBER: US 08/846,017	
22	FILING DATE: 25-APR-1997	
23	APPLICATION NUMBER: US 08/844,419	
24	FILING DATE: 18-APR-1997	
25	APPLICATION NUMBER: US 08/724,643	
26	FILING DATE: 01-OCT-1996	
27	ATTORNEY/AGENT INFORMATION:	
28	NAME: Apple, Randolph T.	
29	REGISTRATION NUMBER: 36,429	
30	REFERENCE/DOCKET NUMBER: 015389-002930US	
31	TELECOMMUNICATION INFORMATION:	
32	TELEPHONE: (415) 576-0200	
33	TELEFAX: (415) 576-0300	
34	INFORMATION FOR SEQ ID NO: 224:	
35	SEQUENCE CHARACTERISTICS:	
36	LENGTH: 4015 base pairs	
37	TYPE: nucleic acid	
38	STRANDEDNESS: single	
39	TOPOLOGY: linear	
40	MOLECULE TYPE: cDNA	
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45	/note= "human telomerase reverse	
46	transcriptase (hTRT) catalytic protein	
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53	Matches 3618; Conservative	0; Mismatches 359; Indels 46; Gaps 5;
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Db		1081	GCCCTCCTTCTACTCAGCTCTCTGAGGCCACGCTG	ACTGGCGCTCGAGGCTCGTGA		1140
OY		1148	GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGG	AGCTCCCCCGCAGGTTGCCCGCGCT		1207
Db		1141	GACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGG	AGCTCCCCCGCAGGTTGCCCGCGCT		1200
OY		1208	GCCCCACGCGCTACTGGCAATGCGGCCCCCTGT	TTCTTGAGAGTGTCTTGGGAACACGCGCA		1267
Db		1201	GCCCCACGCGCTACTGGCAATGCGGCCCCCTGT	TTCTTGAGAGTGTCTTGGGAACACGCGCA		1260
OY		1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTG	CCCCGCTGCCAGCTGCCGTACCCCA	GC	1327
Db		1261	GTGCCCCCTACGGGGTGTCTCTCTCAAGACGCACTG	CCCCGCTGCCAGCTGCCGTACCCCA	GC	1320
OY		1328	AGCCGGTGTCTGTGCCCGGAGAAAGCCCCA	GGGCTCTGTGGCGGCCCCCGAGGAGGAGGA		1387
Db		1321	AGCCGGTGTCTGTGCCCGGAGAAAGCCCCA	GGGCTCTGTGGCGGCCCCCGAGGAGGAGGA		1380

QY	1388	CACAGACCCCCCGTGCCTGGTGACGCTGCTCCGCCACAGCACAGCAGCCCCCTGGCAGGTGTA	1447
Db	1381	CACAGACCCCCCGTGCCTGGTGACGCTGCTCCGCCACAGCACAGCAGCCCCCTGGCAGGTGTA	1440
QY	1448	CGGCTTCGTGCGGGCTGCCTGCCTGCCTGGTGGTCCCCCAGGCTCTGGGGCTCCAGGCA	1507
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QY	1508	CAACGAACCGCCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAGAGATGCCAA	1567
Db	1501	CAACGAACCGCCGCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAGAGATGCCAA	1560
QY	1568	GCTCTCGCTGACGAGAGCTGACGTGGAGATGAGCGTGGGACTGCGCTTGGCTGCGCAG	1627
Db	1561	GCTCTCGCTGACGAGAGCTGACGTGGAGATGAGCGTGGGACTGCGCTTGGCTGCGCAG	1620
QY	1628	GAGCCACAGGGGTGGCTGTGTTCCGGCCGCGACAGCACCGTCTGCTGAGAGATCCTGGC	1687
Db	1621	GAGCCACAGGGGTGGCTGTGTTCCGGCCGCGACAGCACCGTCTGCTGAGAGATCCTGGC	1680
QY	1688	CAAGTTCCTGCATGCGCTGATGAGTGTGACGCGTGCAGCTGCTCAGGTCTTTCTTTTA	1747
Db	1681	CAAGTTCCTGCATGCGCTGATGAGTGTGACGCGTGCAGCTGCTCAGGTCTTTCTTTTA	1740
QY	1748	TGTCACGGAGACCAAGCTTTCAAAGAACAGGCTTTTTTCTACCGGAAGATGCTGGAG	1807
Db	1741	TGTCACGGAGACCAAGCTTTCAAAGAACAGGCTTTTTTCTACCGGAAGATGCTGGAG	1800
QY	1808	CAAGTTGCAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAGCAATTGGAATCAGACAGCACTTGAAGAGGTGCAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCGAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCGAGCATCGGGAAGCCAGGCCGCCCTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGAATACTGCTGGGAGC	1987
Db	1921	CTTCATCCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGGAATACTGCTGGGAGC	1980
QY	1988	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCGAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAGGCACTGTT	2040
QY	2048	CAGCGTGCCTCAACTACAGACGGGCGCGGCCGCCGCCCTCTGGGCGCTCTGTGCTGGG	2107
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QY	2108	CCTGAGCAGATATCCACAGGAGCTGGCGCACCTTCGTGCTGCTGCTGCGGGCCAGGACCC	2167
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QY	2168	GCCGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGGCGCGTACGACACCATCCCCA	2227
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QY	2228	GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2287
Db	2221	GGAACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCCAGAAACAGTACTGCGTGG	2280
QY	2288	TGCGTATGCCGTGTCCAGAAAGGCCGCCATGGGCAAGTCCGCAAGGCTTCAAAGGCCA	2347
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QY	2348	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACTGCAGGA	2407
Db	2341	CGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACTGCAGGA	2400
QY	2408	GACCAAGCCCGCTGAGGAGTCCGCTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2467
Db	2401	GACCAAGCCCGCTGAGGAGTCCGCTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAG	2460
QY	2468	CAGTGGCCTCTTCGACGTCCTTCTACGCTTCATGTGCCACCAAGCCGTGCGCATCAGGG	2527

Db	2461	CAGTGGCCCTCTTGACGCTCTTCTTCAAGCTTCATGTGTCACACGACCGCCGTGCATCAGGGG	2520
QY	2528	CAAGTCCTACGTCACAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTTG	2587
Db	2521	CAAGTCCTACGTCACAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTTG	2580
QY	2588	CAGCCTGTGCTACGCGCACATGAGAACAAAGCTGTTTGCGGGGATTCCGGCGGACGGGCT	2647
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QY	2708	CTTCCTCAGGACCCCTGTCCTCGAAGTGTCCCTGAGTATGGCTGCGTGTGAATTGCGGA	2767
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QY	2768	GACAGTGTGAACCTTCCCTGTAGAGAACGAGGCCCTGGGTGGCAACGCTTTGTTACAT	2827
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Db	2821	GCCGCCCCACGGCCTATTCCCTGTGTGCGGCTGCTGTGATACC CGAACCTGAGGT	2880
QY	2888	GCAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCACTTCAAACG	2947
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QY	3068	CAAGATCCTCCTGCTGACGCGGTACAGGTTTCAACGACATGTGTGTCAGCTCCCATTTCA	3127
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QY	3128	TCAGCAAGTTTGAAGAACCCCAATTTTCTCGCGCGTATCTGTGACACGGCCTCCCT	3187
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QY	3188	CTGCTACTCCATCCTGAAGCCACAGACGCAAGTATGT-----GCAGGTGCTGG	3237
Db	3181	CTGCTACTCCATCCTGAAGCCACAGACGCAAGTATGTGCTGGGGCCAAAGGCGCGCC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTATGTGTCAAGAGACTGATGTAATCTG	3297
Db	3241	CGGCCCTCTGCCCTCCGAGGCCGTGCAGTGCTGTGCCACCAAGCAATTCCTGCTCAAAGT	3300
QY	3298	GGCTTGAAGAAATTTTACCCCTTTTTCGCATCAGGAAGTGTGTTAACCAACCACTGTTCAG	3357
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QY	3358	GCTGCTGTGCCCGCCCTCTGTGTGGGGGTGAGCAGAGCACTGATGGAAGGGACAGAGCTG	3417
Db	3361	GCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCTGTGAAGGCCGACAGCCCGGC	3420
QY	3418	TCTGGAGCTGCCATCTTCCCACTTGTCT-----GCCTG	3454
Db	3421	ACTGCCCTCAGACTTCAAGAACATCCTGACTGATGGCCACCCGCCACAGCCAGGCCGA	3480
QY	3455	GGAAGCGCTGGGGGCTGTCTCTCTCTGTTTGCCCATGTGTGGATTTGGGGGCTTG	3514
Db	3481	GAGCAGACACACGACGCTGTGTACGCGCGGCTTACGTCCAGGAGGAGGGGCGGCC	3540
QY	3515	GCCTCTCTGTTTGGCCCTGTGTGGGATTTGGGCTGTCTCCCGTCCATGTGCATTAAGGCC	3574

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Db 3661 GAGTGTCCAGCACACCTGCGGCTCT-TCACTTCCCAACAGGCTGGCGCTCGGCTCCACCCC 3719

QY 3690 CCAGTCACCGTCCCTCTGCCCCCTGGACACTTTGTCACGATCAGGAGGTTCTGATCCGT 3749

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QY 3810 TTTCTGTGTGTGGAGACCCCTGAGAGGACCCCTGGAGACTCTGGGAATTTGAGTGAACCA 3869

Db 3833 CACCATCCAGGTGGAGACCCCTGAGAGGACCCCTGGAGACTCTGGGAATTTGAGTGAACCA 3892

QY 3870 AAGGTGTCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGCGTCAA 3929

Db 3893 AAGGTGTGCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGCGTCAA 3952

QY 3930 ATTGGGGGGAGGTGTGTGGGAGTAAATACTGAATATATGAGTTTTCAGTTTGA AAA 3989

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QY 3990 AAA 3992

Db 4013 AAA 4015

RESULT 9
US-10-10

Sequence 1, Application US/10105963

Publication No. US20030068818A1

; GENERAL INFORMATION:

APPLICANT: Dennis, Chris

APPLICANT: Clark, A. John

APPLICANT: Schiff, J. Michael

TITLE OF INVENTION: Animal Tissue

TITLE OF INVENTION: Transplantati

TITLE OF INVENTION: Recombination
FILE REFERENCE: 731/002

CURRENT APPLICATION NUMBER: US/10/105.963

CURRENT FILING DATE: 2002-03-21

PRIOR APPLICATION NUMBER: US 60/277,811

PRIOR FILING DATE: 2001-03-2

NUMBER OF SEQ ID NOS: 40

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; SOFTWARE: PACEMCIII VERSION 3.1
; SEND TO NO 1

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LENGTH: 4015

TYPE: DNA

ORGANISM: *Homo sapiens*

FEATURE:

NAME/KEY: CDS (3454)

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; LOCATION: (56) .. (3454)
; OTHER INFORMATION:

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Query Match 82.4%; Score 3306.6; DB 14; Length 4015;

Best Local Similarity 89.9%; Pred. No. 0;

Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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68 GCGCGCTCCCCGCTGCCGAGCCCGTGGCTCCCTGCTGCCGAGCCACTACCGCGAGGTGCT 127

Db 61 GCGGCTCCCGCTGCGAGCCGCTGCTCCCTGCTGCGCAGCACTACCGAGGTGCT 120
QY 128 GCGGCTGCGCAGCTTGTGCGCGCCTGCGGACCCAGGCTGCGGCTGTGACGCGG 187
Db 121 GCGGCTGCGCAGCTTGTGCGCGCCTGCGGACCCAGGCTGCGGCTGTGACGCGG 180
QY 188 GGACCCGCGGCTTCCGCGCTGTGCGCAGTGTGCTGTGCTGTGCTGTGCGGAC 247
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QY 1448 CCGCTTGTGCG 1507
Db 1441 CCGCTTGTGCG 1500
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Db 1501 CAACGAGCGCGCGCTTCTCTCAGAGACCAAGAAATTCTCTCTGCGGAGCA 1560
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QY 1688 CAAGTCTGTGCACTGCGTGTGATGATGTGTGATGATGATGATGATGAT 1747
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RESULT 10

US-10-044-692-1

; Sequence 1, Application US/10044692

; Publication No. US20030096344A1

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Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND

THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-692-1

Query Match 82.4%; Score 3306.6; DB 14; Length 4015;
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Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

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QY 3990 AAA 3992
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RESULT 11

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; Sequence 1, Application US/10044539
; Publication No. US2003010093A1

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APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

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Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse transcriptase (hTERT) catalytic protein component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1

Query Match 82.4%; Score 3306.6; DB 14; Length 4015;
Best Local Similarity 89.9%; Pred. No. 0;
Matches 3618; Conservative 0; Mismatches 359; Indels 46; Gaps 5;

QY 8 GCAGCGTGCCTCTCTGTCGACAGTGGAGACCTTGCCCGGCGACCCCGCATGCC 67
Db 1 GCAGCGTGCCTCTCTGTCGACAGTGGAGACCTTGCCCGGCGACCCCGCATGCC 60
QY 68 GCGCGTCCCGCTGTCGAGCGCGTGCCTCTCTGTCGAGCGACCTTACCGAGGTCT 127
Db 61 GCGCGTCCCGCTGTCGAGCGCGTGCCTCTCTGTCGAGCGACCTTACCGAGGTCT 120
QY 128 GCCGTGCCACGCTTCTGTCGCGCGCTGGGCGCCAGGGCTGGCGCTGTACGCGCG 187
Db 121 GCCGTGCCACGCTTCTGTCGCGCGCTGGGCGCCAGGGCTGGCGCTGTACGCGCG 180
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Db 181 GAACCGCGCGCTTCTGTCGCGCGCTGGGCGCCAGGTGTGTGTGTGTGTGTGTGT 240
QY 248 ACG 307
Db 241 ACG 300
QY 308 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTGTGTGTGTGTGTGT 367
Db 301 CCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGTGTGTGTGTGTGTGT 360
QY 368 GCTGTGAGCG 427
Db 361 GCTGTGAGCG 420
QY 428 CCG 487
Db 421 CCG 480
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Db 481 CCGCGTGGCGAGAGCTGTGTCTTCACTGCTGCGACGCTGGCGCTTTGTGTGTGT 540
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Db 541 GCGTCCAGCTGCGCTTACAGAGTGTGGCGCGCGCGCGCTGTACAGAGTGGCGCTGC 600
QY 608 TCAGGCG 667
Db 601 TCAGGCG 660
QY 668 CTGAACCATAGCTCAGGAGCGCGCGGTCCCGCTGGCGCTGCAAGCCCGGCTGCGAG 727

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Db	721	GAGCGCGGGGCGAGTGCCAGCCGGAAGTCTGCCGTTGCCCAAGAGCCCGAGCGTGCGC	780
Qy	788	TGCCCTGAGCCGAGCGGAGCGCCGTTGGGCAAGGGTCTGGGCCACCCGGCAGGAC	847
Db	781	TGCCCTGAGCCGAGCGGAGCGCCGTTGGGCAAGGGTCTGGGCCACCCGGCAGGAC	840
Qy	848	GCGTGAGCCGAGTGACCGTGTTCTGTGTGTCACTGCCAGACCCCGGAAGAC	907
Db	841	GCGTGAGCCGAGTGACCGTGTTCTGTGTGTCACTGCCAGACCCCGGAAGAC	900
Qy	908	CACCTCTTTGAGAGGCTGCGCTCTTGGCACGCGCACTCCACCCATCCGTGGCGGCCA	967
Db	901	CACCTCTTTGAGAGGCTGCGCTCTTGGCACGCGCACTCCACCCATCCGTGGCGGCCA	960
Qy	968	GCAACCAAGCGGGCCCCCATCCATCCGCGGCCACCACTCCCTGGGACACGCTTTGTCC	1027
Db	961	GCAACCAAGCGGGCCCCCATCCATCCGCGGCCACCACTCCCTGGGACACGCTTTGTCC	1020
Qy	1028	CCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCCTCAGGCGACAAGAGCAGCTGCG	1087
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Qy	1088	GCCCTCCTTCTACTAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAAGGCTCGTGA	1147
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Qy	1148	GACCATCTTCTGAGGTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTGCCCGCCT	1207
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Qy	1208	GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACCAAGCGCA	1267
Db	1201	GCCCCAGCGCTACTGGCAAAATGCGGCCCTGTTTCTGAGCTGCTTGGAAACCAAGCGCA	1260
Qy	1268	GTGCCCCCTACGGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGTCACCCCAGC	1327
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Qy	1328	AGCCCGTGTCTGTGCCCCGGAGAAAGCCCCAGGGCTCTGTGCGCGCCCCCGAGAGAGGA	1387
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Db	1381	CACAGACCCCCGTCGCTGTGTGACGCTGTCTCCGCCAGACAGCAAGCCCCCTGGCAGGTGA	1440
Qy	1448	CGGCTTGTGCGGGGCTGCTCGCCCGGCTGGTGTGCCCCCCAGGCCCTCTGGGGCTCCAGGA	1507
Db	1441	CGGCTTGTGCGGGGCTGCTCGCCCGGCTGGTGTGCCCCCCAGGCCCTCTGGGGCTCCAGGA	1500
Qy	1508	CAACGAACGCGCTTCTCTCAGGAACAACCAAGAAATCAATCTCCCTGGGGAAGCATGCCAA	1567
Db	1501	CAACGAACGCGCTTCTCTCAGGAACAACCAAGAAATCAATCTCCCTGGGGAAGCATGCCAA	1560
Qy	1568	GCTCTCGCTGCAAGAGCTGACCTGGAAGATGAGCGTGGGGGAAGCTGCGCTTGGCTGCGAG	1627
Db	1561	GCTCTCGCTGCAAGAGCTGACCTGGAAGATGAGCGTGGGGGAAGCTGCGCTTGGCTGCGAG	1620
Qy	1628	GAGCCCAAGGGGTTGGCTGTGTTCGGGCGCAGAGCACCGTCTGCGTGAGAGATCTGGC	1687
Db	1621	GAGCCCAAGGGGTTGGCTGTGTTCGGGCGCAGAGCACCGTCTGCGTGAGAGATCTGGC	1680
Qy	1688	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCAGCTGCTCAGGCTCTTCTTTTA	1747
Db	1681	CAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCAGCTGCTCAGGCTCTTCTTTTA	1740
Qy	1748	TGTACGGAGACCAAGTTCAAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGAG	1807

Db	1741	TGTCACGGAGACCACGCTTTCAAAAGAACAGGCTCTTTTCTACCCGGAAAGTGTCTGGAG	1800
QY	1808	CAAGTTGCAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGTGCAGCTGCGGAGCTGTC	1867
Db	1801	CAAGTTGCAAAGCATTTGGAATCAGACAGCACTTGAAGAAGGTGCAGCTGCGGAGCTGTC	1860
QY	1868	GGAAGCAGAGGTCAGGCGAGCATCGGGAAAGCCAGGCGCCCTTGCTGACGTCCAGACTCCG	1927
Db	1861	GGAAGCAGAGGTCAGGCGAGCATCGGGAAAGCCAGGCGCCCTTGCTGACGTCCAGACTCCG	1920
QY	1928	CTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTCGTGGAGC	1987
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QY	1988	CAGAACGTTCCGCAAGAAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT	2047
Db	1981	CAGAACGTTCCGCAAGAAAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAGGCACTGTT	2040
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Db	2041	CAGCGTCTCAACTPACGAGCGGGCGCGCCGCCCTCCTGCGGCGCTCTGTCTGGG	2100
QY	2108	CCTGACGATATCCACAGGGCCTGGCGCACCTTGTGCTGCGTGTGCGGGCCAGAGACC	2167
Db	2101	CCTGACGATATCCACAGGGCCTGGCGCACCTTGTGCTGCGTGTGCGGGCCAGAGACC	2160
QY	2168	GCCGCGCTGAGCTGTACTTTGTCAAGGTGGATGACCGGGCGGTACGACACCATCCCCA	2227
Db	2161	GCCGCGCTGAGCTGTACTTTGTCAAGGTGGATGACCGGGCGGTACGACACCATCCCCA	2220
QY	2228	GGACAGGCTCACGGAGGTCACTGCCAGCATCATCAAAACCCAGAACACGTACTGCGTCCG	2287
Db	2221	GGACAGGCTCACGGAGGTCACTGCCAGCATCATCAAAACCCAGAACACGTACTGCGTCCG	2280
QY	2288	TCCGTATGCCGTGGTCCAGAAAGCCGCCATGGGCACTGCCGAAGGCTTCAAGAGCCA	2347
Db	2281	TCCGTATGCCGTGGTCCAGAAAGCCGCCATGGGCACTGCCGAAGGCTTCAAGAGCCA	2340
QY	2348	CGTCTTACCTTGAACAGACCTCCAGCCGTACATGCGACAGTTGCTGCGTCACTGCAGGA	2407
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QY	2408	GACCAGCCCGCTGAGGGATGCCGTCGTCAATGACAGACAGCTCCTCCCTGAATGAGCCAG	2467
Db	2401	GACCAGCCCGCTGAGGGATGCCGTCGTCAATGACAGACAGCTCCTCCCTGAATGAGCCAG	2460
QY	2468	CAGTGGCCTCTTGCAGCTCTTCTCTACGCTTCAATGTGCCACACGCGCTGCGCATCAGGGG	2527
Db	2461	CAGTGGCCTCTTGCAGCTCTTCTCTACGCTTCAATGTGCCACACGCGCTGCGCATCAGGGG	2520
QY	2528	CAAGTCTACTAGTCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2587
Db	2521	CAAGTCTACTAGTCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTG	2580
QY	2588	CAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTGGGGGATTCGGCGGGAACGGGCT	2647
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QY	2648	GCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGAACACCTCACCTCACCCACGCGAAAC	2707
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QY	2768	GACAGTGTGTAACCTCCCTGTAGAAACGAGCCCTGGGTGGACCGGCTTTTGTTCAGAT	2827
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QY	2828	GCCGGCCACGCGCTATTCCCTGTGTGGCGGCTGCTGTGATACCCGGAACCTTGAGGT	2887
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QY	2888	GCAGAGCGACTACTCCAGCTATATGCCCGGACCTCCATCAGAGCCAGTCTCAACCTTCAACCG	2947
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QY	2948	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3007
Db	2941	CGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGTG	3000
QY	3008	TCACAGCCTGTTTCTGGAATTTGCAGGTGAACAGCCTCCAGACCGGTGTGCACCAACATCTA	3067
Db	3001	TCACAGCCTGTTTCTGGAATTTGCAGGTGAACAGCCTCCAGACCGGTGTGCACCAACATCTA	3060
QY	3068	CAAGATCCTCCTGCTGAGGCGGTACAGGTTTCAACGCAATGTGTCTGCAGCTCCCAATTTCA	3127
Db	3061	CAAGATCCTCCTGCTGAGGCGGTACAGGTTTCAACGCAATGTGTCTGCAGCTCCCAATTTCA	3120
QY	3128	TCAGCAAGTTTGAAGAACCCCAACATTTTCTGCGGTCATCTGTACACAGGCTCCCT	3187
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QY	3188	CTGCTACTCCATCCTGAAAGCCCAAGAACGACAGTATGT-----GCAGTGCCTGG	3237
Db	3181	CTGCTACTCCATCCTGAAAGCCCAAGAACGACAGGATGTGCTGGGGCCAAAGGGCGCGC	3240
QY	3238	CCTCAGTGGCAGCAGTGCCTGCTGCTGTGTAGTGTCTCAGAGACTGAGTGAATCTG	3297
Db	3241	CGGCCCTGTGCTCCGAGGCGGTGACGTGGCTGTGCCAACAAACATTCCTGTCAAAGCT	3300
QY	3298	GGCTTAGGAAGTTCTTAACCCCTTTTCGATCAGAAAGTGTTTAACCACCACTGTTCAG	3357
Db	3301	GACTCGACACCGTGTCACTTACGTGCCACTCCTGGGTCACTCAGACAGCCCAAGCGCA	3360
QY	3358	GCTGCTGCCCGCCCTCTGCTGGGTGAGCAGACCACTGATGGAAGGACAGAGACTG	3417
Db	3361	GCTGAGTCGAAGCTCCCGGGGACGACGCTGACTGCTGGAGCGCAGCCCAACCCGCGC	3420
QY	3418	TCTGGAGCTGCATCCTTCCCACTGTCT-----GCCTG	3454
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QY	3515	GCCTCTCCTGTTTGCCTGTGTGGATTGGGCTGTCTCCCGTCCATGCACTTAAGGCC	3574
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QY	3630	CCCTCTCAGAGCAGAGGCGCGCTATCACCAACGACAGACCCCGCGCGCTCCTGTGCTTC	3689
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QY	3690	CCAGTCACCGTCTCTGCGCCCTGGAACACTTTGTCCAGCATCAGGGAGTTTCTGATCCGT	3749
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QY	3810	TTTCTGTGTGTGAGAACCTCTGAGAAGAACCCCTGGAGCTCTGGGAATTTGGAGTGAACA	3869
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QY	3990	AAA	3992		
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RESULT 12

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: Sequence 1, Application US/10385882
: Publication No. US20030232409A1
: GENERAL INFORMATION:
: APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
: APPLICANT: FARRIS, James
: APPLICANT: FOSTER, Douglas
: APPLICANT: O'GRADY, Scott
: TITLE OF INVENTION: IMMORTAL PORCINE CELLS
: FILE REFERENCE: 110.01700101
: CURRENT APPLICATION NUMBER: US/10/385,882
: CURRENT FILING DATE: 2003-03-11
: PRIOR APPLICATION NUMBER: 60/363,129
: PRIOR FILING DATE: 2002-03-11
: NUMBER OF SEQ ID NOS: 5
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 4027
: TYPE: DNA
: ORGANISM: ARTIFICIAL
: FEATURE:
: OTHER INFORMATION: Nucleotide sequence encoding telomerase reverse transcriptase
US-10-385-882-1

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Query Match	82.4%;	Score 3304.6;	DB 15;	Length 4027;
Best Local Similarity	89.8%;	Pred. No. 0;		
Matches 3619;	Conservative	0;	Mismatches 364;	Indels 46;
				Gaps 5;

QY	13	GCTGCGTCTGCTGCGCAGCAGCTGGGAAAGCCCTGGGCCCCCGGCCAACCCCCCGGATGCGCGG	72
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QY	73	CTCCCCGCTGCGCGAGCCGCTGGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCTGCCG	132
Db	67	CTCCCCGCTGCGCGAGCCGCTGGCGCTCCCTGCTGCGCAGCCACTACCGGAGGTGCTGCCG	126
QY	133	TGGCCACGTTGCTGCGCGCGCGCTGGGGGCCCCAGAGGCTGGCGGCTGTGTGACGCGCGGGACC	192
Db	127	TGGCCACGTTGCTGCGCGCGCGCTGGGGGCCCCAGAGGCTGGCGGCTGTGTGACGCGCGGGACC	186
QY	193	CGGCGGCTTTCCGCGCGCTGTGTGCCCCAGTGCCCTGTGTGCGTGCCCTGGAGCGACGGC	252
Db	187	CGGCGGCTTTCCGCGCGCTGTGTGCCCCAGTGCCCTGTGTGCGTGCCCTGGAGCGACGGC	246
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Db	247	CGCCCCCGCGCGCCCTCTCTTCGCGCAGGTGCTCTGCTGAAGGAGCTGTGGCCGAG	306
QY	313	TGCTGCAGAGGCTGTGCGAGCGCGCGCGCGGAGAACGTGCTGGCCTTCGGCTTCGCGTGC	372
Db	307	TGCTGCAGAGGCTGTGCGAGCGCGCGCGCGGAGAACGTGCTGGCCTTCGGCTTCGCGTGC	366
QY	373	TGACGCGGCCCCCGCGGGGGCCCCCCCCGAGGCTTCAACACAGCGTGCAGCTACTGC	432
Db	367	TGACGCGGCCCCCGCGGGGGCCCCCCCCGAGGCTTCAACACAGCGTGCAGCTACTGC	426
QY	433	CCAACACGGTGAACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGCGCGCGG	492
Db	427	CCAACACGGTGAACCGACGCACTGCGGGGGAGCGGGGCGTGGGGGCTGCTGTCGCCCGG	486
QY	493	TGGCGGACGAGCTGCTGCTGTTCACTGCTGGGACGCTGCGCGCTCTTGTGCTGGTGGCTC	552
Db	487	TGGCGGACGAGCTGCTGCTGTTCACTGCTGGGACGCTGCGCGCTCTTGTGCTGGTGGCTC	546

Db	2707	TCAGGACCCTGTCCGAGGTGTCCCTTGAGTATGGCTGCGGTGTGAACCTTGCAGAAACAG	2766
Qy	2773	TGTTGAACCTTCCCTGTATGAGAAGAGGCCCCCTGGGTGGCACGGCTTTTGTTCAGATGCCG	2832
Db	2767	TGTTGAACCTTCCCTGTATGAGAAGAGGCCCCCTGGGTGGCACGGCTTTTGTTCAGATGCCG	2826
Qy	2833	CCCAAGGCTATTTCCCTGGTGGCGGCTGTGCTGTGATACCCGAGCCCTGAGGTGCAGA	2892
Db	2827	CCCAAGGCTATTTCCCTGGTGGCGGCTGTGCTGTGATACCCGAGCCCTGAGGTGCAGA	2886
Qy	2893	GCGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAACCCGCGCT	2952
Db	2887	GCGACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACTTCAACCCGCGCT	2946
Qy	2953	TCAAGGCTGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGGGCTGAAGTGTACA	3012
Db	2947	TCAAGGCTGGAGGAACATGCGTCCGAAACTCTTTGGGGTCTTGGGCTGAAGTGTACA	3006
Qy	3013	GCCTGTTTCTGATTGTGCAAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAGA	3072
Db	3007	GCCTGTTTCTGATTGTGCAAGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAGA	3066
Qy	3073	TCCTCTCTGTGACGGCGTACAGGTTTACGCGATGTGTGTGACAGCTCCCATTTTATCAGC	3132
Db	3067	TCCTCTCTGTGACGGCGTACAGGTTTACGCGATGTGTGTGACAGCTCCCATTTTATCAGC	3126
Qy	3133	AAGTTTGAAGAACCACCATTTTTCCTGCGCGTATCTGTACACGGGCTCCCTGTGCT	3192
Db	3127	AAGTTTGAAGAACCACCATTTTTCCTGCGCGTATCTGTACACGGGCTCCCTGTGCT	3186
Qy	3193	ACTCCATCCTGAAAGCCAGAAACGACAGTATGT-----GCAGGTGCTGGCCTCA	3242
Db	3187	ACTCCATCCTGAAAGCCAGAAACGACAGTATGTCTGGGGGCCAAGGGCGCGCGCGCC	3246
Qy	3243	GTGGCAGCAGTGCCTGCTGCTGTGTAGTGTGTGACAGACTGAGTGAATCTGGGCTT	3302
Db	3247	CTTGCCTCCGAGGCGCGTGCAGTGGCTGTGCCACAGCATTCCTGCTCAAGCTGACTC	3306
Qy	3303	AGGAAGTCTTACCCTTTTCGATCAGGAAGTGGTTAACCAACCACTGTCAAGCTCG	3362
Db	3307	GACACCGTGTACCTACGTGTGCCACTCTCGGGTCACTAGAGACAGCCAGCGAGCTGA	3366
Qy	3363	TCTGCCCGCCCTCTCGTGGGGTGAACAGACGACCTGATGAAAGGACAGAGAGCTGTCTGG	3422
Db	3367	GTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGAGGCCGACCAACCCGGCACTGC	3426
Qy	3423	GAGCTGCCATCCTTCCCACTTGTCT-----GCTTGGGAA	3459
Db	3427	CCTCAGACTTCAAGACCATCTCTGACTGATGGCCACCCGCCACAGCCAGCGCGAGACA	3486
Qy	3460	GCGCTGGGGGCGCTGTCTCTCTCTGTTTGCCCATGTGTGGATTGGGGGGCGCTGCGCTC	3519
Db	3487	GACACCAAGCAGCCCTGTGTACGCCGGCTCTACGTCCAGGGAGGGAGGGGGCGGCCACAC	3546
Qy	3520	TCCTGTGTTGCCCTGTGTGGGGATTGGGCTGTCTCCCGTCCATGGCACTTAGGGCCCTGT	3579
Db	3547	CCAGGCCCGCACCGCTGGAGTCTGAGGCTGAGTGAAGTGTGGCCGAGGCTTGATGT	3606
Qy	3580	GCAAAACCCAGGCCAAG----GGCTTAGAGAGAGGCCAGCCCAAGCTAACCCCAACCCCTC	3634
Db	3607	CCGGCTGAAGGCTGAGTGTCCGGGCTGAGGCTGAGCGAGTGTCCAGCCAAAGGCTGAGTG	3666
Qy	3635	TCAGGAGCAGAGCGCGCTATTCACACGACAGAGAGCCCGCGCGCTGTGCTTCCAGT	3694
Db	3667	TCCAGCACACCTGCGGTCT-TCACCTTCCCAAGGCTGGCGCTCGGCTCCACCCAGGGC	3725
Qy	3695	CACCGTCTCTGCCCCCTGACACTTTGTCCAGCATCAGGAGGTTTCTGATCCGTCTGAA	3754
Db	3726	CAGCTTTTCTCACCAGAGAGCCCGGCTTCCACTCCCAATAGGAATAGTCATCCCAAG	3785
Qy	3755	ATTCAAGCATGTGAACTGCGGCTCTGAGCTTAAAGCTTCTACTTCTGTCTTCT	3814

Db	3786	ATTGCCAATTGTTCACCCCCT-----CGCCCTGCCCCCTCCCTTTGCTTGCACCCCCCACCACCA	3838
QY	3815	GTGTTGTGAGAGACCCCTGAGAAAGAACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGT	3874
Db	3839	TCCAGGTGAGACCTCTGAGAAAGAACCCCTGGAGCTCTGGGAATTTGAGTGAACCAAGT	3898
QY	3875	GTGCCCTGTACACAGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGG	3934
Db	3899	GTGCCCTGTACACAGCGGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGG	3958
QY	3935	GGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA	3994
Db	3959	GGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTTTTTCAGTTTTTGAAAAAAA	4018
QY	3995	AAAAAAAAA 4003	
Db	4019	AAAAAAAAA 4027	

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RESULT 13
US-09-749-728B-32 ; Sequence 32, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOCYTES
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749, 728B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT-JP00-372826
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: PCT-JP00-01148
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: PCT-JP00-07741
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver.2.0
; SEQ ID NO 32
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: (1)..(3399)
US-09-749-728B-32

Query Match          78.8%; Score 3161.4; DB 9; Length 3396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      63 ATGCCGCGCGCTCCCCGGCTGCAGACCGGTCCCTCCTGCGCAGCACTAACCGCGAG 122
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Db       1 ATGCCGCGCGCTCCCCGGCTGCAGACCGGTCCCTCCTGCGCAGCACTAACCGCGAG 60

QY      123 GTGTCGCCGCTGGCCACGTTGCTGCGCGCGCCTGGGGCCCCAGGGGCTGGCGCTGTGCAG 182
        |||||||
Db       61 GTGTCGCCGCTGGCCACGTTGCTGCGCGCGCCTGGGGCCCCAGGGGCTGGCGCTGTGCAG 120

QY      183 CGCGGGGACCCCGCGGCTTCCGCGCGCTGTGCGCCAGTGCTGTGTGCGTGCCCTGG 242
        |||||||
Db       121 CGCGGGGACCCCGCGGCTTCCGCGCGCTGTGCGCCAGTGCTGTGTGCGTGCCCTGG 180

QY      243 GACGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 302
        |||||||
Db       181 GACGCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240

QY      303 GTGCGCGCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGCGAGAAGACGTGCTGGCCTTGGC 362

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[illegible]

Db	1321	GAGGACACAGACCCCCCTCGCCTGTGTGACGTCCTCCGACAGCACAGCAGCCCTGGCAG	1380
QY	1443	GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGCTGTGTGCCCCCAGGCTCTGGGGCTCC	1502
Db	1381	GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGCTGTGTGCCCCCAGGCTCTGGGGCTCC	1440
QY	1503	AGGCACAACGAACGCGCCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCAT	1562
Db	1441	AGGCACAACGAACGCGCCTTCTCAGGAACACCAAGATTCATCTCCCTGGGGAAGCAT	1500
QY	1563	GCCAAAGCTCTCGCTGACGAGACTGACGTGAAGATGAGCGTGCGGGACTGCGCTTGCTG	1622
Db	1501	GCCAAAGCTCTCGCTGACGAGACTGACGTGAAGATGAGCGTGCGGGACTGCGCTTGCTG	1560
QY	1623	CGCAGAGCCCCAGGGGTTGGCTGTGTTCGCGCCGACAGACCCGTCGTGCTGAGAGATC	1682
Db	1561	CGCAGAGCCCCAGGGGTTGGCTGTGTTCGCGCCGACAGACCCGTCGTGCTGAGAGATC	1620
QY	1683	CTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTATCGTCGAGCTGCTCAGTCTTTC	1742
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QY	1803	TGAGACAAAGTTGCAAAGCATTTGGAATCAGACACTTGAAGAGGGTGCAAGCTCCGGAG	1862
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QY	1863	CTGTGGAAGCAGAGGTCAGGCACGATCGGGAGCCAGCCCGCTGTGAAGTCCAGA	1922
Db	1801	CTGTGGAAGCAGAGGTCAGGCACGATCGGGAGCCAGCCCGCTGTGAAGTCCAGA	1860
QY	1923	CTCCGCTTCATCCCCCAAGCCTGACCGGGCTGCGCCGATTGTGAACATGGAATACTGCTG	1982
Db	1861	CTCCGCTTCATCCCCCAAGCCTGACCGGGCTGCGCCGATTGTGAACATGGAATACTGCTG	1920
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QY	2043	CTGTTACGCGTGTCTCACTACGAGCGGGCGCGCCCGCCTCCTGGCGCCTCTGTG	2102
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QY	2163	GACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCATC	2222
Db	2101	GACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACCATC	2160
QY	2223	CCCCAGACAGGCTCACGAGGTCATCGCCACGATCATCAAACCCAGAACACGTACTGC	2282
Db	2161	CCCCAGACAGGCTCACGAGGTCATCGCCACGATCATCAAACCCAGAACACGTACTGC	2220
QY	2283	GTGCGTCGGTATGCCGTGTGTCAGAAAGGCCGCCATGGGCAAGTCCGCAAGGCTTCAAG	2342
Db	2221	GTGCGTCGGTATGCCGTGTGTCAGAAAGGCCGCCATGGGCAAGTCCGCAAGGCTTCAAG	2280
QY	2343	AGCCACGTCTTACTTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTCACCTG	2402
Db	2281	AGCCACGTCTTACTTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTCACCTG	2340
QY	2403	CAGGAGACCAAGCCCGCTGAGGGATGCCGTGTATCGACAGAGACTCCTCCCTGAATGAG	2462
Db	2341	CAGGAGACCAAGCCCGCTGAGGGATGCCGTGTATCGACAGAGACTCCTCCCTGAATGAG	2400
QY	2463	GCCAGCAGTGGCTCTTCGACGTCCTTCTTACGCTTCATGTGCCAACACGCGCTGCGCATC	2522
Db	2401	GCCAGCAGTGGCTCTTCGACGTCCTTCTTACGCTTCATGTGCCAACACGCGCTGCGCATC	2460

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DB 2521 CTCTGCAAGCTGTGCTACGCGGCAATGGAACAAGCTGTTGCGGGGATTGCGCGGAC 2580
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DB 2701 CGGAAGACAGTGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGCTTTGTT 2760
QY 2823 CAGATGCGGCGCCACGCGCTATTTCCCTGTGCGGCTGCTGCTGATACCCGACCTG 2882
DB 2761 CAGATGCGGCGCCACGCGCTATTTCCCTGTGCGGCTGCTGCTGATACCCGACCTG 2820
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QY 3003 AAGTGTACAGCCTGTTTCTGGAATTGCAAGTGAACAGCCTCCAGAGGCTGACCAAC 3062
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RESULT 14

US-09-843-676-173
Sequence 173, Application US/09843676
Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. US20020164786A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION: /note="preliminary sequence for human TRT cDNA insert of plasmid pGRN121"
US-09-843-676-173
Query Match
Best Local Similarity 78.8%; Score 3159.8; DB 9; Length 4029;
Matches 3577; Conservative 0; Mismatches 412; Indels 55; Gaps 13;
QY 8 GCAGCGCTGCTCTGCTGCGACAGTGGGAAGCCCTGGCCACCCCGGATGCC 67
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DB 61 GCGCGCTCCCGCTGCGGAGCCGCTGCGCTCCCTGCTGCGGACCACTACCGGAGTGTCT 120
QY 128 GCGCGTGGCCACGTTCTGCGGAGCCGCTGGGAGCCCGGATGGCGGCTGTGACGCGG 187
DB 121 GCGCGTGGCCACGTTCTGCGGAGCCGCTGGGAGCCCGGATGGCGGCTGTGACGCGG 180
QY 188 GGACCGGCGGCTTCCGCGGCTGTGCGGACAGTGTCTGTGCGTGGCGGAGCGC 247
DB 181 GGACCGGCGGCTTCCGCGGCTGTGCGGACAGTGTCTGTGCGTGGCGGAGCGC 240
QY 248 ACCGCGGCGGCGGCGGCGGCTCTTCCGCGGAGTGTCTGCTGAAGAGAGTGTGCG 307
DB 241 ANGGCGGCGGCGGCGGCGGCTCTTCCGCGGAGTGTCTGCTGAAGAGAGTGTGCG 300
QY 308 CCGAGTGTGACAGAGCTGTGCGAGCGCGGCGGCGGAGAGTGTGCGCTTGGCTTGGC 367
DB 301 CCGAGTGTGACANANGCTGTGCGAGCGCGGCGGCGGAGAGTGTGCGCTTGGCTTGGC 360
QY 368 GCTGTGACGCGGCGGCGGCGGCGGCGGCGGCGGAGGCTTCAACCAAGCGTGGAGCTA 427
DB 361 GCTGTGACGCGGCGGCGGCGGCGGCGGCGGCGGAGGCTTCAACCAAGCGTGGAGCTA 420
QY 428 CTTGCCCAACAGGTGACGAGCACTGCGGCGGAGCGGCGGCTGTGCTGCG 487

Db 421 CCTGCCCAACACGGGTGACCCGACGCACTGCGGGGAGCCGGGCGTGGGGGCTGCTGCG 480
QY 488 CCGGCTGGGGCGACGACGCTGCTGCTTCACTGCTGCGACGCTGCGGCTCTTTGTGTGTGT 547
Db 481 CCGGCTGGGGCGACGACGCTGCTGCTTCACTGCTGCGACGCTGCGGCTCTTTGTGTGTGT 540
QY 548 GGGTCCCAAGCTGCGCTACCAAGTGTGCGGGGCGCGGCTGTACCAAGCTGCGGCTGCMAC 607
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QY 608 TCAGGCG 667
Db 601 TCAGGCG 658
QY 668 CTGGAACCATAGCGCTCAGGAGGCGCGGGGTCCCGCTGGGCGCTGCGAGCGCGGGTGGAG 727
Db 659 CTGGAACCATAGCGCTCAGGAGGCGCGGGGTCCCGCTGGGCGCTGCGAGCGCGGGTGGAG 717
QY 728 GAGGCGCGGGGCGAGTGCACGCGGAAGTCTGCGCTGCGCAAGAGGCGCAAGCGTGGCGCG 787
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QY 968 GCACCAACGCGGCG 1027
Db 958 GCACCAACGCGGCG 1016
QY 1028 CCGGCTGTACGCGGAGCAACGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1087
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QY 1088 GCGCT 1146
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QY 1207 TGCCCCAGCGCTACTGGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1266
Db 1194 TGCCCCAGCGCTACTGGCAATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1253
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QY 1387 -ACACAGACCGCGCTGCGCTGTGTGAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1445
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Db 1434 TACGCGTTCGTGCGGCG 1493
QY 1506 CACCAACGACGCGCGCTTCTCTAGGAACACCAAGAACTTCTCTCTCTCTCTCTCTCTCTCTCT 1565
Db 1494 CACCAACGACGCGCGCTTCTCTAGGAACACCAAGAACTTCTCTCTCTCTCTCTCTCTCTCTCT 1553

QY 1566 AAGCTCTGCTGACAGAGCTGACGTTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGC 1625
Db 1554 AAGCTCTGCTGACAGAGCTGACGTTGGAAGATGAGCGTGGGAGCTGCGCTTGGCTGCGC 1613
QY 1626 AGGAGCCAGGGGTTGGCTGTGTTCGCGCGCAGAGCAACGCTGCGTGAAGAGATCTCTG 1685
Db 1614 AGGAGCCAGGGGTTGGCTGTGTTCGCGCGCAGAGCAACGCTGCGTGAAGAGATCTCTG 1673
QY 1686 GCCAGTTCTGCACTGGCTGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1745
Db 1674 GCCAGTTCTGCACTGGCTGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1733
QY 1746 TATGTCAACGAGACCAAGCTTTCAAAAGACAGGCTTTTCTACCGGAAGTGTCTGG 1805
Db 1734 TATGTCAACGAGACCAAGCTTTCAAAAGACAGGCTTTTCTACCGGAAGTGTCTGG 1793
QY 1806 AGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACGCTGCGGAGCTG 1865
Db 1794 AGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGTGACGCTGCGGAGCTG 1853
QY 1866 TCGGAAGCAGAGGTCAAGGAGCATCGGGAAGCCAGCGCGCGCGCGCGCGCGCGCGCGCG 1925
Db 1854 TCGGAAGCAGAGGTCAAGGAGCATCGGGAAGCCAGCGCGCGCGCGCGCGCGCGCGCGCG 1913
QY 1926 CGCTTCATCCCAAGCGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1985
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QY 1986 GCCAAGACGTTCCGCAAGAAAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2045
Db 1974 GCCAAGACGTTCCGCAAGAAAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2033
QY 2046 TTCAGCGTGTCAACTTACAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2105
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QY 2346 CAGCTCTTACTTGAAGACCTCCAGCGCTATCGACAGTTCGTGCTCACTGCGAG 2405
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QY 2586 TGACGCTGTGTACGCGCAGATGAGAAACAGCTGTTGCGGAGATTCGCGGAGACGCGG 2645
Db 2574 TGACGCTGTGTACGCGCAGATGAGAAACAGCTGTTGCGGAGATTCGCGGAGACGCGG 2633

QY	2646	CTGCTCCTCGCGTTTGGTGGATGATTCTTGTGTGGTGAACACTCACTCAACCCACGGCAAA	2705
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QY	3066	TACAAGATCCTCCTGCTGCAGGCGGTACAGGTTTCAACGATGTGTGCTGCAGCTCCCATTT	3125
Db	3054	TACAAGATCCTCCTGCTGCAGGCGGTACAGGTTTCAACGATGTGTGCTGCAGCTCCCATTT	3113
QY	3126	CATCAGCAAGTTTGAAGAACCCCAATTTTCTCTGCGGCTCATCTTGACAACGGCTTCC	3185
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QY	3186	CTCTGCTACTCCATCCTTGAAAGCCCAAGAACGCAAGTATGT-----GCAGTGGCTT	3235
Db	3174	CTCTGCTACTCCATCCTTGAAAGCCCAAGAACGCAAGTATGTGGGGGCCAAGGGCGCC	3233
QY	3236	GGCCTCAGTGGCAGCAGTGGCTGCTGCTGTGTAGTGTGTCAGAGACTGAGTGAATC	3295
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QY	3416	TGTCTGGAGCTGCCATCCTTCCCACTTGTCT-----GCC	3452
Db	3414	GCACTGCCCTCAGACTTCAAGACCATCTGTGACTGATGGCAACCGCCACAGCCAGGCC	3473
QY	3453	TGGGGAAGCGCTGGGGGCGCTGCTCTCTCTGTTTGCACCATGTGGATTTGGGGGCC	3512
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Db	3594	TGCATGTTCGGCTGAAGGCTGAGTGTCCGGCTGAGGCGCTGAGCGAGTGTCCAAGCCAAAGG	3653
QY	3628	ACCCCTCTCAGGAGCAGAGGCGCGTATACCAACGACAGAGCCCCGCGCGCTCTGTGCT	3687
Db	3654	CTGAGTGTCCAGCACACCTGTGCTGTCT-TCACTTCCCCACAGGCTGGCGCTCGGCTCCACC	3712
QY	3688	TCCCAGTACCCGCTCTGCGCCCTGGACACTTTGTCCAGATCAAGGAGTTTCTGAATCC	3747

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Db 3773 TCCCCAGATTCGCCCATTTGTTCAACCCCT-----CGCCCTGCCCTCTCTTGCTTCCACC 3825

QY 3808 TCTTCTGTGTGGAGAACCCCTGAGAAAGAACCCCTGGAGCTCTGGAAATTTGAGTGAC 3867

Db 3826 CCCCACCATCCAGGTGAGAGACCCCTGAGAAAGAACCCCTGGAGCTCTGGAAATTTGAGTGAC 3885

QY 3868 CAAAGGTGTGCCCTGTACACAGGCGAGAACCCCTGCACCTGGATGGGGTCCCTGTGGGTC 3927

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QY 3928 AAATTGGGGGAGGTGCTGTGGGAGTAATAATCTGAATATATGAGTTTTCAGTTTTGAA 3987

Db 3946 AAATTGGGGGAGGTGCTGTGGGAGTAATAATCTGAATATATGAGTTTTCAGTTTTGAA 4005

QY 3988 AAAAAAAAAAAAAAAAAAAAAA 4011

Db 4006 AAAAAAAAAAAAAAAAAAAAAA 4029

RESULT 15
US-09-438-486-173
Sequence 173, Application US/09438486
Publication No. US20030009019A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US20030009019A1e1 Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 4029 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY:
LOCATION: 1..4029
OTHER INFORMATION: /note= "preliminary sequence for
OTHER INFORMATION: human TRP cDNA insert of
OTHER INFORMATION: plasmid pGRN121"
US-09-438-486-173

Query Match 78.8%; Score 3159.8; DB 10; Length 4029;
Best Local Similarity 88.5%; Pred. No. 0;
Matches 3577; Conservative 0; Mismatches 412; Indels 55; Gaps 13;

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QY 188 GGAACCCCGCGGCTTTCCGCGCGCTGTGGCCAGTGTCTGTGTGCTGCGCTGGAGCG 247
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QY 968 GCACACG 1027
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Db	2094	GGCTTGAACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCCAGAAC	2153
QY	2166	CCGCGCGCTGAGCTGTACTTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCC	2225
Db	2154	CCGCGCGCTGAGCTGTACTTTTGTCAAGGTGATGTGACGGGCGCGTACGACACCATCCC	2213
QY	2226	CAGGACAGGCTCACGAGGTCAATCGCCAGCATCATCAACCCCGAACAAGTACTGCGTG	2285
Db	2214	CAGGACAGGCTCACGAGGTCAATCGCCAGCATCATCAACCCCGAACAAGTACTGCGTG	2273
QY	2286	CGTCGTATGCCGTGTGCCAAGGCCGCCCATGGGACGTCGCCAAGGCTTCAAGAGC	2345
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QY	2526	GCGAAGTCTTACGTCCAGTGGCCAGGGGATCCCGCAGGCTCCATCCTCTCCACGCTGCTC	2585
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QY	2586	TGCAGCCTGTGCTACGGCGACATGGAAGACAAAGCTGTTTGGGGGATTCCGCCGGGACGGG	2645
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Tue Mar 2 09:53:28 2004

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Db 4006 ||||| 4029

Search completed: March 1, 2004, 23:55:01
Job time : 924.576 secs

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DB 113 GAGTGTGCGCGCTGCGCGAGCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCTG 172
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DB 173 CAGCGCGCGCGCGCGCGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCTGCGCG 232
QY 181 TGGGACGCAAGCG 240
DB 233 TGGGACGCAAGCG 292
QY 241 CTGTGTGCGCGCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGAGAGAGT 300
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DB 353 GCGTTGCGCGCTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CCGAGCTACCTGCGCGCAAGCTGACCGAGCACTGCGCGCGCGCGCGCGCGCGCG 420
DB 413 CCGAGCTACCTGCGCGCAAGCTGACCGAGCACTGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGTGTGCGCGCGCTGCGCGAGCGAGCTGTGCTGCTGCGAGCGCTGCGCGCT 480
DB 473 CTGTGTGCGCGCGCTGCGCGAGCGAGCTGTGCTGCTGCGAGCGCTGCGCGCT 532
QY 481 GTGCTGTGCTGCTGCGAGCTGCGCTACCGAGTGTGCGCGCGCGCGCGCGCTG 540
DB 533 GTGCTGTGCTGCTGCGAGCTGCGCTACCGAGTGTGCGCGCGCGCGCGCGCTG 592
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AR175848
LOCUS AR175848 4015 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 224 from patent US 6309867.
ACCESSION AR175848
VERSION AR175848.1 GI:17917147
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 224 30-OCT-2001;
FEATURES
source location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS E36793 4015 bp DNA linear PAR 18-JUN-2001
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 ACCESSION E36793
 VERSION E36793.1 GI:13022756
 KEYWORDS JP 199253177-A/1.
 SOURCE unidentified
 ORGANISM unidentified.
 unclassified.

REFERENCE 1 (bases 1 to 4015)
 AUTHORS Thomas,R.S., Jochimu,R., Toru,N., Karen,B.C., Greg,B.M.,
 Calvin,B.H. and William,H.A.
 TITLE Human telomerase catalytic subunit promoter
 JOURNAL Patent: JP 199253177-A 1 21-SEP-1999;
 JERON CORP, UNIVERSITY TECHNOLOGY CORP
 COMMENT OS Unidentified
 PN JP 199253177-A/1
 PD 21-SEP-1999
 PF 15-OCT-1998 JP 1998320169

PR 01-OCT-1996 US 08/724,643,18-APR-1997 US 08/844,419, PR
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 09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
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QY	901	GGCGCCGACGACCAACGCGGGCCCCCATCCACATCGCGGCCACACGTCCCTGGACACG	960
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QY	1501	CATGCCAAGCTCTCGCTGAGGAGCTGACGTGGAAGATGACCGTGCGGACTGCGCTTG	1560
Db	1553	CATGCCAAGCTCTCGCTGAGGAGCTGACGTGGAAGATGACCGTGCGGACTGCGCTTG	1612
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Db	1613	CTGCGCAGGAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGCACCGTCTGCGTGAAG	1672
QY	1621	ATCCTGSCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGTCT	1680
Db	1673	ATCCTGSCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGTCT	1732
QY	1681	TTCTTTTATGTACCGAGAACCACTTTCAAAAGACAGGCTTTTTTCTACCGGAGAGT	1740
Db	1733	TTCTTTTATGTACCGAGAACCACTTTCAAAAGACAGGCTTTTTTCTACCGGAGAGT	1792

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Db	2093	GTGCTGGGCTGAGCAGATATCCACAGGCGCTGGCGCACCTTCGTGCTGCGTGGCGGCC	2152
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Db	2153	CAGACCCCGCGCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGGCTACGACACC	2212
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QY	2221	TGCGTCCGTCGGTATGCCGTGTCCTCAGAAAGCCGCCATGGGACAGTCCGCAAGCCTTC	2280
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Db	2633	GACGGGCTGCTCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACTCAACCCAC	2692
QY	2641	GCGAAAAACCTTCTCTCAGGACCCCTGTCCGAGGTGCCCTGAGTATGGCTGCGGTGTGAAC	2700
Db	2693	GCGAAAAACCTTCTCTCAGGACCCCTGTCCGAGGTGCCCTGAGTATGGCTGCGGTGTGAAC	2752
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Db	2753	TTGCGGAGAGACAGTGTGTAACCTTCCCTGTAGAAAGACGAGGCCCTGGGTGGCACGGCTTTT	2812
QY	2761	GTTTCAGATGCCGGCCCCACGCGCTATTTCCCTCGTGTGCGGCTGCTGTGATATCCCGAAC	2820
Db	2813	GTTTCAGATGCCGGCCCCACGCGCTATTTCCCTCGTGTGCGGCTGCTGTGATATCCCGAAC	2872
QY	2821	CTGAGGTGACAGCGCACTACTCCAGCTATAGCCCGGACCTCCATCAGAGCCAGTCTCAC	2880

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RESULT 4
LOCUS AR182221 4015 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6337200.
ACCESSION AR182221
VERSION AR182221.1 GI:20225137
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Morin, G.B.
TITLE Human telomerase catalytic subunit variants
JOURNAL Patent: US 6337200-A 1 08-JAN-2002;
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CAGCGCGGAGCCCGCGGCTTTCCGCGCGCTGTGCGCCAGTGCCTGTGTGCTGCC 180

Db 173 CAGCGCGGAGCCCGCGGCTTTCCGCGCGCTGTGCGCCAGTGCCTGTGTGCTGCC 232
QY 181 TGGAGACGACAGCG 240
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QY 301 GAGTTGCGGCTGCTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GAGTTGCGGCTGCTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGCTACCTGCGCCCAACCGGTGACCGGCACTGCGGGGAGAGCGGGGCTGCGGGGCTG 420
Db 413 CGCAGCTACCTGCGCCCAACCGGTGACCGGCACTGCGGGGAGAGCGGGGCTGCGGGGCTG 472
QY 421 CTGCTGCGCGCGGTGGCGGAGCGAGCTGTGTTCACTGCTGCGACGCTGCGCGCTCTT 480
Db 473 CTGCTGCGCGCGGTGGCGGAGCGAGCTGTGTTCACTGCTGCGACGCTGCGCGCTCTT 532
QY 481 GTGCTGTGCTCCCAAGCTGCGGCTCAAGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 533 GTGCTGTGCTCCCAAGCTGCGGCTCAAGTGTGCGGGCGCGCGCGCGCGCGCGCGCGCGCG 592
QY 541 GCTGCCACTCAGGCG 600
Db 593 GCTGCCACTCAGGCG 652
QY 601 GAACGGGCTGGAACCATAGCGTCAAGGAGCGCGGGTCCCGCTGGCTGCGACGCCCG 660
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QY 661 GGTGCGAGAGCG 720
Db 713 GGTGCGAGAGCG 772
QY 721 CGTGGCGTGCCTCTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
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RESULT 5
LOCUS AR224455 4015 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6440735.
ACCESSION AR224455
VERSION AR224455.1 GI:23333293
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 4015)
TITLE Gaeta, F.C.A.
JOURNAL Dendritic cell vaccine containing telomerase reverse transcriptase
FEATURES for the treatment of cancer
Patent: US 6440735-A 1 27-AUG-2002;
Location/Qualifiers
source 1. 4015
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Query Match 100.0%; Score 3411; DB 6; Length 4015;
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DB 113 GAGTGTGCGCGCTGCGAGCCGCTGCGAGCCGCTGCGAGCCGCTGCGAGCCGCTGCG 172

QY 121 CAGCGCGGAGACCCGCGGCTTCCGCGCGCTGCGAGCCGCTGCGAGCCGCTGCGAGCC 180
DB 173 CAGCGCGGAGACCCGCGGCTTCCGCGCGCTGCGAGCCGCTGCGAGCCGCTGCGAGCC 232

QY 181 TGGAGCGAGCG 240
DB 233 TGGAGCGAGCG 292

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QY 3181 GCGCGCGCGCGCTCTGCTGCTCCGAGCGCGTGAAGTGTGCTGACCAAGCATTCCTG 3240
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RESULT 6
LOCUS AR226390 4015 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6444650.
ACCESSION AR226390
VERSION AR226390.1 GI:27264905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Antisense compositions for detecting and inhibiting telomerase
reverse transcriptase
JOURNAL Patent: US 6444650-A 1 03-SEP-2002;
FEATURES
Source Location/Qualifiers
1..4015
/organism="Unknown"
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ORIGIN
Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAGGTGCTGCGGCTGCGGACAGTTCGTGCGGCGCTGCGGCGGCGGCTGCTGTG 120
DB 113 GAGGTGCTGCGGCTGCGGACAGTTCGTGCGGCGCTGCGGCGGCGGCTGCTGTG 172
QY 121 CAGCGCGGAGACCGCGCGGCTTTCGCGCGGCTGCTGCGGCGGCTGCTGTGCTGCCC 180
DB 173 CAGCGCGGAGACCGCGCGGCTTTCGCGCGGCTGCTGCGGCGGCTGCTGTGCTGCCC 232

QY 181 TGGAGCAGACGGCCGCCCCCGCCCTCTTCCGCAAGTGTCTGCTGAAGAG 240
Db 233 TGGAGCAGACGGCCGCCCCCGCCCTCTTCCGCAAGTGTCTGCTGAAGAG 292
QY 241 CTGCTGCGCCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCAAGACGTGTGCTTC 300
Db 293 CTGCTGCGCCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCAAGACGTGTGCTTC 352
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QY 361 CGCAGCTACTGCGCCACACGGGTGACCGGCACTGCGGGGAGCGGGGCGGTGGGGCTG 420
Db 413 CGCAGCTACTGCGCCACACGGGTGACCGGCACTGCGGGGAGCGGGGCGGTGGGGCTG 472
QY 421 CTGCTGCGCGCGGTGGGCGAGCAGCTGTGTCTCACTGTGCGACGCTGCGCGCTTT 480
Db 473 CTGCTGCGCGCGGTGGGCGAGCAGCTGTGTCTCACTGTGCGACGCTGCGCGCTTT 532
QY 481 GTGCTGTGCTTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGCG 540
Db 533 GTGCTGTGCTTCCAGCTGCGCTTACAGGTGTGCGGGCGCGCGCTGTACAGCTGCG 592
QY 541 GCTGCCACTCAGGCG 600
Db 593 GCTGCCACTCAGGCG 652
QY 601 GAACGGGCGCTGAACCATAGCGTCAGGGAGCGCGGGTCCCGCTGCGCTGCGAGCCCG 660
Db 653 GAACGGGCGCTGAACCATAGCGTCAGGGAGCGCGGGTCCCGCTGCGCTGCGAGCCCG 712
QY 661 GGTGCGAGAGCG 720
Db 713 GGTGCGAGAGCG 772
QY 721 CGTGGCGCTGCGCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 773 CGTGGCGCTGCGCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
QY 781 GGCAGGAGCGGTGACCGAGTGACCGGTGTCTGTGTGTGTGTGTGTGTGTGTGTGT 840
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QY 841 GAAGAAGCCACTCTTTGAGAGGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 893 GAAGAAGCCACTCTTTGAGAGGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 952
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QY 1801 GAGCTGTGGAAGCAGAGGTCAAGCAGCATGCGGAAAGCCAGGCGCGCGCTGCTGACGTCC 1860
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RESULT 7

AR243328
LOCUS AR243328 4015 bp mRNA linear PAT 20-DEC-2002
DEFINITION Sequence 1 from patent US 6475789.
ACCESSION AR243328
VERSION AR243328.1 GI:27290539
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,
Harley,C.B. and Andrews,W.H.
TITLE Human telomerase catalytic subunit: diagnostic and therapeutic
methods
JOURNAL Patent: US 6475789-A 1 05-NOV-2002;
FEATURES
source Location/Qualifiers
1..4015
/organism="unknown"
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ORIGIN
Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	953	GGCCGCGACCAACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACAG	1012
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QY	1021	CAGTGGGGCCCTCCTTCTACTACGCTCTGTAGGCCAGCCCTGACTGGCGCTCGAGG	1080
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QY	1081	CTCGTGAAGACCATCTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGTTG	1140
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QY	1141	CCCCGCTGCCCGACTACTGGCAATGCGGCCCTGTCTGTGAGCTGTGGGAAC	1200
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Db	1253	CACGCGCAGTGCCCCCTACCGGGTGTCTCTAAGACGCACTGCCCGCTGCGAGCTGCGGT	1312
QY	1261	ACCCAGCAGCCCGGTGTGTGTGCCGGGAGAGCCCCAGGGCTGTGGCGGCCCCGAG	1320
Db	1313	ACCCAGCAGCCCGGTGTGTGTGCCGGGAGAGCCCCAGGGCTGTGGCGGCCCCGAG	1372
QY	1321	GAGGAGGACACAGACCCCCCGTGCCTGTGTGAGCTGTCCGCCACAGCAGACCCCTGG	1380
Db	1373	GAGGAGGACACAGACCCCCCGTGCCTGTGTGAGCTGTCCGCCACAGCAGACCCCTGG	1432
QY	1381	CAGGTGTACGGCTTCTGTGCGGGCTGCCTGCGCCGGCTGTGTGCCCCAGGCTTGGGGC	1440
Db	1433	CAGGTGTACGGCTTCTGTGCGGGCTGCCTGCGCCGGCTGTGTGCCCCAGGCTTGGGGC	1492
QY	1441	TCCAGGCAACAAGAACGCGCTTCTCAGGAACACCAAGATTATCTCCCTGGGGAAG	1500
Db	1493	TCCAGGCAACAAGAACGCGCTTCTCAGGAACACCAAGATTATCTCCCTGGGGAAG	1552
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Db	1553	CATGCCAAGCTCTCGCTGAGAGCTGACGTGGAAGATGACGTGCGGACTGCGCTTGG	1612
QY	1561	CTGCGCAGGAGCCGAGGGTTGGCTGTTCGGGCGGACAGCACCCGTCTGCGTGAAGAG	1620
Db	1613	CTGCGCAGGAGCCGAGGGTTGGCTGTTCGGGCGGACAGCACCCGTCTGCGTGAAGAG	1672
QY	1621	ATCCTGGCCAAAGTTCCCTGCACTGGCTGATGAGTGTATAGTCGTGAGCTGCTAAGTCT	1680
Db	1673	ATCCTGGCCAAAGTTCCCTGCACTGGCTGATGAGTGTATAGTCGTGAGCTGCTAAGTCT	1732
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QY	1741	GTCTGAGCAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGTTGACGTGCGG	1800
Db	1793	GTCTGAGCAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGTTGACGTGCGG	1852
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Db	1913	AGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTAC	1972
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Db	1973	GTGGAGCCAGAACGTTCCGAGAGAAAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAG	2032
QY	1981	GCACTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGCGCTCT	2040
Db	2033	GCACTGTTCAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGCGCTCT	2092
QY	2041	GTGCTGGGCTTGAGCGATATCCACAGGGCCTGGCGCACTTCGTGCTGCTGTGGGGCC	2100
Db	2093	GTGCTGGGCTTGAGCGATATCCACAGGGCCTGGCGCACTTCGTGCTGCTGTGGGGCC	2152
QY	2101	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACACACC	2160
Db	2153	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACACACC	2212
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QY	2221	TGCGTGCGTCCGTATGCCGTGTGTCCAGAAAGCCGCCCATGGGCAAGTCCGCAAGCCTTC	2280
Db	2273	TGCGTGCGTCCGTATGCCGTGTGTCCAGAAAGCCGCCCATGGGCAAGTCCGCAAGCCTTC	2332
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QY	2341	CTGCAGAGAGACCAGCCCGCTGAGGGATGCCGTCTCATCGACAGAGACTCCTCCCTGAAT	2400
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QY	2401	GAGGCCAGCAGTGGCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAAGCCGTGCC	2460
Db	2453	GAGGCCAGCAGTGGCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAAGCCGTGCC	2512
QY	2461	ATCAGGGGCAAGTCTTACGTCCAGTGCACAGGGGATCCCGCAGGGCTCCATCTCTCCACG	2520
Db	2513	ATCAGGGGCAAGTCTTACGTCCAGTGCACAGGGGATCCCGCAGGGCTCCATCTCTCCACG	2572
QY	2521	CTGCTCTGCAGCCTGTGTCTACGGCGACATGGAGAACAAAGCTGTTGCGGGGATTCGGCGG	2580
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QY	2581	GACGGGCTGCTCTGCGCTTGTGTGATGATTTCTGTTGTGTGACACCTCACTCAACCCAC	2640
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QY	2641	GCGAAAAACCTTCTCAGGAACCCCTGTGCCAGGTGTCCCTGAGTATGCTGCTGTGTGAAC	2700
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LOCUS AR263555 4015 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 3 from patent US 6331399.
ACCESSION AR263555
VERSION AR263555.1 GI:28075300
KEYWORDS

SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Monia,B.P., Gaarde,W.A. and Wanciewicz,E.
TITLE Antisense inhibition of tert expression
JOURNAL Patent: US 6331399-A 3 18-DEC-2001;
FEATURES
source 1. 4015
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ORIGIN

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LOCUS AR265996
DEFINITION Sequence 3 from patent US 6492171.

ACCESSION AR265996
VERSION AR265996.1 GI:29694842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Monia, B.P., Gaarde, W.A., Freier, S.M. and Wanciewicz, E.
TITLE Antisense modulation of TERT expression
JOURNAL Patent: US 6492171-A 3 10-DEC-2002;
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LOCUS AR390470
DEFINITION Sequence 1 from patent US 6610839.
ACCESSION AR390470
VERSION AR390470.1 GI:40112394
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4015)
AUTHORS Morin, G.B. and Andrews, W.H.
TITLE Promoter for telomerase reverse transcriptase
JOURNAL Patent: US 6610839-A 1 26-AUG-2003;
FEATURES
source location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 3411; DB 6; Length 4015;
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Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1133	CTCGTGAGAGCACTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCCGAGGTTG	1192
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RESULT 12

AR404030

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

ORIGIN

Query Match

Best Local Similarity

Matches 3411; Conservative

Score 3411; DB 6; Length 4015;

Pred. No. 0;

Mismatches 0; Indels 0; Gaps 0;

AR404030

Sequence 1 from patent US 6627619.

AR404030

AR404030.1

GI:40152014

Unknown.

Unknown.

Unclassified.

1 (bases 1 to 4015)

Cech,T.R., Lingner,J., Nakamura,T., Chapman,K.B., Morin,G.B.,

Harley,C.B. and Andrews,W.H.

Antisense compositions for detecting and inhibiting telomerase

reverse transcriptase

Patent: US 6627619-A 1 30-SEP-2003;

Location/Qualifiers

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REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 Dahm, M.W., Phelps, R.C. and Brockmeyer, C.
TITLE Method for quantitatively analyzing tumor cells in a body fluid and test kits suited therefor
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RESULT 15

AX552695

LOCUS AX552695 4015 bp DNA linear PAT 27-NOV-2002

DEFINITION Sequence 1 from Patent WO02074948.

ACCESSION AX552695

VERSION AX552695.1 GI:25896697

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1
AUTHORS Denning, C., Clark, A.J. and Schif, J.M.
TITLE Animal tissue with carbohydrate antigens compatible for human
transplantation
JOURNAL Patent: WO 02074948-A 1 26-SEP-2002;
Geron Corporation (US)
FEATURES
Source location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Tue Mar 2 09:53:24 2004

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Page 28

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PT Proliferation conditions especially cancer and ageing.
XX Claim 5; Fig 16; 387pp; English.

CC The present sequence encodes human telomerase reverse transcriptase
CC (hTERT), which is a ribonucleoprotein. The present invention also
CC describes the following methods: (A) determining whether a test compound
CC is a modulator of hTERT, by detecting the change in hTERT recombinant
CC protein or polynucleotide, on administration of the compound; (B)
CC preparation of recombinant telomerase by contacting a protein preparation
CC of hTERT with a telomerase RNA component; (C) detection of the hTERT RNA or
CC protein in a sample by binding a relevant probe to the sample and
CC detecting the complex formed or in the case of RNA detection, amplifying
CC the product and correlating the presence of complex or amplification
CC product with presence of hTERT in the sample; and (D) increasing the
CC proliferation of a vertebrate cell by increasing hTERT expression; and (E)
CC the use of an agent that causes an increase in cell vertebrate cell
CC proliferation to create a medicament that inhibits ageing. A protein
CC preparation of hTERT and the polynucleotide encoding hTERT can be used in
CC the manufacture of medicaments for inhibiting the effect of ageing or
CC cancer. Inhibitors of telomerase activity can be used to treat conditions
CC that are associated with high telomerase activity. A protein preparation
CC of hTERT can also be used in the new methods

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DB 593 GCTGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTGCTGCGAGCACTACCGC 652
QY 601 GAACGCGGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTGCTGCGAGCACTACCGC 660
DB 653 GAACGCGGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTGCTGCGAGCACTACCGC 712

QY 661 GGTGCGAGGAGCGGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTGCTGCGAGCACTACCGC 720
DB 713 GGTGCGAGGAGCGGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTGCTGCGAGCACTACCGC 772
QY 721 CGTGGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 780
DB 773 CGTGGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 832
QY 781 GGCAGGAGCGGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 840
DB 833 GGCAGGAGCGGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 892
QY 841 GAAGAAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 900
DB 893 GAAGAAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 952
QY 901 GGCAGGAGCGGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 960
DB 953 GGCAGGAGCGGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1012
QY 961 CTTTGTCCCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1020
DB 1013 CTTTGTCCCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1072
QY 1021 CAGTGTGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1080
DB 1073 CAGTGTGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1132
QY 1081 CTGTTGAGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1140
DB 1133 CTGTTGAGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1192
QY 1141 CCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1200
DB 1193 CCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1252
QY 1201 CAGCGGAGTGGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1260
DB 1253 CAGCGGAGTGGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1312
QY 1261 ACCCGAGGAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1320
DB 1313 ACCCGAGGAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1372
QY 1321 GAGGAGGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1380
DB 1373 GAGGAGGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1432
QY 1381 CAGGAGTACGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1440
DB 1433 CAGGAGTACGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1492
QY 1441 TCCAGGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1500
DB 1493 TCCAGGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1552
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DB 1553 CATGCGAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1612
QY 1561 CTGCGAGGAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1620
DB 1613 CTGCGAGGAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1672
QY 1621 ATCTGCGAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1680
DB 1673 ATCTGCGAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1732
QY 1681 TTCTTTATGTACGAGGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1740
DB 1733 TTCTTTATGTACGAGGAGCAGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCGGCTTCCGCGGCTGCTGCGAGCACTACCGC 1792

QY 1741 GTCTGAGCAAGTTGCAAGCATTTGATCAGACGACTTGAAGAGGTGAGCTGCGG 1800
Db 1793 GTCTGAGCAAGTTGCAAGCATTTGATCAGACGACTTGAAGAGGTGAGCTGCGG 1852
QY 1801 GAGCTGTGGAAGCAGAGGTTCAGGACGATCGGGAAGCCAGGCGCCCTGCTGACGTCC 1860
Db 1853 GAGCTGTGGAAGCAGAGGTTCAGGACGATCGGGAAGCCAGGCGCCCTGCTGACGTCC 1912
QY 1861 AGACTCCGCTTCATCCCAAGCCTGACGCGGCTGCGCCGATTTGTAACATGACTACGTC 1920
Db 1913 AGACTCCGCTTCATCCCAAGCCTGACGCGGCTGCGCCGATTTGTAACATGACTACGTC 1972
QY 1921 GTGGAGCCAGAACGTTCCGCAAGAAAAAGAGGCGGAGCGCTCCTCCTGAGGGTGAAG 1980
Db 1973 GTGGAGCCAGAACGTTCCGCAAGAAAAAGAGGCGGAGCGCTCCTCCTGAGGGTGAAG 2032
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Db 2033 GCACTGTTCAGCGTGTCTCACTACGAGCGGCGCGCGCGCGCGCGCGCGCGCGCTCT 2092
QY 2041 GTGCTGGGCTTGACGATATCCACAGGCGCTGCGGCACTTGTGCTGCTGCTGCGGCG 2100
Db 2093 GTGCTGGGCTTGACGATATCCACAGGCGCTGCGGCACTTGTGCTGCTGCTGCGGCG 2152
QY 2101 CAGGACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGCGCGCTACGACACC 2160
Db 2153 CAGGACCCGCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGCGCGCTACGACACC 2212
QY 2161 ATCCCCCAGGACAGGCTCAAGAGGTTCATCGCAGCATCATCAAAACCCAGAACACGTA 2220
Db 2213 ATCCCCCAGGACAGGCTCAAGAGGTTCATCGCAGCATCATCAAAACCCAGAACACGTA 2272
QY 2221 TGCGTGCCTGATGCGGTGCTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 2280
Db 2273 TGCGTGCCTGATGCGGTGCTCCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 2332
QY 2281 AAGAGCCAGCTCTCTACCTTGAAGACCTCCAGCGCTACATGCGACAGTTCGTGCTCAC 2340
Db 2333 AAGAGCCAGCTCTCTACCTTGAAGACCTCCAGCGCTACATGCGACAGTTCGTGCTCAC 2392
QY 2341 CTGCAAGAGACAGCGCGCTGAGGATGCGCGCTCATCGACAGAGTCTCCCTGAAT 2400
Db 2393 CTGCAAGAGACAGCGCGCTGAGGATGCGCGCTCATCGACAGAGTCTCCCTGAAT 2452
QY 2401 GAGGCCAGCAGTGGCTCTTTCGACGCTCTTCTCAAGCTTCTCATGTGCCACACGCGCTGCG 2460
Db 2453 GAGGCCAGCAGTGGCTCTTTCGACGCTCTTCTCAAGCTTCTCATGTGCCACACGCGCTGCG 2512
QY 2461 ATCAGGGGCAAGTCTTACCTTCCAGTGCAGGGAATCCCGCAGGCGCTCATCTCTCCACG 2520
Db 2513 ATCAGGGGCAAGTCTTACCTTCCAGTGCAGGGAATCCCGCAGGCGCTCATCTCTCCACG 2572
QY 2521 CTGCTCTGACGCTGTGCTACGCGCAGCATGGAACAAGCTGTTGGGGGATTCGGCGG 2580
Db 2573 CTGCTCTGACGCTGTGCTACGCGCAGCATGGAACAAGCTGTTGGGGGATTCGGCGG 2632
QY 2581 GACGGGCTGCTCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC 2640
Db 2633 GACGGGCTGCTCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC 2692
QY 2641 GCGAAAAACCTTCTCAGGACCTCTGTCGAGGTGTCCTGAGTATGCTGCTGCTGTAAC 2700
Db 2693 GCGAAAAACCTTCTCAGGACCTCTGTCGAGGTGTCCTGAGTATGCTGCTGCTGTAAC 2752
QY 2701 TTGCGGAAGACAGTGTGAACCTTCTCTGTAAGAAGAGAGGCGCTGGGTGGACAGGCTTTT 2760
Db 2753 TTGCGGAAGACAGTGTGAACCTTCTCTGTAAGAAGAGAGGCGCTGGGTGGACAGGCTTTT 2812
QY 2761 GTTCAGATGCGGCGCCAGCGCTATTCCTCTGCTGCGGCGCTGCTGCTGATACCCGAGAC 2820
Db 2813 GTTCAGATGCGGCGCCAGCGCTATTCCTCTGCTGCGGCGCTGCTGCTGATACCCGAGAC 2872
QY 2821 CTGAGGTGACAGCGACTACTCAGCTATGCGCGGACCTTCATCAGAGCCAGTCTCAC 2880

Db 2873 CTGAGGTGACAGCGACTACTCCAGCTATGCGCGACCTCCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGCGCTTCAAGGCTGGAGGAACATGCTGCAAACTTTGGGGTCTTGGCG 2940
Db 2933 TTCAACCGCGCTTCAAGGCTGGAGGAACATGCTGCAAACTTTGGGGTCTTGGCG 2992
QY 2941 CTGAAGTGCACAGCTGTTTCTGATTTGAGGTGAACAGCCTCCAGAGGCTGACACC 3000
Db 2993 CTGAAGTGCACAGCTGTTTCTGATTTGAGGTGAACAGCCTCCAGAGGCTGACACC 3052
QY 3001 AACATCTACAAGATCCTCTGCTGACGCGTACAGTTTCAAGCATGTGTGCTGACCTC 3060
Db 3053 AACATCTACAAGATCCTCTGCTGACGCGTACAGTTTCAAGCATGTGTGCTGACCTC 3112
QY 3061 CCAATTTCATCAGCAAGTTTGAAGAACCACATTTTCTGCGGCTCATCTGACACG 3120
Db 3113 CCAATTTCATCAGCAAGTTTGAAGAACCACATTTTCTGCGGCTCATCTGACACG 3172
QY 3121 GCCTCCCTCTGCTACTCATCTGAAAGCCAGAACGCAAGGATGTGCTGGGGCCAAAG 3180
Db 3173 GCCTCCCTCTGCTACTCATCTGAAAGCCAGAACGCAAGGATGTGCTGGGGCCAAAG 3232
QY 3181 GCGCGCGCGCGCTCTGCGCTTCCAGAGCGCTGAGTGGCTGTGCCACCAAGATTCTG 3240
Db 3233 GCGCGCGCGCGCTCTGCGCTTCCAGAGCGCTGAGTGGCTGTGCCACCAAGATTCTG 3292
QY 3241 CTCAGCTGACTGACACCGGTGTCACTTACCTGACCTCTGCGGCTCACTCAGGACAGCC 3300
Db 3293 CTCAGCTGACTGACACCGGTGTCACTTACCTGACCTCTGCGGCTCACTCAGGACAGCC 3352
QY 3301 CAGACGAGCTGAGTGGAGAGCTCCCGGGGAGCAGCGCTGACTGCCCTGAGAGCGCAGCC 3360
Db 3353 CAGACGAGCTGAGTGGAGAGCTCCCGGGGAGCAGCGCTGACTGCCCTGAGAGCGCAGCC 3412
QY 3361 AACCCGCACTGCGCTCAGACTTCAAGACCATCTGACTGATGGCCACC 3411
Db 3413 AACCCGCACTGCGCTCAGACTTCAAGACCATCTGACTGATGGCCACC 3463

RESULT 2
AAZ00724
ID AAZ00724 standard; DNA; 4015 BP.
XX
AC AAZ00724;
DT 06-OCT-1999 (first entry)
XX
DE Human telomerase catalytic domain DNA.
XX
KW Telomerase; catalytic domain; human; quantitation; tumour cell; melanoma;
KW body fluid; metastases; T-cell lymphoblastoma; chronic myeloid leukemia;
KW acute lymphatic leukemia; melanoma; pulmonary carcinoma; colon cancer;
KW breast cancer; ss.
XX
OS Homo sapiens.
XX
PN DE19804372-A1.
XX
PD 05-AUG-1999.
XX
PF 04-FEB-1998; 98DE-01004372.
XX
PR 04-FEB-1998; 98DE-01004372.
XX
PA (DAHM/) DAHM M W.
XX
PI Dahm MW;
XX
DR WPI; 1999-431408/37.
XX
PT Quantifying tumor cells by amplifying mRNA encoding the catalytic subunit
PT of telomerase.

XX Example; Fig 1A-B; 26pp; German.

PS This invention describes a novel method for the quantitation of tumour
CC cells in a body fluid which comprises (1) enrichment or isolation of
CC tumour cells in the sample, (2) amplification of mRNA from these cells
CC that encodes the catalytic subunit of telomerase and (3) quantifying the
CC amount of amplified mRNA. The method is applied to tumour cells derived
CC from (micro)metastases, e.g. associated with a wide range of tumours such
CC as T-cell lymphoblastoma, chronic myeloid or acute lymphatic leukemia,
CC melanoma, pulmonary carcinoma, cancer of colon or breast etc. This
CC sequence encodes a human telomerase protein catalytic domain

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 2; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCCGCTGCTCCCTGCTGCGAGCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGAGCCGCTGCTCCCTGCTGCGAGCACTACCGC 112
QY 61 GAGGTGCTGCGCTGCGAGCGTTCGTGCGCGCGCTGCGAGCGCGCTGCGAGCGCTG 120
Db 113 GAGGTGCTGCGCTGCGAGCGTTCGTGCGCGCGCTGCGAGCGCGCTGCGAGCGCTG 172
QY 121 CAGCGCGCGCGCGCGCGCTTTCGCGCGCTGCGAGCGCGCTGCGAGCGCTGCGAGCG 180
Db 173 CAGCGCGCGCGCGCGCGCTTTCGCGCGCTGCGAGCGCGCTGCGAGCGCTGCGAGCG 232
QY 181 TGGGACGACAGCG 240
Db 233 TGGGACGACAGCG 292
QY 241 CTGCTGCGCGCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGCTGCGCGCGAGTGTGCGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GCGTTGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GCGTTGCGCGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGCTACCTGCGCAACAGCGTACCGAGCGCACTGCGCGCGCGCGCGCGCGCGCG 420
Db 413 CGCAGCTACCTGCGCAACAGCGTACCGAGCGCACTGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGCTGCGCGCGCGTGGCGCGAGCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 473 CTGCTGCGCGCGCGTGGCGCGAGCGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 532
QY 481 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 533 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 592
QY 541 GCTGCGCACTCAGCG 600
Db 593 GCTGCGCACTCAGCG 652
QY 601 GAAAGGCGCGTGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAAAGGCGCGTGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGAGCG 720
Db 713 GGTGCGAGAGCG 772
QY 721 CGTGCGCGCTGCG 780
Db 773 CGTGCGCGCTGCG 832
QY 781 GCGAGGAGCGGTGAGCGAGTGAACGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 840

Db 833 GCGAGGAGCGGTGAGCGAGTGAACGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTG 892
QY 841 GAAGAAGCCACCTCTTGGAGGCGTGGCGCTGCGCAAGCGCGCGCGCGCGCGCGCGCG 900
Db 893 GAAGAAGCCACCTCTTGGAGGCGTGGCGCTGCGCAAGCGCGCGCGCGCGCGCGCGCG 952
QY 901 GCG 960
Db 953 GCG 1012
QY 961 CTTTGTCCCGCGGTGTAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
Db 1013 CTTTGTCCCGCGGTGTAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1072
QY 1021 CAGCTGCG 1080
Db 1073 CAGCTGCG 1132
QY 1081 CTGCTGAGAGACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1133 CTGCTGAGAGACCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192
QY 1141 CCG 1200
Db 1193 CCG 1252
QY 1201 CAGCGCGAGTCCCTTACCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1253 CAGCGCGAGTCCCTTACCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312
QY 1261 ACCCGAGAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1313 ACCCGAGAGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1372
QY 1321 GAGGAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Db 1373 GAGGAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1432
QY 1381 CAGGTGTACGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
Db 1433 CAGGTGTACGCGCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1492
QY 1441 TCCAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1500
Db 1493 TCCAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1552
QY 1501 CATGCCAAGCTCTGCGTGCAGGAGCTGACGTTGAAGATGAGCGTGGCGGACTGCGCT 1560
Db 1553 CATGCCAAGCTCTGCGTGCAGGAGCTGACGTTGAAGATGAGCGTGGCGGACTGCGCT 1612
QY 1561 CTGCGGAGAGCG 1620
Db 1613 CTGCGGAGAGCG 1672
QY 1621 ATCCTGCGCAAGTTCTGCACTGCGTGAATGATGTGTACGTCGTCAGCTGCT 1680
Db 1673 ATCCTGCGCAAGTTCTGCACTGCGTGAATGATGTGTACGTCGTCAGCTGCT 1732
QY 1681 TTCTTTATGTCACGGAAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAG 1740
Db 1733 TTCTTTATGTCACGGAAGACCAAGTTCAAAAGAACAGGCTCTTTTCTACCGGAAG 1792
QY 1741 GTCTGAGAGCAAGTTGCAAGCAATGGAATCAGACAGCACTTGAAGAGGCTGAGCT 1800
Db 1793 GTCTGAGAGCAAGTTGCAAGCAATGGAATCAGACAGCACTTGAAGAGGCTGAGCT 1852
QY 1801 GAGCTGTGGAAGCAAGGTCAAGGAGCATCGGGAAGCCAGGCGCGCGCGCGCGCG 1860
Db 1853 GAGCTGTGGAAGCAAGGTCAAGGAGCATCGGGAAGCCAGGCGCGCGCGCGCGCG 1912
QY 1861 AGACTCCGCTTCAATCCCAAGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
Db 1913 AGACTCCGCTTCAATCCCAAGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1972

QY 1921 GTGGAGCCAGAACGTTCCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAG 1980
DB 1973 GTGGAGCCAGAACGTTCCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAG 2032
QY 1981 GCACTGTTCAAGCGTGTCTCACTACGAGCGGGCCGCGGCCCTCTCTGGGGCGCTCT 2040
DB 2033 GCACTGTTCAAGCGTGTCTCACTACGAGCGGGCCGCGGCCCTCTCTGGGGCGCTCT 2092
QY 2041 GTGCTGGGCTTGAACGATATCCACAGGGGCTGGCGCACCTTGTGCTGCTGCTGGCGGC 2100
DB 2093 GTGCTGGGCTTGAACGATATCCACAGGGGCTGGCGCACCTTGTGCTGCTGCTGGCGGC 2152
QY 2101 CAGGACCCCGCGCTGAGCTGTACTTGTCAAGGTGATGACGGGCGCTGACGACACC 2160
DB 2153 CAGGACCCCGCGCTGAGCTGTACTTGTCAAGGTGATGACGGGCGCTGACGACACC 2212
QY 2161 ATCCCCCAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCAGAACAGCTAC 2220
DB 2213 ATCCCCCAGGACAGGCTCACGAGGTCATCGCCAGCATCATCAAAACCAGAACAGCTAC 2272
QY 2221 TGGGTGCGGTATGATCCGCTGTCCAGAAAGCCGCCCATGGGCAAGTCCGAAAGGCTTC 2280
DB 2273 TGGGTGCGGTATGATCCGCTGTCCAGAAAGCCGCCCATGGGCAAGTCCGCAAGGCTTC 2332
QY 2281 AAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCAC 2340
DB 2333 AAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCAC 2392
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DB 2393 CTGACAGAGACCAAGCCCGTGAAGGATGCGCTCATCGACAGAGCTCCTCCTGAAT 2452
QY 2401 GAGGCCAGAGTGGCTCTTTCAGAGCTTCTCTACGCTTATGTGCCAACACCGCGGTGCGC 2460
DB 2453 GAGGCCAGAGTGGCTCTTTCAGAGCTTCTCTACGCTTATGTGCCAACACCGCGGTGCGC 2512
QY 2461 ATCAGGGGCAAGTCTCTACGTCACAGGATCCCGGAGGCTCCATCTCTTCCACG 2520
DB 2513 ATCAGGGGCAAGTCTCTACGTCACAGGATCCCGGAGGCTCCATCTCTTCCACG 2572
QY 2521 CTGCTCTGACGCTGTGTCTACCGGCAATGAGAACAAAGCTGTTGCGGGGATTCGGCGG 2580
DB 2573 CTGCTCTGACGCTGTGTCTACCGGCAATGAGAACAAAGCTGTTGCGGGGATTCGGCGG 2632
QY 2581 GACGGGCTGCTCTCTGCGTTTGGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC 2640
DB 2633 GACGGGCTGCTCTCTGCGTTTGGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC 2692
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DB 2693 GCGAAAACTTCTCTCAGGACCTGTGTCGAGGTGTCCTGATGATGCTGCTGTGAAC 2752
QY 2701 TTGCGAAGACAGTGTGTAATCTCTGTAGAACGAGGCCCTGGTGGACGCGCTTTT 2760
DB 2753 TTGCGAAGACAGTGTGTAATCTCTGTAGAACGAGGCCCTGGTGGACGCGCTTTT 2812
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DB 2933 TTCAACCGCGGCTTCAAGGCTGGGAGAACATGCGTGCAGAACTCTTTGGGGTCTTGCGG 2992
QY 2941 CTGAAGTGTACAGGCTGTTTCTGATTTGACAGTGAACAGCTCCAGACGCTGTGACAC 3000
DB 2993 CTGAAGTGTACAGGCTGTTTCTGATTTGACAGTGAACAGCTCCAGACGCTGTGACAC 3052

QY 3001 AACATCTACAGATCTCTCTGCTGACGGGCTACAGGTTTACCGATGTGTCTGACGCTC 3060
DB 3053 AACATCTACAGATCTCTCTGCTGACGGGCTACAGGTTTACCGATGTGTCTGACGCTC 3112
QY 3061 CCATTTCATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGGCTCATCTGTACACG 3120
DB 3113 CCATTTCATCAGCAAGTTTGGAGAACCCCAATTTTCTGCGGCTCATCTGTACACG 3172
QY 3121 GCCTCCCTGTGCTACTCCATCTTGAAGCCAGAACGACAGGATGTGCTGGGGCCAAAG 3180
DB 3173 GCCTCCCTGTGCTACTCCATCTTGAAGCCAGAACGACAGGATGTGCTGGGGCCAAAG 3232
QY 3181 GGGCGCGCGGCTCTGCTGCTCCAGAGGCGGTGACGTGGCTGTGCAACCAAGCATTTCTG 3240
DB 3233 GGGCGCGCGGCTCTGCTGCTCCAGAGGCGGTGACGTGGCTGTGCAACCAAGCATTTCTG 3292
QY 3241 CTCAAGCTGACTGACACACCGTGTCACTACGTGCCACTCTGGGGTCACTCAGACAGCC 3300
DB 3293 CTCAAGCTGACTGACACACCGTGTCACTACGTGCCACTCTGGGGTCACTCAGACAGCC 3352
QY 3301 CAGACGCACTGAGTGGAGCTCCGGGAGCAGACGCTGACTGACTGAGGCGGACGCC 3360
DB 3353 CAGACGCACTGAGTGGAGCTCCGGGAGCAGACGCTGACTGACTGAGGCGGACGCC 3412
QY 3361 AACCCGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACC 3411
DB 3413 AACCCGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACC 3463

RESULT 3
AAZ20279
ID AAZ20279 standard; cDNA; 4015 BP.
XX
AC AAZ20279;
XX
DT 17-JAN-2000 (first entry)
XX
DE Human telomerase reverse transcriptase (hTERT) cDNA.
XX
KW Telomerase reverse transcriptase; human; hTERT; cell proliferation;
XX cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /*tag= a
XX
PN WO950386-A2.
XX
PD 07-OCT-1999.
XX
PF 31-MAR-1999; 99WO-US007097.
XX
PR 31-MAR-1998; 98US-00052864.
PR 03-AUG-1998; 98US-00128354.
XX
PA (GERO-) GERON CORP.
XX
PI Morin GB;
XX
DR WPI; 1999-610842/52.
DR P-PSDB; AAY32090.
XX
PT New catalytic polypeptide and polymucleotide, useful for increasing
PT catalytic activity in a cell.
XX
PS Disclosure; Fig 2; 24pp; English.
XX
CC This is the nucleotide sequence of cDNA encoding human telomerase reverse
CC transcriptase (hTERT, see AAY32090). Human telomerase is a target for
CC diagnosing and treating diseases relating to cell proliferation and
CC senescence, such as cancer, or for increasing the proliferative capacity

CC of a cell. A claimed method for increasing the proliferative capacity of
CC a vertebrate cell, especially a human or other mammalian cell, involves
CC introducing into the cell a recombinant hTERT polynucleotide encoding an
CC hTERT variant in which residues 192-323, 200-323, 192-271, 200-271, 222-
CC 240, 415-450, 192-323 and 415-450, or 192-271 and 415-450 are deleted. A
CC claimed method for reducing telomerase activity in a cell involves
CC introducing a recombinant polynucleotide encoding an hTERT variant having
CC a deletion of amino acids 192-450, 560-565, 637-660, 638-660, 748-764 or
CC 1055-1071. The polynucleotides are obtained by mutagenesis of the hTERT
CC coding sequence

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 3411; DB 2; Length 4015;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 GCGATGCGCGCGCTCCCGCTGCGGAGCCGCTGCTCCCTGCTGCGCAGCCACTACCGC 60
DB 53 GCGATGCGCGCGCTCCCGCTGCGGAGCCGCTGCTCCCTGCTGCGCAGCCACTACCGC 112
QY 61 GAGTGTCTCCGCTGCGCAGCTGCTGCGGCGCTGCGGCGCCCAAGGCTGCGGCTGTG 120
DB 113 GAGTGTCTCCGCTGCGCAGCTGCTGCGGCGCTGCGGCGCCCAAGGCTGCGGCTGTG 172
QY 121 CAGCGCGGGGAGACCCGCGGCTTTCCGCGCGCTGCTGCGGCGCCCAAGTGTGCTGCGTCCC 180
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QY 301 GGGTTGCGCGCTGTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GGGTTGCGCGCTGTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGGAGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
DB 413 CGGAGTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 473 CTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 532
QY 481 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 533 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 592
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DB 593 GCTGCGCACTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
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DB 713 GGTGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 772
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DB 773 CGTGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
QY 781 GCGAGGAGCGGTGAGACCAATGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB 833 GCGAGGAGCGGTGAGACCAATGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 892
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DB 1013 CTTGTCCCGCGGTGTACGCGGAGAACCAAGCACTTCTCTACTCTCAGGCGCAGAGAG 1072
QY 1021 CAGTGTGCGCGCGCTCTCTCTACTCAGCTCTCTGAGGCGCCAGCGCTGAGCGGCTCGAGG 1080
DB 1073 CAGTGTGCGCGCGCTCTCTCTACTCAGCTCTCTGAGGCGCCAGCGCTGAGCGGCTCGAGG 1132
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DB 1313 ACCCGAGCAGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1372
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DB 1373 GAGGAGGACACAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1432
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DB 1433 CAGGTGTACGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1492
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DB 1853 GAGTGTGGAAGAGAGTCAAGCAGCATGCGGAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1912
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DB 1913 AGACTCGCTTCAATCCCAAGCTGACGCGGTGCGCGGATTTGAAATGAGTACTAGCTC 1972
QY 1921 GTGGAGCGCAGAACTTCCGAGAGAAAAGAGGCGCGAGCGTCTCACTGAGGCTGAAG 1980
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Db 2333 AAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTATGCGACAGTTCGTGCTCAC 2392
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QY 2761 GTTCAGATGCGGGCCACGGCTATTCCCTGTGCGGCGCTGCTGTGATACCCGAGCC 2820
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Db 2873 CTGAGGTGAGAGGCACTACTCCAGCTATGCGCGGACCTCCATCAGAGCCAGTCTCAC 2932
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Db 2993 CTGAAGTGTACAGGCTGTTCTGATTTGAGGTGAACAGCCTCCAGACGCTGTGCACC 3052
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RESULT 4
AAZ30154
ID AAZ30154 standard; cDNA; 4015 BP.
XX
AC AAZ30154;
XX
DT 26-JAN-2000 (first entry)
XX
DE cDNA encoding a human telomerase reverse transcriptase (TRT).
XX
KW Human; telomerase reverse transcriptase; TRT; T lymphocyte activation;
KW dendritic cell; telomerase activity; cancer cell; proliferating cell;
KW immunological destruction; telomerase; cancer; proliferation disease; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
FT
FT
FT
XX
PN WO9950392-A1.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US006898.
XX
PR 31-MAR-1998; 98US-0112006P.
XX
PA (GERO-) GERON CORP.
XX
PI Gaeta FCA;
XX
DR WPI; 1999-610845/52.
DR P-PSDB; AAY43621.
XX
PT Eliciting an in vivo immune response for prevention and treatment of
PT cancers.
XX
PS Disclosure; Fig 2; 26pp; English.
XX
CC The present sequence encodes a human telomerase reverse transcriptase
CC (TRT) polypeptide. The protein is used in the method of the invention.
CC The specification describes a method for activating a T lymphocyte,
CC comprising contacting the T lymphocyte with a dendritic cell that
CC expresses a TRT peptide in the context of a MHC class I or MHC class II

CC molecule. The protein causes induction of an in vivo immunological
CC response to telomerase activity. Cancer cells are characterized by
CC expression of endogenous TRF gene and the presence of detectable
CC telomerase activity. Therefore, by eliciting a specific immune response
CC to TRF or to TRF-expressing cells, it is possible to selectively target
CC proliferating cells for immunological destruction. The method is used for
CC eliciting an in vivo immune response to telomerase by activating a T
CC lymphocyte, and is useful for prevention and treatment of cancers and
CC other proliferation diseases/conditions

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 2; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCCGCGCGCTCCCGCTGCCGAGCCGCTCCCTGCTGCGCAGCCACTACCGC 60
DB 53 GCGATGCCGCGCGCTCCCGCTGCCGAGCCGCTCCCTGCTGCGCAGCCACTACCGC 112
QY 61 GAGTGTCTGCGCTGCGCAGCTTCTGTCGCGCGCTGCGGAGCCGAGGCTGCGGCTGTG 120
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QY 121 CAGCGCGGAGGAGCCCGCGCTTTCGCGCGCTGCGGAGCCGAGTGTGCTGCTGCGTCCC 180
DB 173 CAGCGCGGAGGAGCCCGCGCTTTCGCGCGCTGCGGAGCCGAGTGTGCTGCTGCGTCCC 232
QY 181 TGGAGCGCAGCG 240
DB 233 TGGAGCGCAGCG 292
QY 241 CTGCTGCGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGAGAGAGCTGTGCGCTTC 300
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DB 413 CGCAGCTACTGCG 472
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DB 593 GCTGCCACTCAGGCG 652
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QY 661 GGTGCGAGGAGGCG 720
DB 713 GGTGCGAGGAGGCG 772
QY 721 CGTGGCGCTGCGCGCTGAGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
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DB 833 GGCAGGAGCGGTGAGCGCGAGTACCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 892
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DB 1073 CAGCTGCGCGCGCT 1132
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DB 1433 CAGGTGTACGCGCTTGTGCG 1492
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DB 1793 GTCTGAGCAAGTTGCAAGCATTTGAATCAGACACTTGAAGAGGCTGAGCTGCGG 1852
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DB 1913 AGACTCGGCTTATCCCAAGCCTGACGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1972
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Db 2753 TTGGGGAAGACAGTGTGTAATCTTCCCTGTGAAGACGAGCCCTGGGTGGACGGCTTTT 2812
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Db 3413 AACCGGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGCGCACCC 3463

RESULT 5

AAH45901

ID AAH45901 standard; DNA; 4015 BP.

XX AC AAH45901;

DT 06-SEP-2001 (first entry)

XX DE Human hTERT gene.

XX KW Human; hTERT; telomerase; catalytic subunit; mRNA quantitation;

XX KM detection; beta-region; diagnosis; cancer; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT exon 1.274

FT exon 1.274

FT exon 1.274

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location/Qualifiers
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complement(2311.2325)
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PN	EP1108789-A2.						
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PD	20-JUN-2001.						
XX							
PF	15-DEC-2000; 2000EP-00127228.						
PR	16-DEC-1999; 99US-00465491.						
XX							
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.						
PI	Chang SP, Santini CD;						
DR	WPI; 2001-376930/40.						
XX							
PT	Quantitating expression of mRNA encoding hTERT, the catalytic subunit of telomerase, as an indicator of cancer, by amplifying RNA using primers						
PT	complementary to hTERT gene sequence and quantitating amplified products.						
XX							
PS	Claim 1; Page 5-7; 29pp; English.						
XX							
CC	The present sequence is that of the hTERT gene encoding the catalytic						
CC	subunit of the human telomerase, comprising 16 exons, which is useful in						
CC	a method for quantitating hTERT mRNA. The method is useful for detecting						
CC	the presence of beta-region (a 182 nucleotide region consisting of exons						
CC	7 and 8) of the hTERT-mRNA in a human sample for diagnosis and prognosis						
CC	of cancer. The method provides an accurate measure of telomerase activity						
CC	by selectively measuring mRNA that encodes an active hTERT protein						
XX							
SQ	Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;						
Query Match	100.0%; Score 3411; DB 4; Length 4015;						

	Best Local Similarity	100.0%;	Pred. No. 0;	
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QY	61	GAGTGTGCGCGTGCCAAGTTGTCGCGCGCTGGGGCCCAGGGCTGCGCGTGTG	120	
Db	113	GAGTGTGCGCGTGCCAAGTTGTCGCGCGCGCTGGGGCCCAGGGCTGCGCGTGTG	172	
QY	121	CAGCGCGGGAACCCGCGCTTTCGCGCGCTGGTGGCCAGTGCTGTGTGCTGCC	180	
Db	173	CAGCGCGGGAACCCGCGCTTTCGCGCGCTGGTGGCCAGTGCTGTGTGCTGCC	232	
QY	181	TGGGACGCACGCGCGCCCCCGCGCGCCCCCTCCTCCGCAAGTGTCTCTGTAAGAG	240	
Db	233	TGGGACGCACGCGCGCCCCCGCGCGCCCCCTCCTCCGCAAGTGTCTCTGTAAGAG	292	
QY	241	CTGTGGCCCCGAGTGTGACAAGAGGTGTGCGAGCGCGGCGCGAAGAAGTGTGCTTC	300	
Db	293	CTGTGTGCCCCGAGTGTGACAAGAGGTGTGCGAGCGCGGCGCGAAGAAGTGTGCTTC	352	
QY	301	GCGCTTCGCGCTGTGGAAGGGGCCCCGCGGGGCCCCCGAGGCTTCAACCAAGCGTG	360	
Db	353	GCGCTTCGCGCTGTGGAAGGGGCCCCGCGGGGCCCCCGAGGCTTCAACCAAGCGTG	412	
QY	361	CGCAGCTACCTGCCCCAACACGGTGAACCGCACATGCGGGGAGCGGGCGTGGGGCTG	420	
Db	413	CGCAGCTACCTGCCCCAACACGGTGAACCGCACATGCGGGGAGCGGGCGTGGGGCTG	472	
QY	421	CTGCTGCGCGCGTGGCGGACGAGCTGTGTGTTCACTGTGGACAGCTGCGCGCTCTT	480	
Db	473	CTGCTGCGCGCGTGGCGGACGAGCTGTGTGTTCACTGTGGACAGCTGCGCGCTCTT	532	
QY	481	GTGCTGTGTGCTCCAGCTGCGCTTACCAGTGTGCGGGCGCGCTGTACCAGCTCGC	540	
Db	533	GTGCTGTGTGCTCCAGCTGCGCTTACCAGTGTGCGGGCGCGCTGTACCAGCTCGC	592	
QY	541	GCTGCCACTCAGGCCCGCGCCCCCGCCACACGCTAGTAGACCCCGAAGCGTGTGGATGC	600	
Db	593	GCTGCCACTCAGGCCCGCGCCCCCGCCACACGCTAGTAGACCCCGAAGCGTGTGGATGC	652	
QY	601	GAAACGGGCTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCCCTGGGCTGCCAGCCCCG	660	
Db	653	GAAACGGGCTGGAACCATAGCGTCAAGGAGGCGCGGGTCCCCCTGGGCTGCCAGCCCCG	712	
QY	661	GGTCCGAGGAGGCGCGGGGCGCAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCAAG	720	
Db	713	GGTCCGAGGAGGCGCGGGGCGCAGTGCCAGCCGAAGTCTGCCGTGCCCCAAGAGGCCAAG	772	
QY	721	CGTGGCGTCCCCCTTAGACCGGAGCGGAGCGCCCCGTTGGGCAAGGGTCTGGGCCCAACCG	780	
Db	773	CGTGGCGTCCCCCTTAGACCGGAGCGGAGCGCCCCGTTGGGCAAGGGTCTGGGCCCAACCG	832	
QY	781	GCGCAGGACGCGTGGACCGAGTGAACCGTGTGTTCTGTGTGTGTCACTGCCAGACCCGCC	840	
Db	833	GCGCAGGACGCGTGGACCGAGTGAACCGTGTGTTCTGTGTGTGTCACTGCCAGACCCGCC	892	
QY	841	GAAGAAGCCACCTCTTTGAGAGGGTGCCTCTCTGGCACGCGCCACTCCCAACCATCCGTG	900	
Db	893	GAAGAAGCCACCTCTTTGAGAGGGTGCCTCTCTGGCACGCGCCACTCCCAACCATCCGTG	952	
QY	901	GCGCCGCGCAGCACACGCGGGGCCCCCATTCACATCGGGCCACCAAGTCCCTGGGACACG	960	
Db	953	GCGCCGCGCAGCACACGCGGGGCCCCCATTCACATCGGGCCACCAAGTCCCTGGGACACG	1012	
QY	961	CCTGTGTCCCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGAG	1020	
Db	1013	CCTGTGTCCCCGGTGTACGCGGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAAGAG	1072	
QY	1021	CAGCTGCGGCCCTCTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGG	1080	

[illegible]

QY	2161	ATCCCCCAGSACAGGCTCACGGAGGTATCGCCAGCATCATCAAAACCCAGAACACGTAC	2220
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QY	2221	TGCGTGCCTCGGTATGCCCCGTGCTCCAGAAAGCCGCCCATGCGCACAGTCCCGCAAGCCTTC	2280
Db	2273	TGCGTGCCTCGGTATGCCCCGTGCTCCAGAAAGCCGCCCATGCGCACAGTCCCGCAAGCCTTC	2332
QY	2281	AAGAGCCACGTCCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCAC	2340
Db	2333	AAGAGCCACGTCCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCAC	2392
QY	2341	CTGCAGGAGACCAAGCCCCGTGAGGGATGCCGTCTGTCATCGAGCAGAAGCTCCTCCCTGAAT	2400
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QY	2461	ATCAGGGGCAAGTCTTACGTCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACG	2520
Db	2513	ATCAGGGGCAAGTCTTACGTCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACG	2572
QY	2521	CTGCTCTGCAGCCTGTGTCTACGGCGACATGAGAACAAAGCTGTTGCGGGGATTCGGCGG	2580
Db	2573	CTGCTCTGCAGCCTGTGTCTACGGCGACATGAGAACAAAGCTGTTGCGGGGATTCGGCGG	2632
QY	2581	GACGGGCTGCTCCTGCGTTTGGTGATGATTTCTGTGTGACACCTCACTCAACCCAC	2640
Db	2633	GACGGGCTGCTCCTGCGTTTGGTGATGATTTCTGTGTGACACCTCACTCAACCCAC	2692
QY	2641	GCGAAAACTTCTCAGGAACCCCTGTCCGAGGTGCTCCTGATATGCTGCGTGGAAC	2700
Db	2693	GCGAAAACTTCTCAGGAACCCCTGTCCGAGGTGCTCCTGATATGCTGCGTGGAAC	2752
QY	2701	TTGCGGAGACAGATGTTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTT	2760
Db	2753	TTGCGGAGACAGATGTTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTT	2812
QY	2761	GTTCAGATGCCGCCCAACGGCCTATTTCCCTGTGTCGGCCTGTGCTGATACCCGACC	2820
Db	2813	GTTCAGATGCCGCCCAACGGCCTATTTCCCTGTGTCGGCCTGTGCTGATACCCGACC	2872
QY	2821	CTGAGGTGCAGAGCACTACTCCAGCTATGCCCGAACCTCCATCAGAGCCAGTCTCAC	2880
Db	2873	CTGAGGTGCAGAGCACTACTCCAGCTATGCCCGAACCTCCATCAGAGCCAGTCTCAC	2932
QY	2881	TTCAACCGCGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTGGGGTCTTGCGG	2940
Db	2933	TTCAACCGCGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTGGGGTCTTGCGG	2992
QY	2941	CTGAAGTGTACAGCCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGCACC	3000
Db	2993	CTGAAGTGTACAGCCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGGTGTGCACC	3052
QY	3001	AACATCTACAGATCCTCCTGCTGCAGGCGTACAGTTTACGCATGTGTCTGCAGCTC	3060
Db	3053	AACATCTACAGATCCTCCTGCTGCAGGCGTACAGTTTACGCATGTGTCTGCAGCTC	3112
QY	3061	CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACACG	3120
Db	3113	CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACACG	3172
QY	3121	GCCTCCCTCTGCTACTCCATCCTGAAGCCCAAGACGACGGGATGTGCTGGGGGCCAAG	3180
Db	3173	GCCTCCCTCTGCTACTCCATCCTGAAGCCCAAGACGACGGGATGTGCTGGGGGCCAAG	3232
QY	3181	GGCGCCGCGCGCCTCTGCCCTCCGAGCGCTGCAGTGGCTGTGCCACCAAGCATTCCTG	3240
Db	3233	GGCGCCGCGCGCCTCTGCCCTCCGAGCGCTGCAGTGGCTGTGCCACCAAGCATTCCTG	3292

QY	3241	CTCAAGCTGACTCGACACCGGTGTCA	CACCTTA	CGTGGCACTCTCTGGGGTCACT	CAAGACAGCC	3300
Db	3293	CTCAAGCTGACTCGACACCGGTGTCA	CACCTTA	CGTGGCACTCTCTGGGGTCACT	CAAGACAGCC	3352
QY	3301	CAGACGCAGCTGAGTCTGGAAAGCT	CCCCGGG	ACGACGCTGA	CTGCCCTG	3360
Db	3353	CAGACGCAGCTGAGTCTGGAAAGCT	CCCCGGG	ACGACGCTGA	CTGCCCTG	3412
QY	3361	AACCCGGCACTGCCCCCACAAGTT	CAAGACC	ATCCTG	CACTGATG	3411
Db	3413	AACCCGGCACTGCCCCCACAAGTT	CAAGACC	ATCCTG	CACTGATG	3463

RESULT 6
AADA6821
ID AADA6821 standard; cDNA; 4015 BP.

AC	AAD46821;
XX	
DT	27-JAN-2003 (first entry)
...	

Human telomerase reverse transcriptase (TERT) cDNA.

KM Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; TERT;
KM transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; human; enzyme;
KM telomerase reverse transcriptase; gene; ss.

Homo sapiens.

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FT		/*tag= a
FT		/product= "Human telomerase reverse transcriptase"

PN WO200274948-A2.

PD 26-SEP-2002.

PF 21-MAR-2002; 2002WO-CA0000378.

PR 21-MAR-2001; 2001US-027781P.

PA (GERO-) GERON CORP.

PI Denning C, Clark AJ, Schiff JM;

WPI; 2002-759895/82.

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PT Mammalian cells, useful for producing animal tissues with carbohydrate antigens that are compatible for transplantation into human patients.

PS Disclosure; Page 33-34; 71pp; English.

CC The invention relates to animal tissues with carbohydrate antigens that
CC are compatible for transplantation into human patients. The mammalian
CC cell is inactivated homozygously for expression of alpha(1,3)galactosyl-
CC transferase (alpha1,3GT) gene and comprises a transgene for alpha(1,2)-
CC fucosyltransferase (alpha1,2FT). It is useful for producing animal tissue
CC with carbohydrate antigens that are compatible for transplantation into
CC human patients. The present sequence is human telomerase reverse
CC transcriptase (TERT) cDNA used in the invention

Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match	100.0%;	Score 3411;	DB 6;	Length 4015;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3411; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

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| | | | |
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QY	61	GAGGTGCTGCCGCTGGCCACGTTTCGTGCGGCGCCTGGGGCCCCAGGGCTGCGGGCTGTG	120
Db	113	GAGGTGCTGCCGCTGGCCACGTTTCGTGCGGCGCCTGGGGCCCCAGGGCTGCGGGCTGTG	172
QY	121	CAGCGCGGGGACCCGCGGCTTCCGCGCGCTGTTGACCCAGTGCCTGTGTGCGTCCC	180
Db	173	CAGCGCGGGGACCCGCGGCTTCCGCGCGCTGTTGACCCAGTGCCTGTGTGCGTCCC	232
QY	181	TGGGACGCCACGGCGCCCGCCCGCCCGCCTCTCTTCCGCCAGTGTCTGCTCTGAAGGAG	240
Db	233	TGGGACGCCACGGCGCCCGCCCGCCCGCCTCTCTTCCGCCAGTGTCTCTGCTCTGAAGGAG	292

Qy 241 CTGCTGCCCCGAGTCTCTGCAAGAGCTGTGCGAGCGCGCCGAAGACGTGCTGCGCTTC 300
293 CTGCTGCCCCGAGTCTCTGCAAGAGCTGTGCGAGCGCGCCGAAGACGTGCTGCGCTTC 352
Db

DQ 301 GGCCTTCGCGCTGCTGAACGGGGCCCCCGAGGCTTCAACCAACGCGTG 360
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DB 353 GGCCTTCGCGCTGCTGAACGGGGCCCCCGAGGCTTCAACCAACGCGTG 412

[illegible]

Qy	421	CTGCTGCGCGCGCTGGGCGACGACGTGCTGTTCAACCTGCTGGACGCTGCGGCTCTTT	480
Db	473	CTGCTGCGCGCGCGCTGGGCGACGACGTGCTGTTCAACCTGCTGGACGCTGCGGCTCTTT	532

Qy 481 GTGCTGGTGGCTCCAGCTGGCCCTACCAAGTGTCGGGCGCCGCTGTACCAAGCTCGGC 540
|||
Db 533 GTGCTGGTGGCTCCAGCTGGCCCTACCAAGTGTCGGGCGCCGCTGTACCAAGCTCGGC 592

QY 541 GCTGCCACTCAGGCCGCCGCCCCACACGCTAGTGACCCCGAAGCGCTTGGATGC 600
|||||
Db 593 GCTGCCACTCAGGCCGCCGCCCCACACGCTAGTGACCCCGAAGCGCTTGGATGC 652

QY 601 GAACGGCCCTGAAACCATAGCCCTCAGGGAGGCCCGGGCTCCCCCTGGGCTGCGCAGCCCCG 660

Dp 653 GAACGGGCTGAAACCATAGCCCTCAGGGAGGCCCGGGCTCCCCCTGGGCTGCGCAGCCCCG 712

QY 661 GGTCCGAGGAGCGCGCGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAAG 720

Dh 713 GGTGCGAGGAGGCGCGCGGGGCACTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAAG 772

QY 721 CGTGGCGCTGCCCTGAGCCGGAAGCGGACGCCCGTTGGGCAAGGGTCTGGGCCCAACCG 780

Dh 773 CGTGGCGCTGCCCTGAGCCGGAAGCGGACGCCCGTTGGGCAAGGGTCTGGGCCCAACCG 832

QY 781 GGCAAGACGCGTGGACCCAGTAGACCCTGGTTCTGTGTTGGTGTCACCTGCCAGACCCGCC 840
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Db 833 GGCAGGACGCGCTGAACCCAGTAGACCCTGGTTCTGTGTTGGTGTCACCTGCCAGACCCGCC 892

841 GAAGAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCAAGGCGCACTCCACCCATCCGTG 900

[illegible][illegible]

QY 1021 CAGCTGGGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTGGAGG 108

1081 CTCGTGAGACCATCTTTCTGGGTTCCAGGCCCTGCAATGCCAGGGACTCCCCGAGGTTG 1140

1141 CCCCCCTGCCCAAGCGCTACTGGCAATGCGGCCCTGTCTCGAGCTGCTTGGAAC 1200

Db 1193 CCCCCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGTGTGGAAC 1252
QY 1201 CACGCGAGTGGCCCTACGCGGGTGTCTCTCAAGACGACTGCCCGCTGAGAGTGGCTC 1260
Db 1253 CACGCGAGTGGCCCTACGCGGGTGTCTCTCAAGACGACTGCCCGCTGAGAGTGGCTC 1312
QY 1261 ACCCAGCAGCGCGTGTGTGTGCCCCGAGAGAGCCCGAGGCTGTGGCGGCCCCGAG 1320
Db 1313 ACCCAGCAGCGCGTGTGTGTGCCCCGAGAGAGCCCGAGGCTGTGGCGGCCCCGAG 1372
QY 1321 GAGGAGACACAGAGCCCGCTGCGCTGTGAGCTGCTCCGACAGACAGAGCCCTGG 1380
Db 1373 GAGGAGACACAGAGCCCGCTGCGCTGTGAGCTGCTCCGACAGACAGAGCCCTGG 1432
QY 1381 CAGGTGTACGCGCTTCTGCGGGGCTGCTGCGCGCGCTGTGCCCCAGGCTCTGGGGC 1440
Db 1433 CAGGTGTACGCGCTTCTGCGGGGCTGCTGCGCGCGCTGTGCCCCAGGCTCTGGGGC 1492
QY 1441 TCCAGGACACAGAGCCCGCTTCTCAGAGAACACCAAGAGTTCACTCTCCCTGGGAG 1500
Db 1493 TCCAGGACACAGAGCCCGCTTCTCAGAGAACACCAAGAGTTCACTCTCCCTGGGAG 1552
QY 1501 CATGCCAAGCTCTCGCTGACAGAGCTGACGTGAGAGATGAGCGTGGGGAATGCGCTTGG 1560
Db 1553 CATGCCAAGCTCTCGCTGACAGAGCTGACGTGAGAGATGAGCGTGGGGAATGCGCTTGG 1612
QY 1561 CTGCGCAGAGAGCCAGGGGTTGGCTGTGTTCCGCGCCGACAGACACCTGCTGAGAGAG 1620
Db 1613 CTGCGCAGAGAGCCAGGGGTTGGCTGTGTTCCGCGCCGACAGACACCTGCTGAGAGAG 1672
QY 1621 ATCTGGCCAAAGTTCTCTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAGGTCT 1680
Db 1673 ATCTGGCCAAAGTTCTCTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAGGTCT 1732
QY 1681 TTCTTTATGTACCGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGT 1740
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QY 1741 GTCTGAGCAAGTTGCAAGCAATTGGAATCAGACGACTTGAAGAGGTTGACGCTGCGG 1800
Db 1793 GTCTGAGCAAGTTGCAAGCAATTGGAATCAGACGACTTGAAGAGGTTGACGCTGCGG 1852
QY 1801 GAGCTGTGGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCCCGCTGCTGACGCTCC 1860
Db 1853 GAGCTGTGGAAGCAGAGGTCAGGACGATCGGGAAGCCAGGCCCGCTGCTGACGCTCC 1912
QY 1861 AGACTCCGCTTCACTCCCAAGCCTGACGCGGCTGCGCGCGATTTGAACATGACTACGTC 1920
Db 1913 AGACTCCGCTTCACTCCCAAGCCTGACGCGGCTGCGCGCGATTTGAACATGACTACGTC 1972
QY 1921 GTGGAGCCAGAACTTCCGACAGAGAAAAGAGGCGCAGCGCTCACTCGAGGTTGAAG 1980
Db 1973 GTGGAGCCAGAACTTCCGACAGAGAAAAGAGGCGCAGCGCTCACTCGAGGTTGAAG 2032
QY 1981 GCACTGTTCAAGCTGTCAACTACGAGCGGCGCGCGCGCGCTCTGGGCGCTCT 2040
Db 2033 GCACTGTTCAAGCTGTCAACTACGAGCGGCGCGCGCGCGCTCTGGGCGCTCT 2092
QY 2041 GTGCTGGGCTGACGATATCCACAGGCGCTGGCGCACTTCTGCTGCGTGTGCGGGCC 2100
Db 2093 GTGCTGGGCTGACGATATCCACAGGCGCTGGCGCACTTCTGCTGCGTGTGCGGGCC 2152
QY 2101 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGCGCGCTACGACACC 2160
Db 2153 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGCGCGCTACGACACC 2212
QY 2161 ATCCCCCAGACAGGCTCACGAGGTGATCGCAGCATCATCAACCCAGAACACGCTAC 2220
Db 2213 ATCCCCCAGACAGGCTCACGAGGTGATCGCAGCATCATCAACCCAGAACACGCTAC 2272
QY 2221 TGCGTGCCTGCTATGCGCTGTGCTCAGAGGCGCGCCATGGGCACTCCGCAAGGCTTC 2280

Db 2273 TGCGTGCCTGCTATGCGCTGTGCTCAGAGGCGCGCCCATGGGCACTCCGCAAGGCTTC 2332
QY 2281 AAGAGCACGCTCTTACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2333 AAGAGCACGCTCTTACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2392
QY 2341 CTGCAAGAGACCAAGCGCTGAGGAGATGCGCTGATCGAGCAGAGAGCTCTCCCTGAAT 2400
Db 2393 CTGCAAGAGACCAAGCGCTGAGGAGATGCGCTGATCGAGCAGAGAGCTCTCCCTGAAT 2452
QY 2401 GAGGCGCAGAGTGGCTCTTTCAGAGCTTCTTCAAGCTTCACTGATGTCACACGCGTGC 2460
Db 2453 GAGGCGCAGAGTGGCTCTTTCAGAGCTTCTTCAAGCTTCACTGATGTCACACGCGTGC 2512
QY 2461 ATCAGGGGCAAGTCTTACAGTCCAGTGCAGGAGATCCCGCAGGCTCCATCTCTCCACG 2520
Db 2513 ATCAGGGGCAAGTCTTACAGTCCAGTGCAGGAGATCCCGCAGGCTCCATCTCTCCACG 2572
QY 2521 CTGCTCTGAGCCTGTGCTACGCGCAGATGGAACAAGCTGTTGGCGGGAATTCGCGG 2580
Db 2573 CTGCTCTGAGCCTGTGCTACGCGCAGATGGAACAAGCTGTTGGCGGGAATTCGCGG 2632
QY 2581 GACGGGCTGCTCTGCGTTTGTGATGATTTCTGTTGTGACACCTCACTCAACCCAC 2640
Db 2633 GACGGGCTGCTCTGCGTTTGTGATGATTTCTGTTGTGACACCTCACTCAACCCAC 2692
QY 2641 GCGAAACCTTCTCTCAGAGACCCCTGTCCAGAGTGTCCCTGAGTATGCTGCTGTGAAC 2700
Db 2693 GCGAAACCTTCTCTCAGAGACCCCTGTCCAGAGTGTCCCTGAGTATGCTGCTGTGAAC 2752
QY 2701 TTGCGGAAGACAGTGTGAATTTCCCTGTAGAGACAGAGGCCCTGGGTGCAAGGCTTT 2760
Db 2753 TTGCGGAAGACAGTGTGAATTTCCCTGTAGAGACAGAGGCCCTGGGTGCAAGGCTTT 2812
QY 2761 GTTCAGATGCGCGCCCAAGGCTATTTCCCTGTGTCGCGCTGCTGTGATACCCGAGAC 2820
Db 2813 GTTCAGATGCGCGCCCAAGGCTATTTCCCTGTGTCGCGCTGCTGTGATACCCGAGAC 2872
QY 2821 CTGGAAGTGACAGAGCACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCAC 2880
Db 2873 CTGGAAGTGACAGAGCACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGCGGCTTCAAGGCTGGAGGAGACATGCTGCAAACTCTTTGGGGTCTTGCGG 2940
Db 2933 TTCAACCGCGGCTTCAAGGCTGGAGGAGACATGCTGCAAACTCTTTGGGGTCTTGCGG 2992
QY 2941 CTGAAGTGTACAGGCTGTTTCTGAGTTTGAAGTGAACAGCCTCCAGACGCTGACACG 3000
Db 2993 CTGAAGTGTACAGGCTGTTTCTGAGTTTGAAGTGAACAGCCTCCAGACGCTGACACG 3052
QY 3001 AACATCTACAAGATCTCTGCTGACAGGCTGACAGGTTTCAAGCATGTGCTGACGCTC 3060
Db 3053 AACATCTACAAGATCTCTGCTGACAGGCTGACAGGTTTCAAGCATGTGCTGACGCTC 3112
QY 3061 CCATTTCAAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGCTGATCTGACACG 3120
Db 3113 CCATTTCAAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGCTGATCTGACACG 3172
QY 3121 GCTCCCTCTGCTACTTCACTCTGAAGCCAGAAAGCAGAGGATGCTGGGGCCAAAG 3180
Db 3173 GCTCCCTCTGCTACTTCACTCTGAAGCCAGAAAGCAGAGGATGCTGGGGCCAAAG 3232
QY 3181 GCGCGCGCGCGCTGCTGCGCTCCAGAGCGGTGACGTGCTGTCACCAAGCATTCCTG 3240
Db 3233 GCGCGCGCGCGCTGCTGCGCTCCAGAGCGGTGACGTGCTGTCACCAAGCATTCCTG 3292
QY 3241 CTCAAGCTGACTGACACCGTGTACCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTG 3300
Db 3293 CTCAAGCTGACTGACACCGTGTACCTGACCTGACCTGCTGCTGCTGCTGCTGCTGCTG 3352
QY 3301 CAGACGAGCTGAGTGGAGGCTCCCGGAGACAGCGTGAAGTCTGAGGCGCGAGCC 3360
Db 3353 CAGACGAGCTGAGTGGAGGCTCCCGGAGACAGCGTGAAGTCTGAGGCGCGAGCC 3412

QY 3361 AACCCGGCACTGCCCTCAGACTTCAGACCACTCTGGACTGATGGCCACCC 3411
Db 3413 AACCCGGCACTGCCCTCAGACTTCAGACCACTCTGGACTGATGGCCACCC 3463

RESULT 7
ABA97534
ID ABA97534 standard; DNA; 4015 BP.

AC ABA97534;
XX
DT 05-APR-2002 (first entry)
XX

DE Cancer cell discrimination method related human DNA.

XX Human; telomerase; enzyme; cancer cell discrimination; gene;
KW reverse transcriptase; ds.

XX Homo sapiens.

XX JP2001309791-A.

XX 06-NOV-2001.

XX 02-MAY-2000; 2000JP-00138250.

XX 02-MAY-2000; 2000JP-00138250.

XX (KANE/) KANEUCHI H.
PA (KAMI/) KAMIMORI M.

XX WPI; 2002-134853/18.

PT Discrimination of a cancer cell in a sample tissue, comprises determining
the expression level of a reverse transcriptase component of telomerase
using a hybridization assay.

PS Claim 2; Page 9-10; 16pp; Japanese.

XX The present invention relates to a method for the discrimination of a
cancer cell in a sample tissue, which involves determining the expression
level of a reverse transcriptase component of telomerase in a cell
constituting the sample tissue by an in situ hybridization of the mRNA of
the enzyme, and judging a cell showing a higher expression level than
that of the reverse transcriptase component of telomerase in a normal
cell to be a cancer cell. The present sequence is a human DNA used in the
exemplification of the invention

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 6; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCCGCGCGCTCCCGCTGCCGAGCCGCTGCTCCCTGCTGCCAGCACTACCGC 60
Db 53 GCGATGCCGCGCGCTCCCGCTGCCGAGCCGCTGCTCCCTGCTGCCAGCACTACCGC 112
QY 61 GAGGTGCTGCCGCTGCCAGCTTCGTGCGGCGCTTGCGGCCCAAGGCTGGCGCTGGT 120
Db 113 GAGGTGCTGCCGCTGCCAGCTTCGTGCGGCGCTTGCGGCCCAAGGCTGGCGCTGGT 172
QY 121 CAGCGCGGGGACCGCGCGGCTTCCGCGCGCTGTGGGCCCAAGTCTGTGTGCGTGGCC 180
Db 173 CAGCGCGGGGACCGCGCGGCTTCCGCGCGCTGTGGGCCCAAGTCTGTGTGCGTGGCC 232
QY 181 TGGGACGACAGCG 240
Db 233 TGGGACGACAGCG 292
QY 241 CTGCTGCG 300

Db 293 CTGCTGCG 352
QY 301 GCGTTGCGCGCTGCTGGAACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GCGTTGCGCGCTGCTGGAACGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGCTACCTGCGCCCAACACCGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTG 420
Db 413 CGCAGCTACCTGCGCCCAACACCGGTGACCGACGCACTGCGGGGAGCGGGGCGTGGGGCTG 472
QY 421 CTGCTGCG 480
Db 473 CTGCTGCG 532
QY 481 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 533 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
QY 541 GCTGCCACTCAGGCG 600
Db 593 GCTGCCACTCAGGCG 652
QY 601 GAACGGGCGCTGGAACCATATAGCGTCAAGGAGGCGCGGGTCCCTGCGCGCTGCCAGCCCG 660
Db 653 GAACGGGCGCTGGAACCATATAGCGTCAAGGAGGCGCGGGTCCCTGCGCGCTGCCAGCCCG 712
QY 661 GGTGCGAGGAGGCG 720
Db 713 GGTGCGAGGAGGCG 772
QY 721 CGTGCGCGCTGCGCGCTGAGCGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 773 CGTGCGCGCTGCGCGCTGAGCGCGGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
QY 781 GCGCAGGAGCGCGTGAACCGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 833 GCGCAGGAGCGCGTGAACCGAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892
QY 841 GAAGAAGCCACTCTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 893 GAAGAAGCCACTCTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY 901 GCGCGCGCAGCAACG 960
Db 953 GCGCGCGCAGCAACG 1012
QY 961 CCTGTGCGCGCGCGGTGACGCGCGGAGCAAGCACTTCTCTACTCTCTCAAGCAAGAGAG 1020
Db 1013 CCTGTGCGCGCGCGGTGACGCGCGGAGCAAGCACTTCTCTACTCTCTCAAGCAAGAGAG 1072
QY 1021 CAGCTGCGCGCGCTCTCTCTACTCACTCACTCTGAGGCGCGCGCGCGCGCGCGCGCG 1080
Db 1073 CAGCTGCGCGCGCTCTCTCTACTCACTCACTCTGAGGCGCGCGCGCGCGCGCGCGCG 1132
QY 1081 CTGCTGAGAACATTTTCTGAGTTTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 1133 CTGCTGAGAACATTTTCTGAGTTTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1192
QY 1141 CCGCGCGTGGCG 1200
Db 1193 CCGCGCGTGGCG 1252
QY 1201 CAGCGCAGTGGCG 1260
Db 1253 CAGCGCAGTGGCG 1312
QY 1261 ACCCAGCAGCGCGGTGTGTGTGCGCGGGAAGAGCCCAAGGCTGTGGCGCGCGCGCG 1320
Db 1313 ACCCAGCAGCGCGGTGTGTGTGCGCGGGAAGAGCCCAAGGCTGTGTGGCGCGCGCGCG 1372
QY 1321 GAGGAGACACAGACCCCG 1380
Db 1373 GAGGAGACACAGACCCCG 1432

QY	1381	CAGGTGTA	CGGCTT	CGTGCGGG	CGCTG	CGCTTG	CGCCCGG	CGTGTG	CGCCCC	CAGGCT	CTTGGGC	1440	
Db	1433	CAGGTGTA	CGGCTT	CGTGCGGG	CGCTG	CGCCCGG	CGTGTG	CGCCCC	CAGGCT	CTTGGGC		1492	
QY	1441	TCCAGGCA	CAACGAA	CGCCGCTT	CCTCAG	GAACAC	CAAGAA	GTTCAT	CTCCCTG	GGGAAG		1500	
Db	1493	TCCAGGCA	CAACGAA	CGCCGCTT	CCTCAG	GAACAC	CAAGAA	GTTCAT	CTCCCTG	GGGAAG		1552	
QY	1501	CATGCCAA	AGCTCT	CGCTGCA	GAGCTGA	CGTGA	AAGATGA	CGCTG	CGGGA	CTGCGCTT	GG	1560	
Db	1553	CATGCCAA	AGCTCT	CGCTGCA	GAGCTGA	CGTGA	AAGATGA	CGCTG	CGGGA	CTGCGCTT	GG	1612	
QY	1561	CTGCGGAG	GAGCCCC	CAGGGG	TGGCTGT	GTTC	CGGCGC	CAGACA	CCGTCTG	CGTGA	GAG	1620	
Db	1613	CTGCGGAG	GAGCCCC	CAGGGG	TGGCTGT	GTTC	CGGCGC	CAGACA	CCGTCTG	CGTGA	GAG	1672	
QY	1621	ATCCTG	CCCAAGTT	CCCTGC	ACTG	GTGATG	AGTGTG	TACGTG	AGCTG	CTCAG	GTCT	1680	
Db	1673	ATCCTG	CCCAAGTT	CCCTGC	ACTG	GTGATG	AGTGTG	TACGTG	AGCTG	CTCAG	GTCT	1732	
QY	1681	TTCTTTAT	TATGTCA	CGGAGAC	CACTTTCA	AAAGAC	AGGCTTTT	TTCTAC	CCGGA	GAGT		1740	
Db	1733	TTCTTTAT	TATGTCA	CGGAGAC	CACTTTCA	AAAGAC	AGGCTTTT	TTCTAC	CCGGA	GAGT		1792	
QY	1741	GTCTGAG	CAAGTTG	CAAAAG	CAATTGA	ATCAG	ACACTTGA	AGAGG	TGAC	GTGCGG		1800	
Db	1793	GTCTGAG	CAAGTTG	CAAAAG	CAATTGA	ATCAG	ACACTTGA	AGAGG	TGAC	GTGCGG		1852	
QY	1801	GAGCTGT	CGGAAG	CAGAGGT	CAAGC	ATCGGA	AGCCAG	CCCGC	CTGTGA	CGTCC		1860	
Db	1853	GAGCTGT	CGGAAG	CAGAGGT	CAAGC	ATCGGA	AGCCAG	CCCGC	CTGTGA	CGTCC		1912	
QY	1861	AGACTCG	CTTCAT	CCCCCA	AGCCTGA	CGGGCTG	CGCCGAT	TGTGA	ACATGA	CACTAC	GTG	1920	
Db	1913	AGACTCG	CTTCAT	CCCCCA	AGCCTGA	CGGGCTG	CGCCGAT	TGTGA	ACATGA	CACTAC	GTG	1972	
QY	1921	GTGGGAG	CCAGAAC	GTTCCG	CAGAGAA	AGAGG	CCGAC	GTCTCA	CCCTGA	GGGTGA	AG	1980	
Db	1973	GTGGGAG	CCAGAAC	GTTCCG	CAGAGAA	AGAGG	CCGAC	GTCTCA	CCCTGA	GGGTGA	AG	2032	
QY	1981	GCACTGT	TCAAG	TGCTCA	ACTACG	AGCGG	CGCGCC	CGCCGCT	CTTG	GGCGCT	CT	2040	
Db	2033	GCACTGT	TCAAG	TGCTCA	ACTACG	AGCGG	CGCGCC	CGCCGCT	CTTG	GGCGCT	CT	2092	
QY	2041	GTGCTGG	GCCTGA	CGATAT	CCA	CAGGG	CCCTGG	CGCA	CCTT	CGTGC	GTGCGGG	2100	
Db	2093	GTGCTGG	GCCTGA	CGATAT	CCA	CAGGG	CCCTGG	CGCA	CCTT	CGTGC	GTGCGGG	2152	
QY	2101	CAGGA	CCCCCG	CGCTGA	GTACTTT	GTCA	AGGTGA	TGTGA	CGGG	CGCGTA	CGACAC	2160	
Db	2153	CAGGA	CCCCCG	CGCTGA	GTACTTT	GTCA	AGGTGA	TGTGA	CGGG	CGCGTA	CGACAC	2212	
QY	2161	ATCCCC	CCAGGAC	AGGCTT	CA	CGGAG	GTATCG	CCACAT	CA	TCAA	ACCCCA	GAACAC	2220
Db	2213	ATCCCC	CCAGGAC	AGGCTT	CA	CGGAG	GTATCG	CCACAT	CA	TCAA	ACCCCA	GAACAC	2272
QY	2221	TGCGTGC	GTGCGTAT	GCGGTG	GTCC	AGAA	GGCCG	CCATGG	GCAC	GTCCG	CAAGG	2280	
Db	2273	TGCGTGC	GTGCGTAT	GCGGTG	GTCC	AGAA	GGCCG	CCATGG	GCAC	GTCCG	CAAGG	2332	
QY	2281	AAGAG	CCACGTCT	CTA	CCTTGA	CAGAC	CTCCA	AGCCG	TACATG	CGAC	AGTTG	2340	
Db	2333	AAGAG	CCACGTCT	CTA	CCTTGA	CAGAC	CTCCA	AGCCG	TACATG	CGAC	AGTTG	2392	
QY	2341	CTGCAG	GAGACCA	AGCCGCT	GAGGAT	GCCGTG	TCATCG	AGCAG	AGCTT	CTCC	TGAAT	2400	
Db	2393	CTGCAG	GAGACCA	AGCCGCT	GAGGAT	GCCGTG	TCATCG	AGCAG	AGCTT	CTCC	TGAAT	2452	
QY	2401	GAGGCC	AGCAGT	GCCCTT	TCGAC	GTCTT	CCTAC	GCTTCAT	GTG	CCAC	ACG	2460	
Db	2453	GAGGCC	AGCAGT	GCCCTT	TCGAC	GTCTT	CCTAC	GCTTCAT	GTG	CCAC	ACG	2512	

QY	2461	ATCAGGGGCAAGTCTCTACGTTCCAGTGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACG	2520
Db	2513	ATCAGGGGCAAGTCTCTACGTTCCAGTGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACG	2572
QY	2521	CTGCTCTGCAGCCTGTGTCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCCGGCG	2580
Db	2573	CTGCTCTGCAGCCTGTGTCTACGGCGACATGAGAACAAAGCTGTTTGGGGGATTCCGGCG	2632
QY	2581	GACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACTCAACCCAC	2640
Db	2633	GACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACTCAACCCAC	2692
QY	2641	GCGAAAAACCTTCTCAGAACCTGTGTCCGAGGTGTCCCTAGTATGCGTGCCTGTGAAC	2700
Db	2693	GCGAAAAACCTTCTCAGAACCTGTGTCCGAGGTGTCCCTAGTATGCGTGCCTGTGAAC	2752
QY	2701	TTGCGGAAGACAGTGTGTGAACCTCCCTGTAGAAAGCAGAGCCCTGGGTGCACGGCTTTT	2760
Db	2753	TTGCGGAAGACAGTGTGTGAACCTCCCTGTAGAAAGCAGAGCCCTGGGTGCACGGCTTTT	2812
QY	2761	GTTCAGATGCCGGCCCAAGGCTTATTTCCCTGTGTGCGGCTGTGCTGTGATACCCGACC	2820
Db	2813	GTTCAGATGCCGGCCCAAGGCTTATTTCCCTGTGTGCGGCTGTGCTGTGATACCCGACC	2872
QY	2821	CTGAGGTGCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCAC	2880
Db	2873	CTGAGGTGCAGAGCGACTACTCCAGCTATGCCCGACCTCCATCAGAGCCAGTCTCAC	2932
QY	2881	TTCAACCGCGGCTTCAAGGCTGGAGGAACATGCGTCCAAACTCTTTGGGCTTTGCGG	2940
Db	2933	TTCAACCGCGGCTTCAAGGCTGGAGGAACATGCGTCCAAACTCTTTGGGCTTTGCGG	2992
QY	2941	CTGAAGTGTACAGCCTGTTTCTGATTTGACGTGAACAGCCTCCAGACGCTGTGCACC	3000
Db	2993	CTGAAGTGTACAGCCTGTTTCTGATTTGACGTGAACAGCCTCCAGACGCTGTGCACC	3052
QY	3001	AAATCTACAGATCTCTCTGCTGCAGGCGTACAGCTTTCACGCATGTGTCTGCAGCTC	3060
Db	3053	AAATCTACAGATCTCTCTGCTGCAGGCGTACAGCTTTCACGCATGTGTCTGCAGCTC	3112
QY	3061	CCATTTCATCAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGCGTCACTCTGACACG	3120
Db	3113	CCATTTCATCAGCAAGTTTGGAAAGAACCCCAATTTTCTGCGCGTCACTCTGACACG	3172
QY	3121	GCCTCCCTCTGCTACTCCATCTGAAAGCCAAAGAACGACGGGATGTGCTGGGGGCCAAG	3180
Db	3173	GCCTCCCTCTGCTACTCCATCTGAAAGCCAAAGAACGACGGGATGTGCTGGGGGCCAAG	3232
QY	3181	GGGCGCGCGGCGCTCTGCCCTCCGAGGCGGTGACGTGGTGTGCGCAACCAAGCATTCCTG	3240
Db	3233	GGGCGCGCGGCGCTCTGCCCTCCGAGGCGGTGACGTGGTGTGCGCAACCAAGCATTCCTG	3292
QY	3241	CTCAAGCTGACTGACACCCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGACAGCC	3300
Db	3293	CTCAAGCTGACTGACACCCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGACAGCC	3352
QY	3301	CAGACGCACTGAGTCGGGAAGCTCCCGGGGACGACGCTGACTGCTGAGGCGCAGCC	3360
Db	3353	CAGACGCACTGAGTCGGGAAGCTCCCGGGGACGACGCTGACTGCTGAGGCGCAGCC	3412
QY	3361	AAACCGGCACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCC	3411
Db	3413	AAACCGGCACTGCCCTCAGACTTCAAGACCATCCTGACTGATGGCCACCC	3463

RESULT 8	
ACC58039	
ID	ACC58039 standard; cDNA; 4015 BP
XX	
AC	ACC58039;
XX	
DT	11-AUG-2003 (first entry)
XX	

DE Human telomerase reverse transcriptase cDNA.
XX
KW Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KW short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KW immunosuppressive; antifertility; fungicide; antiparasitic;
KW antiinflammatory; human; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "TERT"
XX WO2003035667-A2.
XX PD 01-MAY-2003.
XX PF 16-OCT-2002; 2002WO-US033065.
XX PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX PA (UTRP) UNIV ROCHESTER.
XX
XX Rowley PT;
XX
XX WPI; 2003-403336/38.
DR P-PSDB; ABR42384.
XX
XX Novel double-stranded short interfering RNA having sense and antisense
PT nucleic acids which are complementary to each other and to target nucleic
PT acid e.g., telomerase RNA or mRNA encoding telomerase reverse
PT transcriptase.
XX
XX Disclosure; Fig 3A-B; 37pp; English.
XX
XX The present sequence is that of human telomerase reverse transcriptase
CC (TERT) cDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 3411; DB 7; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 CTGTGGCCCGAGTGTGTGACAGAGGCTGTGACGCGCGCGGCGGAAGACGCTGCGCTTC 300
DB 293 CTGTGGCCCGAGTGTGTGACAGAGGCTGTGACGCGCGCGGCGGAAGACGCTGCGCTTC 352
QY 301 GAGCTTGGCGCTGTGACG 360
DB 353 GAGCTTGGCGCTGTGACG 412
QY 361 CGAGCTACCTGCCCAACACGCTGACCGCACTGCGGGGAGCGGGGCGTGGGGCTG 420
DB 413 CGAGCTACCTGCCCAACACGCTGACCGCACTGCGGGGAGCGGGGCGTGGGGCTG 472
QY 421 CTGTGCGCGCGGTGGCGGACGAGCTGTGTTCACTGTGCGACGCTGCGGCTCTT 480
DB 473 CTGTGCGCGCGGTGGCGGACGAGCTGTGTTCACTGTGCGACGCTGCGGCTCTT 532
QY 481 GTGCTGTGCTCCCAAGCTGCGCTTACAGGTGTGCGGCGCGCGCTGTACAGCTCGG 540
DB 533 GTGCTGTGCTCCCAAGCTGCGCTTACAGGTGTGCGGCGCGCGCTGTACAGCTCGG 592
QY 541 GCTGCACCTCAGGCG 600
DB 593 GCTGCACCTCAGGCG 652
QY 601 GAACGGGCGCTGAACCATATAGCGTACGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 653 GAACGGGCGCTGAACCATATAGCGTACGAGAGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGAGGCG 720
DB 713 GGTGCGAGAGGCG 772
QY 721 CGTGGCGCTGCCCTTGTAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
DB 773 CGTGGCGCTGCCCTTGTAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
QY 781 GGCAGGACGCGGTGAGACCGAGTACCGGTGTTTCTGTGTGTACCTGCCAGACCGCG 840
DB 833 GGCAGGACGCGGTGAGACCGAGTACCGGTGTTTCTGTGTGTACCTGCCAGACCGCG 892
QY 841 GAAGAAGCCACTTCTTGGAGGCTGCTCTGTGCAAGCGCGCACTCCCAACCATCCGT 900
DB 893 GAAGAAGCCACTTCTTGGAGGCTGCTCTGTGCAAGCGCGCACTCCCAACCATCCGT 952
QY 901 GGGCGGACGACCAAGCG 960
DB 953 GGGCGGACGACCAAGCG 1012
QY 961 CCTGTGCGCGGCTGTAGCGCGGAGCAAGCACTTCTTACTCTCAGGCGACAGAGAG 1020
DB 1013 CCTGTGCGCGGCTGTAGCGCGGAGCAAGCACTTCTTACTCTCAGGCGACAGAGAG 1072
QY 1021 CAGCTGCGGCGCTCTTCTTACTCAGCTCTGTAGGCGCGCAAGCTGCGGCTCGGAG 1080
DB 1073 CAGCTGCGGCGCTCTTCTTACTCAGCTCTGTAGGCGCGCAAGCTGCGGCTCGGAG 1132
QY 1081 CTGTGAGAGCACTTCTTGTGGTTCCAGGCGCTGATGCCAGGAACTCCCGCAGGTTG 1140
DB 1133 CTGTGAGAGCACTTCTTGTGGTTCCAGGCGCTGATGCCAGGAACTCCCGCAGGTTG 1192
QY 1141 CCGCGGCTGCG 1200
DB 1193 CCGCGGCTGCG 1252
QY 1201 CAGCGGCACTGCG 1260
DB 1253 CAGCGGCACTGCG 1312
QY 1261 ACCCAGAGCGCGGTGTGTGTGCGCGCGGAGAGAGCGCGCGCTGTGCGCGCGCGCGAG 1320
DB 1313 ACCCAGAGCGCGGTGTGTGTGCGCGCGGAGAGAGCGCGCGCTGTGCGCGCGCGCGAG 1372

QY	1321	GAGGAGGACACAGACCCCGCTGCGCTTGAGTGCAGCTGCTCCGCCAGACACAGACGCCCTGG	1380
Db	1373	GAGGAGGACACAGACCCCGCTGCGCTTGAGTGCAGCTGCTCCGCCAGACACAGACGCCCTGG	1432
QY	1381	CAGGTGTAAGCGCTTCGTGCGGGCGCTGCGCTGCGCGCGGTGTTGCGCCCAAGCCCTGCGGC	1440
Db	1433	CAGGTGTAAGCGCTTCGTGCGGGCGCTGCGCTGCGCGCGGTGTTGCGCCCAAGCCCTGCGGC	1492
QY	1441	TCCAGGCACAACGAACCGCGCTTCCCTCAGGAACACCAAGAACTCATCTCCCTGGGGAAG	1500
Db	1493	TCCAGGCACAACGAACCGCGCTTCCCTCAGGAACACCAAGAACTCATCTCCCTGGGGAAG	1552
QY	1501	CATGCCAAGCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGCTTGG	1560
Db	1553	CATGCCAAGCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGCTTGG	1612
QY	1561	CTGCGCAGAGACCCAGGGGTTGCTGTGTTCCGGCCGACAGACACCGTCTGCGTAGAGAG	1620
Db	1613	CTGCGCAGAGACCCAGGGGTTGCTGTGTTCCGGCCGACAGACACCGTCTGCGTAGAGAG	1672
QY	1621	ATCCTGCGCAAGTTCCTGCACTGCGTGAATGAGTGTACGTCGTGAGCTGCTCAGSTCT	1680
Db	1673	ATCCTGCGCAAGTTCCTGCACTGCGTGAATGAGTGTACGTCGTGAGCTGCTCAGSTCT	1732
QY	1681	TTCCTTTATGTCAACGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCCGGAAGT	1740
Db	1733	TTCCTTTATGTCAACGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCCGGAAGT	1792
QY	1741	GTCGTGAGCAAGTTGCAABAGCATTTGAATCAGACAGCACTTGAAGAGGATGACGTGCGG	1800
Db	1793	GTCGTGAGCAAGTTGCAABAGCATTTGAATCAGACAGCACTTGAAGAGGATGACGTGCGG	1852
QY	1801	GAGCTGTCCGGAAGCAGAGGTCAAGCCAGCATCGGGAAGCCAGGCCCGCCCTGCTACGTC	1860
Db	1853	GAGCTGTCCGGAAGCAGAGGTCAAGCCAGCATCGGGAAGCCAGGCCCGCCCTGCTACGTC	1912
QY	1861	AGACTCCGCTTCATCCCCAGCGCTGAACGGGCTGCGGCGCGATTGTGAACATGACTACGTC	1920
Db	1913	AGACTCCGCTTCATCCCCAGCGCTGAACGGGCTGCGGCGCGATTGTGAACATGACTACGTC	1972
QY	1921	GTTGGAGCCAGAACGTTCCCGCAGAGAAAAAGAGGGCCGAGCGTCTCACTCGAGGATGAAG	1980
Db	1973	GTTGGAGCCAGAACGTTCCCGCAGAGAAAAAGAGGGCCGAGCGTCTCACTCGAGGATGAAG	2032
QY	1981	GCACTGTTCAAGCTGCTCAACTACGAGCGGGCGCGCGCCCGGCTCTCTGGCGCCTCT	2040
Db	2033	GCACTGTTCAAGCTGCTCAACTACGAGCGGGCGCGCGCCCGGCTCTCTGGCGCCTCT	2092
QY	2041	GTCCTGGGCTTGACGATATCCACAGGGCCTGGCGCACTTCGTGCTGCGTGTGCGGGCC	2100
Db	2093	GTCCTGGGCTTGACGATATCCACAGGGCCTGGCGCACTTCGTGCTGCGTGTGCGGGCC	2152
QY	2101	CAGGACCCGCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACC	2160
Db	2153	CAGGACCCGCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACC	2212
QY	2161	ATCCCCCAGGACAGGCTCAACGGAAGTCAATCGCCAGCATCATCAAAACCCCAAGAACAGTAC	2220
Db	2213	ATCCCCCAGGACAGGCTCAACGGAAGTCAATCGCCAGCATCATCAAAACCCCAAGAACAGTAC	2272
QY	2221	TGCGTGCCTGGTATGCGCGTGTGTCCAGAAAGGCCGCCCATGGGCAAGTCCGCAAGGCTTTC	2280
Db	2273	TGCGTGCCTGGTATGCGCGTGTGTCCAGAAAGGCCGCCCATGGGCAAGTCCGCAAGGCTTTC	2332
QY	2281	AAGAGCCACGTTCTACCTTGACAGACCTCAAGCCGTACATGCGACAGTTCTGGCTCAC	2340
Db	2333	AAGAGCCACGTTCTACCTTGACAGACCTCAAGCCGTACATGCGACAGTTCTGGCTCAC	2392
QY	2341	CTGCAGAGACCAAGCCCGCTGAGGGATGCCGTGTCTATCGAGCAGAGCTCTCCCTGAAT	2400
Db	2393	CTGCAGAGACCAAGCCCGCTGAGGGATGCCGTGTCTATCGAGCAGAGCTCTCCCTGAAT	2452
QY	2401	GAGGCCACAGTGGCTCTTCGACGTCTTCTCAAGCTTCAATGTGCCACCAAGCCGTGCGC	2460

ID	ACC57552	standard; cDNA; 4015 BP.
Db	2453	GAGGCCAGAGTGGCCCTCTTTCAGCCTTCTCTACGCTTTCATGTGCCACCACGCGGTGGC
Qy	2461	ATCAGGGGGAAGTCTTACGTCCAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCCACG
Db	2513	ATCAGGGGCAAGTCTTACGTCAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCCACG
Qy	2521	CTGCTCTGCAGCCTGTGTCTACGCGGACATGAGAACAAAGCTGTTTCCGGGGAATTCGGCG
Db	2573	CTGCTCTGCAGCCTGTGTCTACGCGGACATGAGAACAAAGCTGTTTCCGGGGAATTCGGCG
Qy	2581	GACGGCTGCTCCTCGCTTGGTGATGATTTCTTGTGTGACACCTCACCTCACCCAC
Db	2633	GACGGCTGCTCCTCGCTTGGTGATGATTTCTTGTGTGACACCTCACCTCACCCAC
Qy	2641	GCGAAACCTTCTCAGAGACCTGTGTCGAGGTGTCCTGAGTATGGCTGCGTGGAAC
Db	2693	GCGAAACCTTCTCAGAGACCTGTGTCGAGGTGTCCTGAGTATGGCTGCGTGGAAC
Qy	2701	TTGCGGAGAAGTAGTGTGAATTCCTGTAGAAAGACGAGCCCTGGGTGCACGCTTTT
Db	2753	TTGCGGAGAAGTAGTGTGAATTCCTGTAGAAAGACGAGCCCTGGGTGCACGCTTTT
Qy	2761	GTTCAAGTGCAGGCGCCCAACGCGCTATTTCCCTGTGTGCGGCTCTGTGATACCGGACC
Db	2813	GTTCAAGTGCAGGCGCCCAACGCGCTATTTCCCTGTGTGCGGCTCTGTGATACCGGACC
Qy	2821	CTGAGGTGCAGAGCGCACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAC
Db	2873	CTGAGGTGCAGAGCGCACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAC
Qy	2881	TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCCGCAAACTCTTTGGGGTCTTGGG
Db	2933	TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCCGCAAACTCTTTGGGGTCTTGGG
Qy	2941	CTGAAGTGCACAGCCTGTTTCTGGATTGTCAGGTGAACAAGCTCCAGACGGTGTGACC
Db	2993	CTGAAGTGCACAGCCTGTTTCTGGATTGTCAGGTGAACAAGCTCCAGACGGTGTGACC
Qy	3001	AACATCTACAAGATCCTCTCTGCTGTCAGGCGGTACAGGTTTCAACGATGTGTGTCAGCTC
Db	3053	AACATCTACAAGATCCTCTCTGCTGTCAGGCGGTACAGGTTTCAACGATGTGTGTCAGCTC
Qy	3061	CAATTTTCATCAGCAAGTTTGGAAAGAACCCACATTTTCTCTGCGGCTCATCTGTGACAG
Db	3113	CAATTTTCATCAGCAAGTTTGGAAAGAACCCACATTTTCTCTGCGGCTCATCTGTGACAG
Qy	3121	GCTCCTCTGTCTACTCTCATCTCTGAAGCCAAAGACGAGGATGTGCTGGGGCCAAAG
Db	3173	GCTCCTCTGTCTACTCTCATCTCTGAAGCCAAAGACGAGGATGTGCTGGGGCCAAAG
Qy	3181	GAGCGCGCGGCGCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTG
Db	3233	GAGCGCGCGGCGCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTG
Qy	3241	CTCAAGCTGACTGCACACCGTGTCACTTACGTCGCACTCCTGCGGCTCATCTCAGGACAGCC
Db	3293	CTCAAGCTGACTGCACACCGTGTCACTTACGTCGCACTCCTGCGGCTCATCTCAGGACAGCC
Qy	3301	CAGACGAGCTGAGTCCGGAAGCTCCCGGGGACGACGCTGACTGCCCTTGAGGCGCGAGCC
Db	3353	CAGACGAGCTGAGTCCGGAAGCTCCCGGGGACGACGCTGACTGCCCTTGAGGCGCGAGCC
Qy	3361	AACCCGGCACTGCCCTCAGACTTCAAGACCATCTCTGACTGATGGCCACC 3411
Db	3413	AACCCGGCACTGCCCTCAGACTTCAAGACCATCTCTGACTGATGGCCACC 3463

XX 28-JUL-2003 (first entry)
DT Human telomerase reverse transcriptase cDNA.
XX
DE
XX
KM Telomerase reverse transcriptase; TERT; enzyme; RNA interference;
KM short interfering RNA; siRNA; cancer; tumour; cytostatic; contraceptive;
KM immunosuppressive; antifertility; fungicide; antiparasitic;
KM antiinflammatory; human; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag= a
FT /product= "TERT"
XX
PN WO2003034985-A2.
XX
PD 01-MAY-2003.
XX
PF 16-OCT-2002; 2002WO-US033146.
XX
PR 22-OCT-2001; 2001US-0345326P.
PR 20-FEB-2002; 2002US-0359196P.
PR 22-MAY-2002; 2002US-0383195P.
XX
PA (UVRP) UNIV ROCHESTER.
XX
PI Rowley PI;
XX
DR MPI; 2003-403289/38.
DR P-PSDB; ABR42063.
XX
XX
PT Novel nucleic acid encoding or comprising interfering RNAs which target
PT telomerase RNA, useful for inhibiting telomerase activity for treating
PT cancer, infertility and disorders of the immune system.
XX
XX
PS Disclosure; Fig 3; 52pp; English.
XX
XX The present sequence is that of human telomerase reverse transcriptase
CC (TERT) cDNA. The invention relates to the discovery that double-stranded
CC interfering RNAs, such as short interfering RNAs (siRNA), which target
CC telomerase RNA or TERT mRNA are capable of inhibiting telomerase
CC activity. Inhibition of telomerase in cancer cells leads to telomere
CC shortening, end-to-end chromosomal fusion, and apoptosis. Interference of
CC telomerase activity can also be used for treatment of infertility, for
CC contraception or sterilisation, for immunosuppression, for treatment of
CC yeast, parasite and fungal infections, and in antiinflammatory therapies.
CC As telomerase is active in a limited number of cell types, e.g. tumour
CC cells, germline cells, certain stem cells of the haematopoietic system, T
CC and B cells, sun-damaged skin, and proliferative cervix, most normal
CC cells are not affected by telomerase RNA interference therapy
XX
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 7; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCCGCTGCTCCCTGCTGCGCAGCCACTACCGC 60
DB 53 GCGATGCGCGCGCTCCCGCTGCGAGCCGCTGCTCCCTGCTGCGCAGCCACTACCGC 112
QY 61 GAGGTGCTGCGCTGCGCAGCTTCTGCGCGCGCTGCGGCCCGCAGGGCTGCGGCTG 120
DB 113 GAGGTGCTGCGCTGCGCAGCTTCTGCGCGCGCTGCGGCCCGCAGGGCTGCGGCTG 172
QY 121 CAGCGCGGAGACCGCGCGCTTTCGCGCGCTGCTGCGCCAGTGCCTGTGCTGCGCC 180
DB 173 CAGCGCGGAGACCGCGCGCTTTCGCGCGCTGCTGCGCCAGTGCCTGTGCTGCGCC 232
QY 181 TGGGACGACG 240

DB 233 TGGGACGACG 292
QY 241 CTGCTGCGCGCGAGTCTGACAGAGGCTGTGCGAGCGCGCGCGCGCGAGAGACGCTGCGCTTC 300
DB 293 CTGCTGCGCGCGAGTCTGACAGAGGCTGTGCGAGCGCGCGCGCGCGAGAGACGCTGCGCTTC 352
QY 301 GCGTTGCGCGCTGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GCGTTGCGCGCTGCTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGGAGCTACCTGCGCCACACCGGTGACCGGACCGGACCGGAGCGCGCGCGCGCGCGCG 420
DB 413 CGGAGCTACCTGCGCCACACCGGTGACCGGACCGGAGCGCGCGCGCGCGCGCGCGCTG 472
QY 421 CTGCTGCGCGCGCGTGGCGGACGACGCTGCTGCTTCACTGCTGACGCTGCGCGCTCTT 480
DB 473 CTGCTGCGCGCGCGTGGCGGACGACGCTGCTGCTTCACTGCTGACGCTGCGCGCTCTT 532
QY 481 GTGCTGTGCTGCTGCGCGCGCTGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCTG 540
DB 533 GTGCTGTGCTGCTGCGCGCGCTGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCTG 592
QY 541 GCTGCCACTCAGGCG 600
DB 593 GCTGCCACTCAGGCG 652
QY 601 GAACGGGCGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 653 GAACGGGCGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGGAGCG 720
DB 713 GGTGCGAGGAGCG 772
QY 721 CGTGCGGCTGCG 780
DB 773 CGTGCGGCTGCG 832
QY 781 GGCAGGACGCGTGAACCGAGTGACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 833 GGCAGGACGCGTGAACCGAGTGACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 892
QY 841 GAAGAAGCCACTCTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
DB 893 GAAGAAGCCACTCTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY 901 GCGCGCGAGCACG 960
DB 953 GCGCGCGAGCACG 1012
QY 961 CTTGTCGCGCGGTGACGCGGAGACCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1020
DB 1013 CTTGTCGCGCGGTGACGCGGAGACCACTTCTCTACTCTCTCTCTCTCTCTCTCTCTCT 1072
QY 1021 CAGCTGCGCGCGCT 1080
DB 1073 CAGCTGCGCGCGCT 1132
QY 1081 CTGCTGAGACACATCTTCTGAGTTCAAGGCGCGCTGATGACAGGACTCCCGCAGGTTG 1140
DB 1133 CTGCTGAGACACATCTTCTGAGTTCAAGGCGCGCTGATGACAGGACTCCCGCAGGTTG 1192
QY 1141 CCGCGCGTCCCGCAGCGCTACTGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
DB 1193 CCGCGCGTCCCGCAGCGCTACTGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1252
QY 1201 CACGCGAGTCCCGCTACGCGGCTGCTCTCAAGACGACCTGCGCGCTGCGAGCTGCGGTC 1260
DB 1253 CACGCGAGTCCCGCTACGCGGCTGCTCTCAAGACGACCTGCGCGCTGCGAGCTGCGGTC 1312
QY 1261 ACCCGAGAGCGCGGTGTGTGCGCGGAGAGCCCGCAGGCTCTGTGCGCGCGCGCGAG 1320

Db 1313 ACCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAGCCCCAGGGCTCTGTGGCGCCCCGAG 1372
QY 1321 GAGGAGGACACAGACCCCCCTGCGCTGTGTGAGCTGTCTCCGACAGACAGACCCCTGG 1380
Db 1373 GAGGAGGACACAGACCCCCCTGCGCTGTGTGAGCTGTCTCCGACAGACAGACCCCTGG 1432
QY 1381 CAGGTGTACGGCTTCTGTGCGGCTGTGCTGCGCCGGCTGTGCCCCAGGCTCTGGGGC 1440
Db 1433 CAGGTGTACGGCTTCTGTGCGGCTGTGCTGCGCCGGCTGTGCCCCAGGCTCTGGGGC 1492
QY 1441 TCCAGGACAAACGAGCCGCTTCTCAGGAACACCAAGATTCTCTCCCTGGGGAAG 1500
Db 1493 TCCAGGACAAACGAGCCGCTTCTCAGGAACACCAAGATTCTCTCCCTGGGGAAG 1552
QY 1501 CATGCCAAGCTCTCGCTGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTG 1560
Db 1553 CATGCCAAGCTCTCGCTGAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGCGCTTG 1612
QY 1561 CTGCGCAGGAGCCCGAGGGTGTGCTGTGTTCCGGCCGACAGACACCGTCTGGGTAGAG 1620
Db 1613 CTGCGCAGGAGCCCGAGGGTGTGCTGTGTTCCGGCCGACAGACACCGTCTGGGTAGAG 1672
QY 1621 ATCTTGGCCAAGTCTCTGCACTGGCTGATGATGATGATGATGATGATGATGATGAT 1680
Db 1673 ATCTTGGCCAAGTCTCTGCACTGGCTGATGATGATGATGATGATGATGATGATGAT 1732
QY 1681 TTCTTTATGTACGAGACACGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAGAGT 1740
Db 1733 TTCTTTATGTACGAGACACGTTTCAAAAGAACAGGCTCTTTTCTAACCGAAGAGT 1792
QY 1741 GTCTGAGCAGAGTTGCAAGCATTTGGAATCAGACACACTTGAAGAGGGTGCAGCTGCG 1800
Db 1793 GTCTGAGCAGAGTTGCAAGCATTTGGAATCAGACACACTTGAAGAGGGTGCAGCTGCG 1852
QY 1801 GAGCTGTCCGAGCAGAGGTCAGGCAAGCATCCGGAAGCCAGCCCGCTGTGACGTCC 1860
Db 1853 GAGCTGTCCGAGCAGAGGTCAGGCAAGCATCCGGAAGCCAGCCCGCTGTGACGTCC 1912
QY 1861 AGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGCCGATTTGTGAACATGACTACGTC 1920
Db 1913 AGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGCCGATTTGTGAACATGACTACGTC 1972
QY 1921 GTGGGAGCCAGAACGTTCCGACAGAAAAGAGGGCCGAGCGTCTCACTTGAAGGGTGAAG 1980
Db 1973 GTGGGAGCCAGAACGTTCCGACAGAAAAGAGGGCCGAGCGTCTCACTTGAAGGGTGAAG 2032
QY 1981 GCACTGTTCAGCGTGTCTAACTACGAGCGGGCGGGCGCCCGGCTCTTGGGGCGCTCT 2040
Db 2033 GCACTGTTCAGCGTGTCTAACTACGAGCGGGCGGGCGCCCGGCTCTTGGGGCGCTCT 2092
QY 2041 GTGCTGGGCTTGACGATATCCACAGGGCCCTGGGCACTTGTGCTGCTGCTGGGGCC 2100
Db 2093 GTGCTGGGCTTGACGATATCCACAGGGCCCTGGGCACTTGTGCTGCTGCTGGGGCC 2152
QY 2101 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGCGGCTACGACACC 2160
Db 2153 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGCGGCTACGACACC 2212
QY 2161 ATCCCCCAGGACAGGCTACGAGAGTTCATCCGACATCATCAAAACCCAGAACACGTAC 2220
Db 2213 ATCCCCCAGGACAGGCTACGAGAGTTCATCCGACATCATCAAAACCCAGAACACGTAC 2272
QY 2221 TGCCTGCTGCTATGCTGTGTCCAGAGGCGCCCATGGGCAAGTCCGCAAGGCTTC 2280
Db 2273 TGCCTGCTGCTATGCTGTGTCCAGAGGCGCCCATGGGCAAGTCCGCAAGGCTTC 2332
QY 2281 AAGAGCCACGCTCTACTTACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTAC 2340
Db 2333 AAGAGCCACGCTCTACTTACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTAC 2392
QY 2341 CTGACGAGACACCGCGCTGAGGATGCTGCTGCTACGAGACAGCTCTCCCTGAAT 2400
Db 2393 CTGACGAGACACCGCGCTGAGGATGCTGCTGCTACGAGACAGCTCTCCCTGAAT 2452

QY 2401 GAGGCCACGAGTGGCTCTTTCAGACGTTCTTCTTACGCTTTCATGTGCCACCACGCGCTGGC 2460
Db 2453 GAGGCCACGAGTGGCTCTTTCAGACGTTCTTCTTACGCTTTCATGTGCCACCACGCGCTGGC 2512
QY 2461 ATCAGGGGCAAGTCTTACGTTCCAGTGCAGGGGATCCCGCAGAGGCTCCATCTTCCACG 2520
Db 2513 ATCAGGGGCAAGTCTTACGTTCCAGTGCAGGGGATCCCGCAGAGGCTCCATCTTCCACG 2572
QY 2521 CTGCTCTGACGCTGTGTGCGGCGACATGAGAAACAAGCTTTTGGGGGATTCGGCGG 2580
Db 2573 CTGCTCTGACGCTGTGTGCGGCGACATGAGAAACAAGCTTTTGGGGGATTCGGCGG 2632
QY 2581 GACGGGCTGCTCTGCGTTTGTGTGATGATTTCTTGTGTGACACCTCACCTCACCCAC 2640
Db 2633 GACGGGCTGCTCTGCGTTTGTGTGATGATTTCTTGTGTGACACCTCACCTCACCCAC 2692
QY 2641 GCCAAAACCTTCTCAGACCTGTGTCGAGAGTGTCCCTGAGTATGCTGCTGTGAAC 2700
Db 2693 GCCAAAACCTTCTCAGACCTGTGTCGAGAGTGTCCCTGAGTATGCTGCTGTGAAC 2752
QY 2701 TTGCGGAAGACAGTGTGAACCTTCCCTGTGAAGAAGAGGCCCTGGGTGCAAGCTTTT 2760
Db 2753 TTGCGGAAGACAGTGTGAACCTTCCCTGTGAAGAAGAGGCCCTGGGTGCAAGCTTTT 2812
QY 2761 GTTCAGATGCGGCGCCACGCGCTATTCCCTGTGCGGCTGTGCTGTGAATCCCGAAC 2820
Db 2813 GTTCAGATGCGGCGCCACGCGCTATTCCCTGTGCGGCTGTGCTGTGAATCCCGAAC 2872
QY 2821 CTGAGAGTGACAGAGCACTCTCAGCTATGCCGGAACCTCCATCAGAGCCAGTCTCAC 2880
Db 2873 CTGAGAGTGACAGAGCACTCTCAGCTATGCCGGAACCTCCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTGAACCTTTGGGGTCTTGGCG 2940
Db 2933 TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTGAACCTTTGGGGTCTTGGCG 2992
QY 2941 CTGAAGTGTACAGCGCTTTCTGATTTGCAAGTGAACAGCTCCAGACGGTGTGACAC 3000
Db 2993 CTGAAGTGTACAGCGCTTTCTGATTTGCAAGTGAACAGCTCCAGACGGTGTGACAC 3052
QY 3001 AACATCTACAGATCTCTGCTGACGGCGTACAGTTTCAAGCATGTGTGTGACGCTC 3060
Db 3053 AACATCTACAGATCTCTGCTGACGGCGTACAGTTTCAAGCATGTGTGTGACGCTC 3112
QY 3061 CCAATTCTACAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACACG 3120
Db 3113 CCAATTCTACAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACACG 3172
QY 3121 GCCTCCCTCTGCTACTCTCTGAAGCCAGAAACGCAAGGATGTGCTGGGGGCCAAG 3180
Db 3173 GCCTCCCTCTGCTACTCTCTGAAGCCAGAAACGCAAGGATGTGCTGGGGGCCAAG 3232
QY 3181 GGGCGCGCGGCTCTGCGCTTCCGAGGGCGGTGCAAGTGTGTGACCAAGCATTCCTG 3240
Db 3233 GGGCGCGCGGCTCTGCGCTTCCGAGGGCGGTGCAAGTGTGTGACCAAGCATTCCTG 3292
QY 3241 CTCAAGCTGACTGACACCGTGTCACTTACGTGCCACTCTTGGGGTCACTCAGAGACAGCC 3300
Db 3293 CTCAAGCTGACTGACACCGTGTCACTTACGTGCCACTCTTGGGGTCACTCAGAGACAGCC 3352
QY 3301 CAGACGAGCTGAGTGGAAAGCTCCCGGGGAGACGCTGACTGCGCTGAGAGCGCGAGCC 3360
Db 3353 CAGACGAGCTGAGTGGAAAGCTCCCGGGGAGACGCTGACTGCGCTGAGAGCGCGAGCC 3412
QY 3361 AACCCGGCACTGCTCAGACTTCAAGACCACTCTGAGTGTGAGGCAACC 3411
Db 3413 AACCCGGCACTGCTCAGACTTCAAGACCACTCTGAGTGTGAGGCAACC 3463

RESULT 10
ABZ22474
ID ABZ22474 standard; cdna; 4015 BP.

XX AC ABZ22474;
XX DT 25-MAR-2003 (first entry)
XX DE Human telomerase reverse transcriptase encoding cDNA SEQ ID NO:1.
XX KM Human; telomerase reverse transcriptase; enzyme; hTERT; chromosome 5;
XX KM vulnery; antilicer; epithelial cell migration promoter; wound;
XX KM epithelisation; skin wound; lesion; burn; surgical incision; ulcer;
XX KM epithelial cell; keratinocyte; epidermal; mucosal; gene; ss.
XX OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 56..3454
FT /tag=a
FT /product="human telomerase reverse transcriptase"
XX PN WO200291999-A2.
XX PD 21-NOV-2002.
XX PF 09-MAY-2002; 2002WO-US014867.
XX PR 09-MAY-2001; 2001US-0289903P.
XX PA (GERO-) GERON CORP.
XX PI Jiang X, Chiu C, Harley CB;
XX DR WPI; 2003-120591/11.
XX DR P-PSDB; ABP56676.
XX PT Composition for treating wounds and enhancing epithelization of a skin
XX PT surface, comprises vector encoding telomerase reverse transcriptase or
XX PT telomerized epithelial cells on a microparticle or a matrix.
XX PS Disclosure; Page 31-32; 68pp; English.
XX CC The present invention describes a pharmaceutical composition (I)
XX CC comprising a vector encoding telomerase reverse transcriptase (TERT) in
XX CC an excipient or device, or comprises telomerized epithelial cells on a
XX CC microparticle or a matrix suitable for topical administration or
XX CC administration to a wound site. (I) has vulnery and antilicer
XX CC activities and can be used to promote epithelial cell migration. (I) is
XX CC useful for treating a wound and enhancing epithelisation of a skin
XX CC surface. The wound is especially skin wound including acute lesion such
XX CC as traumatic lesion, burn, or surgical incision, chronic lesion such as
XX CC chronic venous ulcer, diabetic ulcer or compression ulcer and the wound
XX CC is further monitored for closure. The telomerase activity or TERT
XX CC expression is increased in epithelial cells at the site of treatment and
XX CC also in fibroblasts or endothelial cells at the site of treatment. The
XX CC epithelial cells are especially keratinocytes. A polynucleotide encoding
XX CC TERT is useful for the preparation of a medicament for treatment of a
XX CC wound or an epithelial surface in a human or animal. An epithelial cell
XX CC with increased telomerase activity or increased expression of TERT is
XX CC useful for preparation of a medicament for the treatment of a wound in a
XX CC human or animal. (I) is also useful for treating wounds of other
XX CC epidermal surfaces including mucosal surfaces such as bronchus, mouth,
XX CC nose, oesophagus, stomach, or intestine. The present sequence encodes
XX CC human TERT (hTERT), which is given in the exemplification of the present
XX CC invention. hTERT is located to chromosome 5
SQ Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 7; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGGCTCCCGCTGCGAGCGGTGCTCCCTGCTGCGAGCCACTACCGC 60
DB 53 GCGATGCGCGGCTCCCGCTGCGAGCGGTGCTCCCTGCTGCGAGCCACTACCGC 112

QY 61 GAGGTGCTGCGGCTGCGACGTTGCTGCGGCGCTGGGGCCCGAGGGCTGCGCGGTG 120
DB 113 GAGGTGCTGCGGCTGCGACGTTGCTGCGGCGCTGGGGCCCGAGGGCTGCGCGGTG 172
QY 121 CAGCGCGGAGACCGCGGCTTCCGCGCGCTGGTGCCAGTGCCCTGTGTGCGTGCC 180
DB 173 CAGCGCGGAGACCGCGGCTTCCGCGCGCTGGTGCCAGTGCCCTGTGTGCGTGCC 232
QY 181 TGGAGCGACG 240
DB 233 TGGAGCGACG 292
QY 241 CTGTTGCGCGGAGTGCTGACAGGCTGTGCGAGCGCGCGCGCGAGAGAGAGAGAG 300
DB 293 CTGTTGCGCGGAGTGCTGACAGGCTGTGCGAGCGCGCGCGAGAGAGAGAGAGAG 352
QY 301 GCGTTGCGCGGCTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GCGTTGCGCGGCTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGCTACCTGCGCCACACAGGTGACCGACGACCTGCGGGGAGAGCGGGCGTG 420
DB 413 CGCAGCTACCTGCGCCACACAGGTGACCGACGACCTGCGGGGAGAGCGGGCGTG 472
QY 421 CTGTTGCGCGGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 473 CTGTTGCGCGGCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 532
QY 481 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 533 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
QY 541 GCTGCGCACTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
DB 593 GCTGCGCACTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 652
QY 601 GAACGGGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 660
DB 653 GAACGGGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGAGAGCG 720
DB 713 GGTGCGAGAGAGCG 772
QY 721 CGTGGCGCTGCG 780
DB 773 CGTGGCGCTGCG 832
QY 781 GGCAGGAGCGGTGAGCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 840
DB 833 GGCAGGAGCGGTGAGCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 892
QY 841 GAAGAAGCCACTCTTTGAGAGGTGCGCTCTGTGCGACGCGCGCACTCCCAACCC 900
DB 893 GAAGAAGCCACTCTTTGAGAGGTGCGCTCTGTGCGACGCGCGCACTCCCAACCC 952
QY 901 GGCAGGAGCGGTGAGCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 960
DB 953 GGCAGGAGCGGTGAGCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 1012
QY 961 CTTGTGCGCGGCTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
DB 1013 CTTGTGCGCGGCTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1072
QY 1021 CAGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1073 CAGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1132
QY 1081 CTGTTGAGAGACCATCTTCTGTTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1140
DB 1133 CTGTTGAGAGACCATCTTCTGTTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 1192

QY 1141 CCCCCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGCTGCTTGGGAAC 1200
DB 1193 CCCCCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGCTGCTTGGGAAC 1252
QY 1201 CAGCGCAGTGGCCCCCTACCGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTC 1260
DB 1253 CAGCGCAGTGGCCCCCTACCGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGCTGCGGTC 1312
QY 1261 ACCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAGCCCCAGGGCTCTGTGGCGGCCCGAG 1320
DB 1313 ACCCCAGCAGCCGGTGTCTGTGCCCCGGGAGAGCCCCAGGGCTCTGTGGCGGCCCGAG 1372
QY 1321 GAGGAGGACACAGACCCCCCTGCGCTGTGTGAGCTGTCTCCGACAGACAGAGCCCTGG 1380
DB 1373 GAGGAGGACACAGACCCCCCTGCGCTGTGTGAGCTGTCTCCGACAGACAGAGCCCTGG 1432
QY 1381 CAGGTGTACGGCTTCTGTGCGGGCTGCTGCGCCGCTGTGTGCCAGGCTCTGGGGC 1440
DB 1433 CAGGTGTACGGCTTCTGTGCGGGCTGCTGCGCCGCTGTGTGCCAGGCTCTGGGGC 1492
QY 1441 TCCAGGCAACAAGACCGCGCTTCTCAGGAACAACAAGATTCTATCTCCCTGGGAAG 1500
DB 1493 TCCAGGCAACAAGACCGCGCTTCTCAGGAACAACAAGATTCTATCTCCCTGGGAAG 1552
QY 1501 CATGCCAAGCTCTGCTGAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTG 1560
DB 1553 CATGCCAAGCTCTGCTGAGAGCTGACGTGAAGATGAGCGTGGGAGCTGCGCTTG 1612
QY 1561 CTGGCAGAGAGCCCCAGGGTGGCTGTGTCTCCGCGCAGAGACACCGCTGCGTGAAGAG 1620
DB 1613 CTGGCAGAGAGCCCCAGGGTGGCTGTGTCTCCGCGCAGAGACACCGCTGCGTGAAGAG 1672
QY 1621 ATCTGGCCAAAGTCTCTGCACTGGCTGATGAGTGTATCGTCTGAGCTGCTCAGTCT 1680
DB 1673 ATCTGGCCAAAGTCTCTGCACTGGCTGATGAGTGTATCGTCTGAGCTGCTCAGTCT 1732
QY 1681 TTCTTTTATGTACCGAGACACAGCTTCAAAAGAACAGGCTTTTCTAACCGGAAGAGT 1740
DB 1733 TTCTTTTATGTACCGAGACACAGCTTCAAAAGAACAGGCTTTTCTAACCGGAAGAGT 1792
QY 1741 GTCTGAGCAAGTTGTCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAAGT 1800
DB 1793 GTCTGAGCAAGTTGTCAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAAGT 1852
QY 1801 GAGCTGTCCGAGACAGAGGTTCAGGCAAGCATCGGGAAGCCAGCCGCTGTGACGTCC 1860
DB 1853 GAGCTGTCCGAGACAGAGGTTCAGGCAAGCATCGGGAAGCCAGCCGCTGTGACGTCC 1912
QY 1861 AGACTCCGCTTCACTCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTC 1920
DB 1913 AGACTCCGCTTCACTCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTC 1972
QY 1921 GTGGAGACCCAGAACGTTCCCGACAGAAAAAGAGGGCGGAGCGTCTCACTGAGGGTGAAG 1980
DB 1973 GTGGAGACCCAGAACGTTCCCGACAGAAAAAGAGGGCGGAGCGTCTCACTGAGGGTGAAG 2032
QY 1981 GCACTGTTCAGCGTGTCTCACTACGAGCGGGCGCGGCCCTCTGAGGGCGCTCT 2040
DB 2033 GCACTGTTCAGCGTGTCTCACTACGAGCGGGCGCGGCCCTCTGAGGGCGCTCT 2092
QY 2041 GTGCTGGGCTTGAAGCATATCCACAGGGCCTGGCGCACTTCTGCTGCTGTGCGGGCC 2100
DB 2093 GTGCTGGGCTTGAAGCATATCCACAGGGCCTGGCGCACTTCTGCTGCTGTGCGGGCC 2152
QY 2101 CAGGACCCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCTACGACACC 2160
DB 2153 CAGGACCCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCTACGACACC 2212
QY 2161 ATCCCCCAGGACAGGCTACAGGAGGTCTACGCAAGCATCATCAAAACCCAGAACAGCTAC 2220
DB 2213 ATCCCCCAGGACAGGCTACAGGAGGTCTACGCAAGCATCATCAAAACCCAGAACAGCTAC 2272
QY 2221 TGGGTGCTGGTATGCGGTGTCTCAGAGGCGCGCCATGGGACGTCGCAAGGCTTTC 2280

DB 2273 TGGGTGCTGGTATGCGGTGTCTCAGAGGCGCGCCATGGGACGTCGCAAGGCTTTC 2332
QY 2281 AAGAGCCACGCTCTCTACCTTGAAGACCTCCAGCCGCTACATGGCAGAGTCTGCTGCTAC 2340
DB 2333 AAGAGCCACGCTCTCTACCTTGAAGACCTCCAGCCGCTACATGGCAGAGTCTGCTGCTAC 2392
QY 2341 CTGACGAGAGACCAAGCCCGCTGAGGGATGCGGCTGCTCATCGACAGAGCTCTCCCTGAAT 2400
DB 2393 CTGACGAGAGACCAAGCCCGCTGAGGGATGCGGCTGCTCATCGACAGAGCTCTCCCTGAAT 2452
QY 2401 GAGGCCAGCAGTGGGCTCTTGAACGCTCTTCTCTACGCTTCACTGTGCCACCAAGCCGCTGCC 2460
DB 2453 GAGGCCAGCAGTGGGCTCTTGAACGCTCTTCTCTACGCTTCACTGTGCCACCAAGCCGCTGCC 2512
QY 2461 ATCAGGGGCAAGTCTCTACGCTCAGTGCACAGGGGATCCCGCAGAGGCTCCATCTCTCCACG 2520
DB 2513 ATCAGGGGCAAGTCTCTACGCTCAGTGCACAGGGGATCCCGCAGAGGCTCCATCTCTCCACG 2572
QY 2521 CTGCTCTGACGCTGTGCTACGGCGCAGCATGAGAACAAAGCTGTTGGCGGGATTGCGCGG 2580
DB 2573 CTGCTCTGACGCTGTGCTACGGCGCAGCATGAGAACAAAGCTGTTGGCGGGATTGCGCGG 2632
QY 2581 GACGGGCTCTCTCTGCGTTGGTGGATGATTTCTGTTGGTGAACACCTCACTCAACCCAC 2640
DB 2633 GACGGGCTCTCTCTGCGTTGGTGGATGATTTCTGTTGGTGAACACCTCACTCAACCCAC 2692
QY 2641 GCGAAAACCTTCTCTCAGAACCTGTGTCGAGAGTCTCTGAGTATGGCTGCTGCTGAAC 2700
DB 2693 GCGAAAACCTTCTCTCAGAACCTGTGTCGAGAGTCTCTGAGTATGGCTGCTGCTGAAC 2752
QY 2701 TTGCGAAGACAGTGTGAATTTCCCTGTAGAAGACAGGCCCTGGTGGACGAGCTTTT 2760
DB 2753 TTGCGAAGACAGTGTGAATTTCCCTGTAGAAGACAGGCCCTGGTGGACGAGCTTTT 2812
QY 2761 GTTCAGATCCGCGCCACGCGCTATTCCCTGTGCGGCTGTGCTGATACCGGAGAC 2820
DB 2813 GTTCAGATCCGCGCCACGCGCTATTCCCTGTGCGGCTGTGCTGATACCGGAGAC 2872
QY 2821 CTGAGGTGACAGAGCAGCTCTCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAC 2880
DB 2873 CTGAGGTGACAGAGCAGCTCTCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGAACTCTTTGGGGCTTTGCGG 2940
DB 2933 TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGAACTCTTTGGGGCTTTGCGG 2992
QY 2941 CTGAAGTGTACAGCCTGTTCTGATTGTGAGTGAACAGCCTCCAGACGGTGTGACAC 3000
DB 2993 CTGAAGTGTACAGCCTGTTCTGATTGTGAGTGAACAGCCTCCAGACGGTGTGACAC 3052
QY 3001 AACATCTACAAGATCCTCTGCTGACAGGCTTCAAGCATGTGTGTGACGCTC 3060
DB 3053 AACATCTACAAGATCCTCTGCTGACAGGCTTCAAGCATGTGTGTGACGCTC 3112
QY 3061 CCAATTCTACGCAAGTTGGAAGAACCCCACTTTTCTGCGGCTCATCTTGAACAG 3120
DB 3113 CCAATTCTACGCAAGTTGGAAGAACCCCACTTTTCTGCGGCTCATCTTGAACAG 3172
QY 3121 GCTTCCCTCTGCTACTCTCATCTCTGAAGCCCAAGAACGCAAGGATGTGCTGGGGCCCAAG 3180
DB 3173 GCTTCCCTCTGCTACTCTCATCTCTGAAGCCCAAGAACGCAAGGATGTGCTGGGGCCCAAG 3232
QY 3181 GGGGCGCGCGCGCTCTGCGCTCCGAGCGGCTGAGTGGCTGTGCCACCAAGCATCTCTG 3240
DB 3233 GGGGCGCGCGCGCTCTGCGCTCCGAGCGGCTGAGTGGCTGTGCCACCAAGCATCTCTG 3292
QY 3241 CTCAAGTGAAGTGAACCGGTGTACCTACGTGCACTCTCTGGGGTCACTCAAGACAGCC 3300
DB 3293 CTCAAGTGAAGTGAACCGGTGTACCTACGTGCACTCTCTGGGGTCACTCAAGACAGCC 3352
QY 3301 CAGACGAGCTGAGTGGAAAGCTCCCGGGGACAGCGCTGACTGCGCTGGAAGCGCGAGCC 3360

Db 3353 CAGACGACGCTGAGTGGAACTCCGGGAGCAGCTGACTGCCCTGAGAGCCGACGCC 3412

QY 3361 AACCCGGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACC 3411

Db 3413 AACCCGGCACTGCCCTCAGACTTCAAGACCATCTGACTGATGGCCACC 3463

RESULT 11

ID ACC44482 standard; DNA; 4015 BP.

XX ACC44482;

AC ACC44482;

DT 29-AUG-2003 (first entry)

DE Human telomerase reverse transcriptase gene.

XX Gene; ds; human; telomerase reverse transcriptase; adipogenic capacity;
KW primary preadipocyte cell; adipogenesis; obesity; adipocytokine;
KM anorectic; adiponectin; insulin.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 56..3454

FT /tag= a

FT /product= "telomerase reverse transcriptase"

PN WO2003031640-A2.

PD 17-APR-2003.

PF 07-OCT-2002; 2002WO-US031635.

PR 06-OCT-2001; 2001US-0327650P.

PR 06-OCT-2001; 2001US-0327651P.

PA (BOST-) BOSTON MEDICAL CENT CORP.

PI Kirkland J, Tchkonja T;

DR WPI; 2003-421278/39.

DR P-PSDB; ABR58045.

XX New primary preadipocyte strain expressing telomerase reverse
PT transcriptase, useful in research applications, screening assays,
PT clinical applications, and in the administration of therapeutic agents,
PT particularly for obesity.

PS Disclosure; Page 11-13; 53pp; English.

XX The invention relates to the generation of primary preadipocyte cell
CC strains that express telomerase reverse transcriptase (TERT- the
CC catalytic subunit of telomerase), and maintain and/or enhance replicative
CC potential and maintain adipogenic capacity of the cell. This sequence
CC represents the gene encoding the TERT protein. The cell strain can be
CC used in research to study all aspect of adipogenesis, especially in
CC relation to researching treatments for e.g. obesity. The cell can also be
CC used to identify adipogenesis modulators for use as therapeutic agents
CC such as hormones, growth factors, cytokines, enzymes, cholesterol binding
CC proteins, cholesterol removing proteins or their combinations.
CC Alternatively, the therapeutic agent may be an adipocytokine, preferably
CC adiponectin, or insulin

XX Sequence 4015 BP; 663 A; 1363 C; 1275 G; 714 T; 0 U; 0 Other;

QY Query Match 100.0%; Score 3411; DB 7; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Db 53 GCGATGCCGCGCTCCCGCTGCGAGCGCTGCGCTCCCTGCTGCGAGCCACTACCGC 60

1132

QY 61 GAGTGTCTGCGCTGCGCACTTCTGTGCGGCGCTGAGGCCCCAGGCGCTGCGCTGTG 120

Db 113 GAGTGTCTGCGCTGCGCACTTCTGTGCGGCGCTGAGGCCCCAGGCGCTGCGCTGTG 172

QY 121 CAGCGCGGGGACCCCGGCTTCCGCGCGCTGCTGAGGCCCCAGGCGCTGCTGCTGCTG 180

Db 173 CAGCGCGGGGACCCCGGCTTCCGCGCGCTGCTGAGGCCCCAGGCGCTGCTGCTGCTG 232

QY 181 TGGGACGCAAGCG 240

Db 233 TGGGACGCAAGCG 292

QY 241 CTGCTGCGCGCGCTGCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 300

Db 293 CTGCTGCGCGCGCTGCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 352

QY 301 GAGTGTCTGCGCTGCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 360

Db 353 GAGTGTCTGCGCTGCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 412

QY 361 GCGAGCTACCTGCGCGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 420

Db 413 GCGAGCTACCTGCGCGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 472

QY 421 CTGCTGCGCGCGCTGCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 480

Db 473 CTGCTGCGCGCGCTGCTGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 532

QY 481 GTGCTGTGCTGCTGCGCGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 540

Db 533 GTGCTGTGCTGCTGCGCGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCTT 592

QY 541 GCTGCCACTCAGGCG 600

Db 593 GCTGCCACTCAGGCG 652

QY 601 GAACGGGCGCTGGAACCATAGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCT 660

Db 653 GAACGGGCGCTGGAACCATAGCGTCAAGGAGGCGCGCGCGCGCGCGCGCGCGCGCT 712

QY 661 GGTGCGAGGAGGCG 720

Db 713 GGTGCGAGGAGGCG 772

QY 721 CGTGGCGCTGCGCGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCT 780

Db 773 CGTGGCGCTGCGCGCAAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCT 832

QY 781 GCGAGGAGCGCGTGAACCGAGTACCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 840

Db 833 GCGAGGAGCGCGTGAACCGAGTACCGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 892

QY 841 GAAGAAGCCACTTCTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900

Db 893 GAAGAAGCCACTTCTTGAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 952

QY 901 GCGCGCGAGCAACG 960

Db 953 GCGCGCGAGCAACG 1012

QY 961 CCTGTGCGCGCGTGTACGCGCGAGCAACCACTTCTTCTTCTTCTTCTTCTTCTTCTT 1020

Db 1013 CCTGTGCGCGCGTGTACGCGCGAGCAACCACTTCTTCTTCTTCTTCTTCTTCTTCTT 1072

QY 1021 CAGCTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1080

Db 1073 CAGCTGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1132

QY 1081 CTGCTGAGAGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1140

Db 1133 CTGCTGAGAGCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1192

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Db 1193 CCCCCCTGCCCCAGCGCTACTGCAATGCGGCCCTGTTCTGAGCTGCTTGGGAAC 1252
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Db 1253 CACGCGAGTGGCCCCCTACGGGGGTGCTCTCAAGACGACTGCGCGCTGCGAGCTGCGGTC 1312
QY 1261 ACCCCAGCAGCCGGTGTCTGTGCCCGGAGAAAGCCCCAGGGCTGTGTGGCGGCCCGGAG 1320
Db 1313 ACCCCAGCAGCCGGTGTCTGTGCCCGGAGAAAGCCCCAGGGCTGTGTGGCGGCCCGGAG 1372
QY 1321 GAGGAGACACAGACCCCCCGCTGCGCTGTGACAGCTGTCTCCGCAACACAGAGCCCTGG 1380
Db 1373 GAGGAGACACAGACCCCCCGCTGCGCTGTGACAGCTGTCTCCGCAACACAGAGCCCTGG 1432
QY 1381 CAGGTGTACGGCTTCTGTGCGGGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Db 1433 CAGGTGTACGGCTTCTGTGCGGGCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1492
QY 1441 TCCAGGCAACAACGAAACCGCGCTTCTCAAGAAACACCAAGAGTTTCTCTCCCTGGGGAAG 1500
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Db 1553 CATGCCAAGCTCTGCTGCAAGAGCTGAGAGATGAGCGTGGCGGAGCTGCGCTGG 1612
QY 1561 CTGCGCAGAGAGCCCAAGGGGTGCTGTGTTCCGCGCAGAGACCGTCTGCTGAGAG 1620
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QY 1621 ATCTGCGCAAGTTCTCTGCACTGCTGATGAGTGTGTAAGTCTGAGCTGCTCAGGTCT 1680
Db 1673 ATCTGCGCAAGTTCTCTGCACTGCTGATGAGTGTGTAAGTCTGAGCTGCTCAGGTCT 1732
QY 1681 TTCTTTATGTCAAGAGACCAAGTTCAAAAAGACAGGCTTTTCTAACCAGAGAGT 1740
Db 1733 TTCTTTATGTCAAGAGACCAAGTTCAAAAAGACAGGCTTTTCTAACCAGAGAGT 1792
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Db 1793 GTCTGAGCAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGTGAGCTGCGG 1852
QY 1801 GAGCTGTGGAAGCAGAGGTGAGGACATCGGGAAGCCAGGCCCGCTGCTGAGCTCC 1860
Db 1853 GAGCTGTGGAAGCAGAGGTGAGGACATCGGGAAGCCAGGCCCGCTGCTGAGCTCC 1912
QY 1861 AGACTCCGCTTCATCCCCAAGCTGACGGGCTGCGCGCAATTGTAACATGACTAAGTC 1920
Db 1913 AGACTCCGCTTCATCCCCAAGCTGACGGGCTGCGCGCAATTGTAACATGACTAAGTC 1972
QY 1921 GTGGAGCAGAAAGCTTCCGAGAGAAAAGAGGGCCGAGGCTCACCTCGAGGTGAAG 1980
Db 1973 GTGGAGCAGAAAGCTTCCGAGAGAAAAGAGGGCCGAGGCTCACCTCGAGGTGAAG 2032
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Db 2033 GCACTGTTCAGCGTGTCAACTACGAGCGGGCGCGGCCCGGCTCTCTGGGCGCTCT 2092
QY 2041 GTGCTGGGCTTGACGATATCCAGAGGGCTGCGCACTTCTGTGCTGCTGCTGGGGCC 2100
Db 2093 GTGCTGGGCTTGACGATATCCAGAGGGCTGCGCACTTCTGTGCTGCTGCTGGGGCC 2152
QY 2101 CAGGACCCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGACGGCGCTACGACACC 2160
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QY 2221 TGCGTGGTGGTATGCGGTGTTCAGAGGCGGCCCATGGGCACTCCGCAAGGCTTC 2280
QY 2273 TGCGTGGTGGTATGCGGTGTTCAGAGGCGGCCCATGGGCACTCCGCAAGGCTTC 2332
QY 2281 AAGAGCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCAC 2340
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QY 2341 CTGAGAGAGACAGCCCGCTGAGGGATGCGTGTATCGAGCAGAGCTCTCCCTGAAT 2400
Db 2393 CTGAGAGAGACAGCCCGCTGAGGGATGCGTGTATCGAGCAGAGCTCTCCCTGAAT 2452
QY 2401 GAGGCCAGAGTGGCTCTTTCGACGCTTCTTACGCTTCATGTCACCAAGCCGTGCGC 2460
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QY 2521 CTGCTGTGACGCTGTGCTACGGCGACATGAGAAACAAAGCTTTTGGGGGATTGGCGCG 2580
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QY 2581 GACGGGCTGCTCTGCTGCTTGTGTGATGATTTCTGTGTGTGACACTTCACTCAACCAC 2640
Db 2633 GACGGGCTGCTCTGCTGCTTGTGTGATGATTTCTGTGTGTGACACTTCACTCAACCAC 2692
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Db 2693 GCGAAAACCTTCTCAGGACCCCTGCTGAGGTGTCCCTGAGTATGCTGCTGTGTGAAC 2752
QY 2701 TTGCGGAAGACAGTGTGTAACCTTCTGTGTAAGAAAGAGGCGCTGGGTGGACAGGCTTTT 2760
Db 2753 TTGCGGAAGACAGTGTGTAACCTTCTGTGTAAGAAAGAGGCGCTGGGTGGACAGGCTTTT 2812
QY 2761 GTTCAAGATGCGGGCCCAAGGCTGATTTCCCTGTGTGCGGCTGCTGTGATACCCGAGC 2820
Db 2813 GTTCAAGATGCGGGCCCAAGGCTGATTTCCCTGTGTGCGGCTGCTGTGATACCCGAGC 2872
QY 2821 CTGAGGTGAGAGGAGCTACTTCAAGTATGCCCCGAGCTTCATCAGAGCCAGTCTCAC 2880
Db 2873 CTGAGGTGAGAGGAGCTACTTCAAGTATGCCCCGAGCTTCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGGCTTCAAGGCTGGAGAAACATGCTGCAAACTTTGGGGCTTTGCGG 2940
Db 2933 TTCAACCGGCTTCAAGGCTGGAGAAACATGCTGCAAACTTTGGGGCTTTGCGG 2992
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Db 2993 CTGAAGTGTCAAGCTGTTTCTGATTTGAGGTGAACAGCTTCAGAGGTGTGAC 3052
QY 3001 AACATCTAACAGATCTCTGCTGAGGCGGTACAGGTTTCAAGCATGTGTGCTGAGCTC 3060
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QY 3181 GCGCGCGCGCGCTCTGCTGCTGAGGCGGTGAGTGTGCTGCAACCAAGCATTCCTG 3240
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Db 3293 CTCAAGTGAAGTGAACAGGTGCACTTACGTGCACTCTGCGGTCACTCAGAGAGCC 3352
QY 3301 CAGAGCAGCTGAGTGGAGAGCTCCCGGAGCAGAGCTGAGCTGAGGCGCGAGCC 3360
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Db 3353 CAGACGAGCTGAGTGGAGCTCCCGGGAGCAGCTGACTGCTGAGGCGGAGCC 3412
QY 3361 AACCGGCACTGCTCCAGACTTCAAGACCATCTGAGTATGAGCCACC 3411
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RESULT 12

ABZ18391
ID ABZ18391 standard; cDNA; 4015 BP.

AC ABZ18391;

DT 23-JAN-2003 (first entry)

DE Group III cDNA cancer related clone SEQ ID NO:817.

KW Human; cancer; tumour; therapy; diagnosis; CT antigen; CP antigen;
immune response; virology; immunology; microbiology; molecular biology;
recombinant DNA technology; gene; ss.

OS Homo sapiens.

PN WO200278516-A2.

PD 10-OCT-2002.

PF 28-MAR-2002; 2002WO-US010421.

PR 30-MAR-2001; 2001US-0280255P.

PR 28-AUG-2001; 2001US-0315563P.

PR 09-JAN-2002; 2002US-0347313P.

PA (CORI-) CORIXA CORP.

PI Wang T, Wang S, Bangur CS, Gaiger A;

DR WPI; 2003-058387/05.

PT New immunogenic polynucleotides or polypeptides useful for diagnosing,
preventing and treating cancer expressing CT or CP mRNA antigens, and in
virology, immunology, microbiology, molecular biology and recombinant DNA
techniques.

PS Claim 1; SEQ ID NO 817; 207pp; English.

CC ABQ17575 to ABQ20506 represent isolated polynucleotide (I) sequences, and
CC ABP54446 to ABP54472 represent protein (II) sequences, from the present
CC invention. (I) and (II) have cytostatic activity and can be used in gene
CC therapy and vaccines. (I), (II), antibodies and compositions from the
CC present invention are useful for diagnosing, preventing and treating
CC cancer, which expresses CT or CP mRNA antigens. They are useful for
CC stimulating immune response. They can also be useful in virology,
CC immunology, microbiology, molecular biology and recombinant DNA
CC techniques. N.B. The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 4015 BP; 664 A; 1363 C; 1275 G; 713 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 7; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGGCTCCCGGCTGCGAGCGCTGCTGCTGCGGAGCCACTACCGC 60
Db 53 GCGATGCGCGGCTCCCGGCTGCGAGCGCTGCTGCTGCGGAGCCACTACCGC 112
QY 61 GAGGTGCTGCGGCTGCGGAGCTGCTGCGGCGCTGCGGCGCCAGGCGCTGGTG 120
Db 113 GAGGTGCTGCGGCTGCGGAGCTGCTGCGGCGCTGCGGCGCCAGGCGCTGGTG 172
QY 121 CAGCGCGGAGCCCGGCGCTTCCGCGGCTGCTGCGGCGGAGTGTCTGTGTGCGTGC 180

Db 173 CAGCGCGGAGACCCCGGCTTTCGCGCGCTGTGAGCCAGTGCTGTGTGCTGCC 232
QY 181 TGGAGCGCACG 240
Db 233 TGGAGCGCACG 292
QY 241 CTGTGAGCCCGAGTGTGAGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGTGAGCCCGAGTGTGAGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GGTTCGCGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GGTTCGCGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGCTACTGCGCCCAACACGCTGACCGAGCACTGCGGGGAGCGGGCGTGGGCTG 420
Db 413 CGCAGCTACTGCGCCCAACACGCTGACCGAGCACTGCGGGGAGCGGGCGTGGGCTG 472
QY 421 CTGTGCGCGCGCTGCGGCGAGCAGCGTGTGCTGCTGCTGCGAGCGCTGCGCTTT 480
Db 473 CTGTGCGCGCGCTGCGGCGAGCAGCGTGTGCTGCTGCTGCGAGCGCTGCGCTTT 532
QY 481 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 533 GTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 592
QY 541 GCTGCACTCAGGCG 600
Db 593 GCTGCACTCAGGCG 652
QY 601 GAAAGGCGCTGGAACCAATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAAAGGCGCTGGAACCAATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCG 712
QY 661 GGTGCGAGGAGCG 720
Db 713 GGTGCGAGGAGCG 772
QY 721 CGTGGCGCTGCG 780
Db 773 CGTGGCGCTGCG 832
QY 781 GGCAGGAGCGCTGAGCCAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 833 GGCAGGAGCGCTGAGCCAGTGAACGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 892
QY 841 GAGAAGCCACTCTTTGAGAGGCTGCGCTCTGCGACGCGCGCGCGCGCGCGCGCG 900
Db 893 GAGAAGCCACTCTTTGAGAGGCTGCGCTCTGCGACGCGCGCGCGCGCGCGCGCG 952
QY 901 GGCAGGAGCCAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 953 GGCAGGAGCCAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1012
QY 961 CTTGTGCGCGCGCTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
Db 1013 CTTGTGCGCGCGCTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1072
QY 1021 CAGCTGCGCGCGCTCTCTACTCAGCTCTGTGAGCGCGCGCGCGCGCGCGCGCG 1080
Db 1073 CAGCTGCGCGCGCTCTCTACTCAGCTCTGTGAGCGCGCGCGCGCGCGCGCGCG 1132
QY 1081 CTGCTGAGAGCACTTTTCTGAGGCTTCCAGGCGCTGATGCCAGGAGTCCCGCAGG 1140
Db 1133 CTGCTGAGAGCACTTTTCTGAGGCTTCCAGGCGCTGATGCCAGGAGTCCCGCAGG 1192
QY 1141 CCGCGCGCTGCG 1200
Db 1193 CCGCGCGCTGCG 1252
QY 1201 CAGCGGAGTGCCTTACGCGGCTGTCTTCAAGAGCACTGCGCGCGCGCGCGCG 1260

Db 1253 CACGCGCAGTGCCTTACGGGGTGCTCCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTC 1312
QY 1261 ACCCAGCAGCCGGTGTGTGCCCCGGAGAGACCCAGGGCTTGTGGCCCCCGAG 1320
Db 1313 ACCCAGCAGCCGGTGTGTGCCCCGGAGAGACCCAGGGCTTGTGGCCCCCGAG 1372
QY 1321 GAGGAGGACACAGACCCCGCTGCGCTGTGAGCTGTCCGACAGACAGACCCCTGG 1380
Db 1373 GAGGAGGACACAGACCCCGCTGCGCTGTGAGCTGTCCGACAGACAGACCCCTGG 1432
QY 1381 CAGGTGTACGGCTTGTGGGGGGCTGCGCTGCGCGGCTGGTGCCCCCAGGCTTGGGGC 1440
Db 1433 CAGGTGTACGGCTTGTGGGGGGCTGCGCTGCGCGGCTGGTGCCCCCAGGCTTGGGGC 1492
QY 1441 TCCAGGACACAGACCCCGCTTCTTCAAGAACCAAGATTCTCTCTGGGAG 1500
Db 1493 TCCAGGACACAGACCCCGCTTCTTCAAGAACCAAGATTCTCTCTGGGAG 1552
QY 1501 CATGCCAAGCTCTCGCTGACAGGAGCTGACCTGGAAGATGAGCGTGGGGAATGGCTTGG 1560
Db 1553 CATGCCAAGCTCTCGCTGACAGGAGCTGACCTGGAAGATGAGCGTGGGGAATGGCTTGG 1612
QY 1561 CTGCGCAGGAGCCCGAGGGGTGGCTGTGTTCCGGCCGACAGACACCTGTCTGCTGAGAG 1620
Db 1613 CTGCGCAGGAGCCCGAGGGGTGGCTGTGTTCCGGCCGACAGACACCTGTCTGCTGAGAG 1672
QY 1621 ATCTTGCCCAAGTTCTGCACTGGCTGATGATGTGTACGTCTGCAAGTGTCTAGGCTCT 1680
Db 1673 ATCTTGCCCAAGTTCTGCACTGGCTGATGATGTGTACGTCTGCAAGTGTCTAGGCTCT 1732
QY 1681 TTCTTTATGTACAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAT 1740
Db 1733 TTCTTTATGTACAGGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAT 1792
QY 1741 GTCTGAGCAAGTTGCAAGCATTTGGAATCAGACACTTGAAGAGGTGACGCTGCGG 1800
Db 1793 GTCTGAGCAAGTTGCAAGCATTTGGAATCAGACACTTGAAGAGGTGACGCTGCGG 1852
QY 1801 GAGCTGTGGAAGCAGAGGTGAGGAGCATCGGAAGCCAGGCTCGCTGCTGACGCTC 1860
Db 1853 GAGCTGTGGAAGCAGAGGTGAGGAGCATCGGAAGCCAGGCTCGCTGCTGACGCTC 1912
QY 1861 AGACTCCGCTTCACTCCCAAGCCTGACGGGCTGCGGCGGCTGCTGAGACTAGCTC 1920
Db 1913 AGACTCCGCTTCACTCCCAAGCCTGACGGGCTGCGGCGGCTGCTGAGACTAGCTC 1972
QY 1921 GTGGAGCCAGAACGTTCCGACAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGTTAAG 1980
Db 1973 GTGGAGCCAGAACGTTCCGACAGAGAAAAGAGGGCCGAGCGTCTCACTCGAGGTTAAG 2032
QY 1981 GCACTGTTCAGCGTCTCACTACAGAGCGGCGGCGGCGGCTCTGCGGCGCTCT 2040
Db 2033 GCACTGTTCAGCGTCTCACTACAGAGCGGCGGCGGCGGCTCTGCGGCGCTCT 2092
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Db 2093 GTGCTGGGCTGAGCATATCCACAGGGCTGGCGCACCTTCTGCTGCTGCTGCGGCGC 2152
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Db 2153 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGCTACGACACC 2212
QY 2161 ATCCCCCAGAGAGGCTCAAGAGGTCACTGCGCAGCATCATAAACCCAGAACAGCTAC 2220
Db 2213 ATCCCCCAGAGAGGCTCAAGAGGTCACTGCGCAGCATCATAAACCCAGAACAGCTAC 2272
QY 2221 TGGCTGCGTGGTATGCGGTGTGTCAGAAAGCCCGCATGGGCACTCCGCAAGGCTTC 2280
Db 2273 TGGCTGCGTGGTATGCGGTGTGTCAGAAAGCCCGCATGGGCACTCCGCAAGGCTTC 2332
QY 2281 AAGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCAAGTTCGTGCTCAC 2340
Db 2333 AAGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCAAGTTCGTGCTCAC 2392

QY 2341 CTGACAGAGACCAAGCCCGCTGAGGAGTGCCTGCTCATCGACAGAGCTCTCTCTGAAT 2400
Db 2393 CTGACAGAGACCAAGCCCGCTGAGGAGTGCCTGCTCATCGACAGAGCTCTCTCTGAAT 2452
QY 2401 GAGCCAGCAGTGGCTCTTCAAGCTCTTCAAGCTTCACTGTCACAGAGCGCTGGCGC 2460
Db 2453 GAGCCAGCAGTGGCTCTTCAAGCTCTTCAAGCTTCACTGTCACAGAGCGCTGGCGC 2512
QY 2461 ATCAGGGGCAAGTCTTACGTCCAGTGCCAGGGGATCCCGCAGGAGCTCCATCTCCACG 2520
Db 2513 ATCAGGGGCAAGTCTTACGTCCAGTGCCAGGGGATCCCGCAGGAGCTCCATCTCCACG 2572
QY 2521 CTGCTCTGAGCCTGTGCTACGGGACATGAGAAACAAGCTGTTGGGGGATTCGGCGG 2580
Db 2573 CTGCTCTGAGCCTGTGCTACGGGACATGAGAAACAAGCTGTTGGGGGATTCGGCGG 2632
QY 2581 GACGGGCTGCTCTGCGTTTGGTGATGATTTCTGTTGTTGACACCTCACTCAACCCAC 2640
Db 2633 GACGGGCTGCTCTGCGTTTGGTGATGATTTCTGTTGTTGACACCTCACTCAACCCAC 2692
QY 2641 GCGAAACCTTCTTCAAGACCCCTGTCCAGAGTCTCCCTGAGTATGGCTGCTGTGAAC 2700
Db 2693 GCGAAACCTTCTTCAAGACCCCTGTCCAGAGTCTCCCTGAGTATGGCTGCTGTGAAC 2752
QY 2701 TTGCGGAAGACAGTGTGAACCTTCCCTGTAAAGACAGAGCCCTGGTGGACCGGCTTTT 2760
Db 2753 TTGCGGAAGACAGTGTGAACCTTCCCTGTAAAGACAGAGCCCTGGTGGACCGGCTTTT 2812
QY 2761 GTTCAAGTCCGGCCCAAGGCTTATCCCTGTGCTGCGGCTGCTGTGATACCCGGAC 2820
Db 2813 GTTCAAGTCCGGCCCAAGGCTTATCCCTGTGCTGCGGCTGCTGTGATACCCGGAC 2872
QY 2821 CTGAGGTGACAGGCACTACTCCAGCTATGCGCGGACCTCCATCAGAGCAAGTCTCAC 2880
Db 2873 CTGAGGTGACAGGCACTACTCCAGCTATGCGCGGACCTCCATCAGAGCAAGTCTCAC 2932
QY 2881 TTCAACCGGGCTTCAAGGCTGGGAGGAACATGCGTCCAAACTCTTTGGGGTCTTGCGG 2940
Db 2933 TTCAACCGGGCTTCAAGGCTGGGAGGAACATGCGTCCAAACTCTTTGGGGTCTTGCGG 2992
QY 2941 CTGAAGTGTACAGCCTGTTTCTGATTTGAGGTGAACAGCCTCCAGACGCTGTGACCC 3000
Db 2993 CTGAAGTGTACAGCCTGTTTCTGATTTGAGGTGAACAGCCTCCAGACGCTGTGACCC 3052
QY 3001 AACATCTACAAGATCTCTGCTGACGGGCTACAGGTTTCAAGCATGTGTCTGACGCTC 3060
Db 3053 AACATCTACAAGATCTCTGCTGACGGGCTACAGGTTTCAAGCATGTGTGTGACGCTC 3112
QY 3061 CCATTTATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACACG 3120
Db 3113 CCATTTATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACACG 3172
QY 3121 GCCTCCCTGTCTACTCATCTGAAAGCCAAAGACGAGGAGTGTGCGGGCCAAAG 3180
Db 3173 GCCTCCCTGTCTACTCATCTGAAAGCCAAAGACGAGGAGTGTGCGGGCCAAAG 3232
QY 3181 GGGCGCGCGGCTCTGCGCTCCGAGGCGGTGACAGTGTGTCACCAAGCATTCCTG 3240
Db 3233 GGGCGCGCGGCTCTGCGCTCCGAGGCGGTGACAGTGTGTCACCAAGCATTCCTG 3292
QY 3241 CTCAAGCTGACTGACACCGGTGTACCTTACGTGCACTCTGGGGTCACTCAGACAGCC 3300
Db 3293 CTCAAGCTGACTGACACCGGTGTACCTTACGTGCACTCTGGGGTCACTCAGACAGCC 3352
QY 3301 CAGACGAGCTGAGTGGAAAGTCCCGGGGACGACGCTGACTGCGCTGGAAGCCGACCC 3360
Db 3353 CAGACGAGCTGAGTGGAAAGTCCCGGGGACGACGCTGACTGCGCTGGAAGCCGACCC 3412
QY 3361 AACCGGCACTGCGCTCAGACTTGAAGACCATCTGACTGATGGCCACCC 3411
Db 3413 AACCGGCACTGCGCTCAGACTTGAAGACCATCTGACTGATGGCCACCC 3463

RESULT 13
AAV72117
ID AAV72117 standard; cDNA; 4042 BP.
XX
AC AAV72117;
XX
DT 24-MAY-1999 (first entry)
XX
DE Human catalytic telomerase sub-unit cDNA.
XX
KW Human; catalytic telomerase subunit; therapy; diagnosis; htc; assay;
KW modulator; treatment; inhibit; cellular disorder; death; defect; cancer;
KW ageing; antisense; neoplastic cell; telomerase-related condition;
KW tumour cell; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 63..3461
FT /*tag= a
FT /product= "catalytic telomerase subunit"
XX
PN WO9859040-A2.
XX
PD 30-DEC-1998.
XX
PF 09-JUN-1998; 98WO-EP003468.
XX
PR 20-JUN-1997; 97DE-01026329.
PR 26-MAR-1998; 98DE-01013274.
PR 14-APR-1998; 98DE-01016496.
XX
PA (FARB) BAYER AG.
XX
PI Hagen G, Siegmund H, Weichel W, Wick M, Zubov D;
XX
DR WPI: 1999-081276/07.
DR P-PSDB; AAM90251.
XX
PT New catalytically active subunit of human telomerase - used in the
PT modulation of telomerase activity, particularly for treating cancer and
PT ageing.
XX
PS Claim 4; Fig 1; 76pp; German.
XX
CC This sequence encodes a novel human catalytic telomerase sub-unit (htc).
CC The encoded protein can be used in screening assays to identify
CC modulators of telomerase and to treat or inhibit cellular disorders,
CC death, defects and/or other pathological processes involving telomerase,
CC particularly cancer and ageing (also suitable for this are agents that
CC stimulate, inhibit or mimic the activity of the subunit). Antisense
CC nucleic acids inhibit telomerase action (by binding to specific mRNA),
CC particularly in neoplastic cells and may be expressed in vivo. Antibodies
CC and fragments of the protein, used as probes or primers, are used to
CC diagnose telomerase-related conditions (especially neoplasia) by (1)
CC detecting abnormal levels of the subunit protein in body fluids or
CC tissues or (ii) by measuring the amount of the encoding nucleic acid.
CC Expression of the nucleic acid encoding the subunit mRNA is confined to
CC tumour cells, in contrast to the ubiquitous expression of the telomerase
CC RNA subunit
XX
SQ Sequence 4042 BP; 684 A; 1364 C; 1277 G; 717 T; 0 U; 0 Other;

Query Match 100.0%; Score 3411; DB 2; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGGAGCCACTACCGC 60
Db 60 GCGATGCGCGCGCTCCCGCTGCGAGCGCGCTCCCTGCTGCGGAGCCACTACCGC 119
QY 61 GAGGTGCTGCGCGCTGCGGAGCGCTGCTGCGGCGCGCTGCGGCGCGCTGCTG 120

Db 120 GAGGTGCTGCGCGCTGCGGAGCGCTGCTGCGGCGCGCTGCGGCGCGCTGCTG 179
QY 121 CAGCGCGGGGAGACCCCGGCTTTCCCGCGCGCTGCTGCGGAGCCAGTGCCTGCTGCGGCC 180
Db 180 CAGCGCGGGGAGACCCCGGCTTTCCCGCGCGCTGCTGCGGAGCCAGTGCCTGCTGCGGCC 239
QY 181 TGGGACGACAGCG 240
Db 240 TGGGACGACAGCG 299
QY 241 CTGCTGCGCGCGAGTCTGCTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 300 CTGCTGCGCGCGAGTCTGCTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 359
QY 301 GCGTTGCGCGCTGCTGACAGCG 360
Db 360 GCGTTGCGCGCTGCTGACAGCG 419
QY 361 CGCAGCTACCTGCG 420
Db 420 CGCAGCTACCTGCG 479
QY 421 CTGCTGCG 480
Db 480 CTGCTGCG 539
QY 481 GTGCTGCTGCTGCTGCG 540
Db 540 GTGCTGCTGCTGCTGCG 599
QY 541 GCTGCACTCAGGCG 600
Db 600 GCTGCACTCAGGCG 659
QY 601 GAACGGCGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 660 GAACGGCGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 719
QY 661 GGTGCGAGGAGCG 720
Db 720 GGTGCGAGGAGCG 779
QY 721 CGTGCGCGCTGCG 780
Db 780 CGTGCGCGCTGCG 839
QY 781 GCGAGAGCGGTGAGCGAGTACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 840 GCGAGAGCGGTGAGCGAGTACCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
QY 841 GAAGAAGCCACTTTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 900 GAAGAAGCCACTTTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 959
QY 901 GCGCGCGAGCAGCG 960
Db 960 GCGCGCGAGCAGCG 1019
QY 961 CTTGTGCGCGCGGTGAGCG 1020
Db 1020 CTTGTGCGCGCGGTGAGCG 1079
QY 1021 CAGCTGCGCGCGCTTCTTCTACTCAGCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
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QY 1081 CTGCTGAGAGCACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Db 1140 CTGCTGAGAGCACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1199
QY 1141 CCGCGCGTGCAGCGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200

Db 1200 CCCCCCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTTGGGAAC 1259
QY 1201 CAGCGCAGTGCCTTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGGCGTC 1260
Db 1260 CAGCGCAGTGCCTTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGCTGGCGTC 1319
QY 1261 ACCCAGCAGCGGCTGTCTGTGCCCGGAGAGAGCCCGAGGGCTCTGTGGCGCCCCGAG 1320
Db 1320 ACCCAGCAGCGGCTGTCTGTGCCCGGAGAGAGCCCGAGGGCTCTGTGGCGCCCCGAG 1379
QY 1321 GAGAGGACACAGACCCCGCTGCTGTGTCAGCTGCTCCGCGACACAGAGCCCTGG 1380
Db 1380 GAGAGGACACAGACCCCGCTGCTGTGTCAGCTGCTCCGCGACACAGAGCCCTGG 1439
QY 1381 CAGGTGTACGGCTTCTGTGGGGCTGCTGCTGCGCGGCTGTGCCCCCGAGCTTGGGGC 1440
Db 1440 CAGGTGTACGGCTTCTGTGGGGCTGCTGCTGCGCGGCTGTGCCCCCGAGCTTGGGGC 1499
QY 1441 TCCAGGCACACGAAACCGGCTTCTCAAGAACACCAAGATTCTCTCTGGGGAAG 1500
Db 1500 TCCAGGCACACGAAACCGGCTTCTCAAGAACACCAAGATTCTCTCTGGGGAAG 1559
QY 1501 CATGCCAAGCTCTCGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGGAAGCTGCGCTTGG 1560
Db 1560 CATGCCAAGCTCTCGCTGACGAGAGCTGACGTGGAAGATGAGCGTGGGGAAGCTGCGCTTGG 1619
QY 1561 CTGCGCAGAGAGCCCGAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTAGAGAG 1620
Db 1620 CTGCGCAGAGAGCCCGAGGGGTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTAGAGAG 1679
QY 1621 ATCCTGGCCAAAGTTCTCTGCACTGGCTGATGATGTGTACGTCGTCGAGCTGCTCAGGTCT 1680
Db 1680 ATCCTGGCCAAAGTTCTCTGCACTGGCTGATGATGTGTACGTCGTCGAGCTGCTCAGGTCT 1739
QY 1681 TTCTTTATGTACGAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGT 1740
Db 1740 TTCTTTATGTACGAGAGACCAAGTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGT 1799
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Db 1800 GTCTGAGCAAGTTGCAAAAGCATTTGAATCAGACACATTGAAGAGGCTGAGCTGCGG 1859
QY 1801 GAGCTGTGGAAGCAGAGGTGAGGAGCAGCATCGGGAAGCCAGGCGCGCTGCTGAGCTGC 1860
Db 1860 GAGCTGTGGAAGCAGAGGTGAGGAGCAGCATCGGGAAGCCAGGCGCGCTGCTGAGCTGC 1919
QY 1861 AGACTCCGCTTCAATCCCAAGCCTGACGGGCTGCGCGCATTTGTAACATGACTACGTG 1920
Db 1920 AGACTCCGCTTCAATCCCAAGCCTGACGGGCTGCGCGCATTTGTAACATGACTACGTG 1979
QY 1921 GTGGAGCCAGAACGTTCCGACAGAAAAGAGGCGGAGCGTCTCACTCGAGGAGTGAAG 1980
Db 1980 GTGGAGCCAGAACGTTCCGACAGAAAAGAGGCGGAGCGTCTCACTCGAGGAGTGAAG 2039
QY 1981 GCACTGTTCAAGCTGCTCAACTACGAGCGGCGCGCGCGCTCTCTGGGCGCTCT 2040
Db 2040 GCACTGTTCAAGCTGCTCAACTACGAGCGGCGCGCGCGCTCTCTGGGCGCTCT 2099
QY 2041 GTGCTGGGCTGAGCATATCCACAGGGCTGGCGCACTTCTGTGCTGCTGTGCGGGC 2100
Db 2100 GTGCTGGGCTGAGCATATCCACAGGGCTGGCGCACTTCTGTGCTGCTGTGCGGGC 2159
QY 2101 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCTACGACACC 2160
Db 2160 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCTACGACACC 2219
QY 2161 ATCCCCCAGGACAGGCTCACGAGGTCAATGCCAGCATCAAAACCCAGAACACGTAAC 2220
Db 2220 ATCCCCCAGGACAGGCTCACGAGGTCAATGCCAGCATCAAAACCCAGAACACGTAAC 2279
QY 2221 TGGCTGCTGCTATGCTGCTGTGCTCAAGAGCGCGCCATGGGCACTGCGCAAGGCTTTC 2280
Db 2280 TGGCTGCTGCTATGCTGCTGTGCTCAAGAGCGCGCCATGGGCACTGCGCAAGGCTTTC 2339

QY 2281 AAGAGCCAGTCTCTACTTGAACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCAC 2340
Db 2340 AAGAGCCAGTCTCTACTTGAACAGACCTCCAGCCGTACATGCGACAGTTGCTGCTCAC 2399
QY 2341 CTGCAAGAGACCAAGCCCGCTGAGGATGCGGTGCTCATCGAGCAGAGCTCTCCCTGAAT 2400
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QY 2401 GAGGCCAGCAGTGAAGCTTTCAGCGTCTTCTCAAGCTTCAATGTGCCACAGCGCGTGGC 2460
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QY 2461 ATCAGGGGCAAGTCTCTAGTCCAGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCTCCACG 2520
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QY 2521 CTGCTCTGACGCTGTGCTACGGCGACATGAGAAACAAGCTGTTTGGGGGATTCGGCGG 2580
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Db 2640 GACGGGCTGCTCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACTCACCCAC 2699
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Db 2700 GCGAAAACTTCTCTAGAGACCTCTGTCAGAGGTCTCTGATGATGCTGCGTGTGAAC 2759
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Db 2760 TTGCGGAAGACAGTGTGAACCTTCCCTGTAGAAAGCAGAGCCCTGGGTGCAAGGCTTTT 2819
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QY 2821 CTGAGGTGACAGGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCACTCTCAC 2880
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QY 3001 AACATCTACAAGATCTCTGCTGACAGGCTACAGGTTTCAAGCATGTGTGACAGCTC 3060
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QY 3061 CCATTTATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACACG 3120
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QY 3121 GCCTCCCTGTGTAATCCATCTGAAAGCAAGAACGACAGGATGCTGGGGCCAAAG 3180
Db 3180 GCCTCCCTGTGTAATCCATCTGAAAGCAAGAACGACAGGATGCTGGGGCCAAAG 3239
QY 3181 GCGCGCGCGGCTCTGCGCTCCGAGCGCTGACGTGCTGTGCAACCAAGCATTCCTG 3240
Db 3240 GCGCGCGCGGCTCTGCGCTCCGAGCGCTGACGTGCTGTGCAACCAAGCATTCCTG 3299
QY 3241 CTCAAGTGAATGACACCGTGTCACTACGTGCACTCTGGGGTCACTCAGACAGCC 3300
Db 3300 CTCAAGTGAATGACACCGTGTCACTACGTGCACTCTGGGGTCACTCAGACAGCC 3359
QY 3301 CAGACGAGCTGAGTGGAGGCTCCGGGGGACGACGCTGACTGCTGAGAGCGCGACGC 3360
Db 3360 CAGACGAGCTGAGTGGAGGCTCCGGGGGACGACGCTGACTGCTGAGAGCGCGACGC 3419

QY	1261	ACCCACAGACCCGGTGTCTGTGCCCCGGAGAAAGCCCCAGAGGCTTGTGGCGGCCCCCGAG	1320
Db	1333	ACCCACAGACCCGGTGTCTGTGCCCCGGAGAAAGCCCCAGAGGCTTGTGGCGGCCCCCGAG	13922
QY	1321	GAGGAGGACACAGACCCCCCGTCCGCTTGATGACGTGCTCCGCCAGACAAGACAGCCCTTG	13800
Db	1393	GAGGAGGACACAGACCCCCCGTCCGCTTGATGACGTGCTCCGCCAGACAAGACAGCCCTTG	14522
QY	1381	CAGGTGTACGGCTTCTGTGCGGGCTGECTGCGCCGGCTGTTGCCCCCCAGGCTCTGGGC	14400
Db	1453	CAGGTGTACGGCTTCTGTGCGGGCTGECTGCGCCGGCTGTTGCCCCCCAGGCTCTGGGC	15122
QY	1441	TCCAGGCAACAAGAACCGCGCTTCTCAGGAAACACCAAGAGTTCACTCCCTGGGGAAG	15000
Db	1513	TCCAGGCAACAAGAACCGCGCTTCTCAGGAAACACCAAGAGTTCACTCCCTGGGGAAG	15722
QY	1501	CATGCCAAGCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGACTGCGCTTG	15600
Db	1573	CATGCCAAGCTCTCGCTGACGAGCTGACGTGGAAGATGAGCGTGGGACTGCGCTTG	16322
QY	1561	CTGCGCAGAGACCCAGGGGTTGGCTGTGTTCCGGCCGACAGACCGTCTGCTGAGGAG	16200
Db	1633	CTGCGCAGAGACCCAGGGGTTGGCTGTGTTCCGGCCGACAGACCGTCTGCTGAGGAG	16922
QY	1621	ATCCTGGCCAAAGTTCCCTGCACTGGCTGATGAGTGTGTAAGTGTGAGCTGCTCAGTCT	16800
Db	1693	ATCCTGGCCAAAGTTCCCTGCACTGGCTGATGAGTGTGTAAGTGTGAGCTGCTCAGTCT	17522
QY	1681	TTCTTTTATGTACCGAGACCAAGCTTCAAAAGACAGGCTCTTTTCTACCCGAAGAT	17400
Db	1753	TTCTTTTATGTACCGAGACCAAGCTTCAAAAGACAGGCTCTTTTCTACCCGAAGAT	18122
QY	1741	GTTCTGAGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAAGGTGCAAGTCCGG	18000
Db	1813	GTTCTGAGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAAGGTGCAAGTCCGG	18722
QY	1801	GAGCTGTCCGGAAGCAGAGGTCAAGGACGATCGGGAAGCCAGGCCCTGCTGACGTCC	18600
Db	1873	GAGCTGTCCGGAAGCAGAGGTCAAGGACGATCGGGAAGCCAGGCCCTGCTGACGTCC	19322
QY	1861	AGACTCCGCTTCATCCCCAGAGCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTC	19200
Db	1933	AGACTCCGCTTCATCCCCAGAGCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTC	19922
QY	1921	GTTGGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACCTCGAGGCTGAAG	19800
Db	1993	GTTGGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACCTCGAGGCTGAAG	20522
QY	1981	GCACTGTTCAAGCTGTCAACTACGAGCGGGCGCGGCCCTCCTGCGGCGCTCT	20400
Db	2053	GCACTGTTCAAGCTGTCAACTACGAGCGGGCGCGGCCCTCCTGCGGCGCTCT	21122
QY	2041	GTTGCTGGGCTTGAGCATATTCACAGGGCCTGGCGCACTTCTGTTGCTGCTGTGCGGGCC	21000
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QY	2161	ATCCCCCAGGACAGGCTCACGGAAGGTATCGCCAGACATCATCAACCCAGAACACAGTAC	22200
Db	2233	ATCCCCCAGGACAGGCTCACGGAAGGTATCGCCAGACATCATCAACCCAGAACACAGTAC	22922
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Db	2353	AAAGACCAAGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGTGCTCAC	24122
QY	2341	CTGCAGAGACCAAGCCCGCTGAGGGATGCCGTGCTCATCGAGCAGAGCTTCTCCCTGAAT	24000

Db	2413	CTGCAGGAGACCAAGCCCGCTGAGGGATGCCCGTGTGATCGAGCAGAGACTCCTCCCTGAAT	2472
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Db	2473	GAGGCCAGCAGTGGCCTCTTTCGACGTCTTCTACGCTTCATGTGCCACCAAGCGGTGCC	2532
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QY	2581	GACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCAC	2640
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QY	2641	GCGAATAACCTTCTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGGGTGAAC	2700
Db	2713	GCGAATAACCTTCTCCTCAGGACCCCTGGTCCGAGGTGTCCTGAGTATGGCTGGGTGAAC	2772
QY	2701	TTGCCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTT	2760
Db	2773	TTGCCGGAAGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGACGGCTTTT	2832
QY	2761	GTTTCAGATGCCGGGCCACGGCCTATTCCCTGGTGGCGGCTGTGCTGTAACCCGGACC	2820
Db	2833	GTTTCAGATGCCGGGCCACGGCCTATTCCCTGGTGGCGGCTGTGCTGTAACCCGGACC	2892
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QY	2941	CTGAAGTGTACAGCCTGTTTCTGTGATTTGAGGTGAACAGCCTCCAGACGGTGTGCACC	3000
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QY	3001	AACATCTACAAGATCCTCTGTGTGAGGCGTACAGGTTTACGCGATGTGTCTGCAGCTC	3060
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Db	3433	AAACCGGCACTGCCCTCAGACTTCAAGACCATCCTGAGCTGATGGCCACCC 3483	

RESULT 15

AAV27876
ID AAV27876 standard; cDNA; 3798 BP.
XX AAV27876;
AC
XX 25-MAR-2003 (revised)
DT 12-OCT-1998 (first entry)
XX
DE Human telomerase protein 2 (TP2) full-length cDNA.
XX
KM TP2; human; telomerase protein 2; cancer; AIDS; ageing; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..3466
FT /*tag= a
XX
XX MO9821343-A1.
XX
XX 22-MAY-1998.
XX
XX 13-NOV-1997; 97WO-US021248.
XX
XX 15-NOV-1996; 96US-00751189.
XX 11-JUN-1997; 97US-00873039.
XX 16-OCT-1997; 97US-00951733.
XX
XX (AMGE-) AMGEN INC.
XX (AMGE-) AMGEN CANADA INC.
XX
XX Harrington LA, Robinson MO;
XX
XX WPI; 1998-297946/26.
XX P-PSDB; AAV27876.
XX
XX
XX New nucleic acid encoding human telomerase protein-2 - used for
PT regulating telomerase activity, e.g. for treating cancer or acquired
PT immune deficiency syndrome.
XX
XX
XX Claim 1c; Fig 8; 150pp; English.
XX
XX This full-length cDNA clone codes for a human telomerase protein 2 (TP2,
CC see AAW61350), a novel protein of the telomerase complex. The sequence
CC was deduced from overlapping partial clones #32 (see AAV27872) and TP2-15
CC (see AAV27875), which were obtained from a human colon tumour cell line
CC LIM1863 cDNA. Expressing TP2 genes in a cell is used to increase
CC telomerase activity and thus proliferation for treatment of e.g. HIV
CC infection, AIDS and ageing disorders, while expressing an inactive mutant
CC of TP2 (or molecule antisense to the gene) is used to decrease telomerase
CC activity, e.g. for treatment of cancer. TP2 polypeptides can also be used
CC to screen for agents that inhibit TP2 activity or its binding to TRF1
CC (see AAW61347) or telomerase RNA, potentially useful therapeutically,
CC also to raise specific antibodies useful in immunoassays and
CC therapeutically as inhibitors. Nucleic acid fragments are used as
CC diagnostic probes for detecting/quantifying TP2 DNA. Also contemplated
CC are transgenic animals in which the TP2 gene has been inactivated or is
CC overexpressed. TP2 polypeptides are administered i.v., s.c. or orally, or
CC they are delivered from engineered cells or gene therapy vectors.
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX
SQ Sequence 3798 BP; 613 A; 1311 C; 1212 G; 662 T; 0 U; 0 Other;
Query Match 100.0%; Score 3409.4; DB 2; Length 3798;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 121 CAGCCGGGGGACCCCGGGGCTTTCCGCGCGCTGTGTGGCCAGTGCTGGTGTGCTGCCCC 180
Db 185 CAGCCGGGGGACCCCGGGGCTTTCCGCGCGCTGTGTGGCCAGTGCTGGTGTGCTGCCCC 244
QY 181 TGGGACGCAAGCG 240
Db 245 TGGGACGCAAGCG 304
QY 241 CTGCTGGCCCGAGTGTGTCAGAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCTT 300
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Db 605 GCTGCCACTCAGGCG 664
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QY 661 GGTGCGAGAGCG 720
Db 725 GGTGCGAGAGCG 784
QY 721 CGTGCCTGCTGCTGAGCG 780
Db 785 CGTGCCTGCTGCTGAGCG 844
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Db 965 GGCGCGCAGCACG 1024
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Db 1025 CCTTGTCCCGGTGTACGCGCGAGACCAAGCACTTCTTACTCTCTAGGCGACAAGAG 1084
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Tue Mar 2 09:53:25 2004

us-09-424-686f-11.rng

Page 32

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 19:45:38 ; Search time 6913.91 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3411	100.0	3411	20	US-09-424-686F-11
2	3411	100.0	3798	13	US-08-951-733-19
3	3411	100.0	4015	1	PCT-US01-15774-3
4	3411	100.0	4015	1	PCT-US02-10421-817
5	3411	100.0	4015	1	PCT-US02-14667-1
6	3411	100.0	4015	1	PCT-US02-31635-1
7	3411	100.0	4015	1	PCT-US02-33146-19
8	3411	100.0	4015	1	PCT-US03-19844-1
9	3411	100.0	4015	1	PCT-US99-06898-1
10	3411	100.0	4015	1	PCT-US99-07097-1
11	3411	100.0	4015	1	PCT-US99-07160-1
12	3411	100.0	4015	13	US-08-974-549-1
13	3411	100.0	4015	14	US-09-052-864-1
14	3411	100.0	4015	20	US-09-432-503-1
15	3411	100.0	4015	25	US-09-601-645-10
16	3411	100.0	4015	25	US-09-601-645A-10
17	3411	100.0	4015	31	US-09-721-477-1
18	3411	100.0	4015	31	US-09-721-506-1
19	3411	100.0	4015	34	US-09-843-676-224
20	3411	100.0	4015	39	US-09-949-016-455
21	3411	100.0	4015	42	US-09-990-080-1
22	3411	100.0	4015	43	US-10-044-539-1
23	3411	100.0	4015	43	US-10-044-592-1
24	3411	100.0	4015	44	US-10-053-758-224
25	3411	100.0	4015	44	US-10-054-295-224
26	3411	100.0	4015	44	US-10-054-611-224
27	3411	100.0	4015	45	US-10-105-863-1
28	3411	100.0	4015	45	US-10-112-699-817
29	3411	100.0	4015	45	US-10-143-536-1
30	3411	100.0	4015	47	US-10-208-243-1
31	3411	100.0	4015	49	US-10-325-810-1
32	3411	100.0	4015	50	US-10-388-578-1
33	3411	100.0	4015	50	US-10-389-431-1
34	3411	100.0	4015	51	US-10-449-565-1
35	3411	100.0	4015	53	US-10-602-441-1
36	3411	100.0	4042	20	US-09-424-686B-1
37	3411	100.0	4042	20	US-09-424-686F-1
38	3411	100.0	4042	24	US-09-582-246-2
39	3411	100.0	7029	13	US-08-911-312A-1
40	3411	100.0	7029	13	US-08-911-312A-1
41	3409.4	100.0	4015	46	US-10-170-235-38656
42	3407.8	99.9	4016	81	US-60-245-223-3
43	3407.8	99.9	4023	14	US-09-026-981-35
44	3407.8	99.9	4027	1	PCT-US03-07526-1
45	3407.8	99.9	4027	14	US-09-063-657-1

ALIGNMENTS

RESULT 1
US-09-424-686F-11
; Sequence 11, Application US/09424686F
; GENERAL INFORMATION:
; APPLICANT: Hagen, Gustav
; APPLICANT: Siegmund, Hans-Ulrich
; APPLICANT: Weichel, Walter
; APPLICANT: Wick, Mareisa
; APPLICANT: Zubov, Dmitry
; TITLE OF INVENTION: Human Catalytic Telomerase Sub-Unit and its Diagnostic and Therap
; FILE REFERENCE: Bayer 10,203
; CURRENT APPLICATION NUMBER: US/09/424,686F
; PRIOR APPLICATION NUMBER: 1999-11-29
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microsoft Word
; SEQ ID NO 11

LENGTH: 3411
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3411)
; OTHER INFORMATION: Nucleotides 1-59 and 3471-4042 of SEQ ID NO 1 were deleted to
; US-09-424-686F-11
; provide this sequence.
Query Match
Best Local Similarity 100.0%; Score 3411; DB 20; Length 3411;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGATGCGCGCGCTCCCGCTGCGCGAGCGCTGCTCCCTGCTGCGAGCCACTACCGC 60
Db 1 GCGATGCGCGCGCTCCCGCTGCGCGAGCGCTGCTCCCTGCTGCGAGCCACTACCGC 60
QY 61 GAGGTGCTGCGCTGCGCGAGCGCTGCTGCGCGAGCGCTGCGCGAGCGCTGCGCGAG 120
Db 61 GAGGTGCTGCGCTGCGCGAGCGCTGCTGCGCGAGCGCTGCGCGAGCGCTGCGCGAG 120
QY 121 CAGCGCGCGAGCGCGCGCTTCCCGCGCGCTGCTGCGCGAGCGCTGCTGCGCGAGCG 180
Db 121 CAGCGCGCGAGCGCGCGCTTCCCGCGCGCTGCTGCGCGAGCGCTGCTGCGCGAGCG 180
QY 181 TGGAGCGAGCG 240
Db 181 TGGAGCGAGCG 240
QY 241 CTGCTGCGCGCGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 241 CTGCTGCGCGCGAGCTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 301 GCGTTCGCGCTGCGAGCG 360
Db 301 GCGTTCGCGCTGCGAGCG 360
QY 361 CGCAGCTACCTGCG 420
Db 361 CGCAGCTACCTGCG 420
QY 421 CTGCTGCG 480
Db 421 CTGCTGCG 480
QY 481 GTGCTGCTGCTGCG 540
Db 481 GTGCTGCTGCTGCG 540
QY 541 GCTGCG 600
Db 541 GCTGCG 600
QY 601 GAACG 660
Db 601 GAACG 660
QY 661 GGTGCGAGAGCG 720
Db 661 GGTGCGAGAGCG 720
QY 721 CGTGGCGCTGCG 780
Db 721 CGTGGCGCTGCG 780
QY 781 GCGAGAGCG 840
Db 781 GCGAGAGCG 840
QY 841 GAAGAAGCG 900
Db 841 GAAGAAGCG 900

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Db		901	GGCCCGCAGCACCAACGCGGGCCCCCATTCACATCGCGGCCAACCACTCCCTGGGACACG	960
QY		961	CTTTGTCCCCCGGTGTACGCCGAGACCAGAAGCACTTCTCTACTCTCTCAGCGACAAGAG	1020
Db		961	CTTTGTCCCCCGGTGTACGCCGAGACCAGAAGCACTTCTCTACTCTCTCAGCGACAAGAG	1020
QY		1021	CAGCTGCGGCCCTCTCTCTACTCAGCTCTCTGAGGCCAAGCCTGACTGGCGCTCGAAG	1080
Db		1021	CAGCTGCGGCCCTCTCTCTACTCAGCTCTCTGAGGCCAAGCCTGACTGGCGCTCGAAG	1080
QY		1081	CTCGTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCAGGGAACTCCCCGACAGTTG	1140
Db		1081	CTCGTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCAGGGAACTCCCCGACAGTTG	1140
QY		1141	CCCCGCTGCCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTGAGCTGCTTGGAA	1200
Db		1141	CCCCGCTGCCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTGAGCTGCTTGGAA	1200
QY		1201	CACGCGCAGTCCCCCTACGGGGTGCTCTCAAGACGCACTGCCGCTGCAGCTCGGTC	1260
Db		1201	CACGCGCAGTCCCCCTACGGGGTGCTCTCAAGACGCACTGCCGCTGCAGCTCGGTC	1260
QY		1261	ACCCGAGCAGCCGGTGTCTGTGCCCCGGAGAACCCCAAGGGCTCTGTGCGCGCCCCGAG	1320
Db		1261	ACCCGAGCAGCCGGTGTCTGTGCCCCGGAGAACCCCAAGGGCTCTGTGCGCGCCCCGAG	1320
QY		1321	GAGGAGCACACAGACCCCCTGCTGTGCTGTGAGCTGCTCCGACAGACAGACAGCCCTGG	1380
Db		1321	GAGGAGCACACAGACCCCCTGCTGTGCTGTGAGCTGCTCCGACAGACAGACAGCCCTGG	1380
QY		1381	CAGGTGTACGAGCTTGTGCGGGCTGCTGCGCGCGGTGTGCCCCCAGGCTCTGGGGC	1440
Db		1381	CAGGTGTACGAGCTTGTGCGGGCTGCTGCGCGCGGTGTGCCCCCAGGCTCTGGGGC	1440
QY		1441	TCCAGGCAACAAGAACGCGCGTTCTCAGGAACAACCAAGAATTCACTCCCTGGGGAAG	1500
Db		1441	TCCAGGCAACAAGAACGCGCGTTCTCAGGAACAACCAAGAATTCACTCCCTGGGGAAG	1500
QY		1501	CATGCCAAGCTCTCGCTGACAGGAGTGAAGTGAAGCTGCGGGACTGCCCTTG	1560
Db		1501	CATGCCAAGCTCTCGCTGACAGGAGTGAAGTGAAGCTGCGGGACTGCCCTTG	1560
QY		1561	CTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCCTGCGTAGAGAG	1620
Db		1561	CTGCGCAGGAGCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCCTGCGTAGAGAG	1620
QY		1621	ATCCTGSCCAAGTTCCTGCACTGEGCTGATGAGTGTGTAAGTCTGAGCTGCTCAGGCT	1680
Db		1621	ATCCTGSCCAAGTTCCTGCACTGEGCTGATGAGTGTGTAAGTCTGAGCTGCTCAGGCT	1680
QY		1681	TTCTTTTATGTACGGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGT	1740
Db		1681	TTCTTTTATGTACGGGAGACCAAGCTTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGT	1740
QY		1741	GTCTGAGCAAGTTGCAAAGCATTTGAATCAGACAGCACTTGAAGAAGGTGCACTGCGG	1800
Db		1741	GTCTGAGCAAGTTGCAAAGCATTTGAATCAGACAGCACTTGAAGAAGGTGCACTGCGG	1800
QY		1801	GAGCTGTCCGAAAGCAGAGSTCAGGCAAGCATCGGGAAGCCAAGCCCGCTGCTGACGTCC	1860
Db		1801	GAGCTGTCCGAAAGCAGAGSTCAGGCAAGCATCGGGAAGCCAAGCCCGCTGCTGACGTCC	1860
QY		1861	AGACTCCGCTTCAATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTC	1920
Db		1861	AGACTCCGCTTCAATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGACTACGTC	1920
QY		1921	GTGGAGCCAGAACGTTCCGACAGAAAAAGAGGSCCGAGCGTCTCAACCTCGAGGGGTGAAG	1980
Db		1921	GTGGAGCCAGAACGTTCCGACAGAAAAAGAGGSCCGAGCGTCTCAACCTCGAGGGGTGAAG	1980

QY	1981	GCACTGTTACGCTGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGCGCCTCT	2040
Db	1981	GCACTGTTACGCGTGTCTCAACTACGAGCGGGCGCGGCCCGCCCTCCTGGCGCCTCT	2040
QY	2041	GTGCTGGGCGCTGGACGATATCCACAGAGGCGCTGGCGCACTTTCGTGCTGCGTGTGCGGCGC	2100
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QY	2101	CAGAGACCGCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACC	2160
Db	2101	CAGAGACCGCGCGCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGCTACGACACC	2160
QY	2161	ATCCCCCAGGACAGGCTCACGGAGGTCAATGCCAGCATCATCAAACCCAGAACACGTAC	2220
Db	2161	ATCCCCCAGGACAGGCTCACGGAGGTCAATGCCAGCATCATCAAACCCAGAACACGTAC	2220
QY	2221	TGCGTGCGTGGTATGCGGTGTCCAGAAAGCGGCCCATATGGGCAAGTCCGCAAGGCTTTC	2280
Db	2221	TGCGTGCGTGGTATGCGGTGTCCAGAAAGCGGCCCATATGGGCAAGTCCGCAAGGCTTTC	2280
QY	2281	AAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTACATCGACAGTTGTTGGCTCAC	2340
Db	2281	AAGAGCCAGCTCTCTACCTTGACAGACCTCCAGCCGTACATCGACAGTTGTTGGCTCAC	2340
QY	2341	CTGACGAGACAGCCCGCTGAGGGATGCCGTGTCATCGACAGAGTCTCCCTGAAT	2400
Db	2341	CTGACGAGACAGCCCGCTGAGGGATGCCGTGTCATCGACAGAGTCTCTCCCTGAAT	2400
QY	2401	GAGGCCAGAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCAAGCCGTGCGC	2460
Db	2401	GAGGCCAGAGTGGCCTCTTCGACGTCTTCTACGCTTCATGTGCCACCAAGCCGTGCGC	2460
QY	2461	ATCAGGGGCAAGTCTTAAGTCCAGTCCAGGCGGATCCCGAGGGCTCCATCTCTCCACG	2520
Db	2461	ATCAGGGGCAAGTCTTAAGTCCAGTCCAGGCGGATCCCGAGGGCTCCATCTCTCCACG	2520
QY	2521	CTGCTCTGCAGCCTGTGCTACGGCGACATGGAAGAACAGCTGTTTGGGGGATTCGGCGG	2580
Db	2521	CTGCTCTGCAGCCTGTGCTACGGCGACATGGAAGAACAGCTGTTTGGGGGATTCGGCGG	2580
QY	2581	GACGGGCTGTCTCTGCGTTTGGTGAATTTCTTGTGTGACACCTCAACCTCAACCCAC	2640
Db	2581	GACGGGCTGTCTCTGCGTTTGGTGAATTTCTTGTGTGACACCTCAACCTCAACCCAC	2640
QY	2641	GCGAAAACCTTCTCTCAGGACCCCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGAAC	2700
Db	2641	GCGAAAACCTTCTCTCAGGACCCCTGTCGAGGTGTCCCTGAGTATGGCTGCGTGAAC	2700
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Db	2701	TTGCGGAAGACAGTGTGAATTCCTGTAGAAGACGAGGCCCTGGGTGGCAACGCGCTTTT	2760
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Db	2761	GTTCAGATGCGGGCCCAAGGCTATTCCTGCTGTGCGGCGCTGCTGTGATACCCGGACC	2820
QY	2821	CTGAGGTGCAAGAGGACTACTCCAGCTATGCCCGGAGCCTCCATCAGAGCCAGTCTCAC	2880
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QY	2881	TTCAACCGCGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGCGG	2940
Db	2881	TTCAACCGCGGCTTCAAGGCTGGAGGAACATGCGTCGCAAACTTTTGGGGTCTTGCGG	2940
QY	2941	CTGAAGTGTCAACAGCCTGTTTCTGGAATTTGCAAGGTGAACAGCCTTCCAGACGGTGTGACC	3000
Db	2941	CTGAAGTGTCAACAGCCTGTTTCTGGAATTTGCAAGGTGAACAGCCTTCCAGACGGTGTGACC	3000
QY	3001	AACATCTACAAGATCTCTCTGCTGCAAGCGGTACAGGTTTCAACGATGTGTGCTGACGCTC	3060
Db	3001	AACATCTACAAGATCTCTCTGCTGCAAGCGGTACAGGTTTCAACGATGTGTGCTGACGCTC	3060
QY	3061	CCAATTTCATCAGCAAGTTTGGAAAGAACCCCACTTTTTCCTGCGCGTCAATCTGTACACG	3120

Db 3061 CCAATTCATCAGCAGATTGGAGAAGAACCCCACTTTTCTCTGCGCTACTCTGACACG 3120
QY 3121 GCTTCCCTCTGCTACTCATCTGAAAGCCAGAAAGCAGGAGATGTCGTCGGGGCCAAAG 3180
Db 3121 GCTTCCCTCTGCTACTCATCTGAAAGCCAGAAAGCAGGAGATGTCGTCGGGGCCAAAG 3180
QY 3181 GGGCGCCGCGCCCTCTGCTCCGAGGCGCTGCACTGGCTGTGCCACCAAGCATTCCTG 3240
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QY 3241 CTCAGCTGACTGACACACCGTGTACCTACCTGTCCTGCTGCTGCTGCTGCTGCTGCTG 3300
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QY 3301 CAGACGAGCTGAGTCGGAAGCTCCCGGGGAGACGCTGACTGCTGCTGCTGCTGCTGCTG 3360
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QY 3361 AACCCGCACTGCTCTCAAGACTTCAAGACCACTCTGACTGATGCGCAACC 3411
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RESULT 2

US-08-951-733-19

Sequence 19, Application US/08951733

GENERAL INFORMATION:

APPLICANT: Harrington, Lea A.

APPLICANT: Robinson, Murray O.

TITLE OF INVENTION: NOVEL GENES ENCODING TELOMERASE PROTEINS

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: One Amgen Center Drive

CITY: Thousand Oaks

STATE: CA

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/951,733

FILING DATE: 16-OCT-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/873,039

FILING DATE: 11-JUN-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/751,189

FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Oleski, Nancy A.

REGISTRATION NUMBER: 34,688

REFERENCE/DOCKET NUMBER: A-433B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (805) 447-6504

TELEFAX: (805) 499-8011

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 3798 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-951-733-19

Query Match 100.0%; Score 3411; DB 13; Length 3798;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCCGCGGCTCCCGCTGCGGAGCCGTCGCTCCCTGCTGCGGAGCCACTACCGC 60
Db 65 GCGATGCCGCGGCTCCCGCTGCGGAGCCGTCGCTCCCTGCTGCGGAGCCACTACCGC 124
QY 61 GAGGTGCTGCGGCTGCGGAGCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 120
Db 125 GAGGTGCTGCGGCTGCGGAGCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 184
QY 121 CAGCGCGGAGCCGCGGCTTCCGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 180
Db 185 CAGCGCGGAGCCGCGGCTTCCGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 244
QY 181 TGGAGCGACG 240
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QY 241 CTGCTGCGCGGAGTCGTCGAGAGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 300
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QY 301 GCGCTTGGCGCTGTCGAGCGGCG 360
Db 365 GCGCTTGGCGCTGTCGAGCGGCG 424
QY 361 CGCAGCTACTGCGCCACACACGCTGACCGACACTGCGGCGGAGCGCGGCTGCGGCGCTG 420
Db 425 CGCAGCTACTGCGCCACACACGCTGACCGACACTGCGGCGGAGCGCGGCTGCGGCGCTG 484
QY 421 CTGCTGCGCGGAGTCGTCGAGAGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 480
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QY 661 GGTGCGAGGAGCG 720
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QY 721 CGTGGCGCTGCGCGCTGAGCGCGGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
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Db 905 GAAGAAGCCACTCTTTGAGAGGTCGCTCTCTGCGAGCGCGCACTCCCAACCATTCGCTG 964
QY 901 GGGCGGAGCAGCAGCG 960
Db 965 GGGCGGAGCAGCAGCG 1024
QY 961 CCTTGTCCCGGCTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGAGAGAG 1020
Db 1025 CCTTGTCCCGGCTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGAGAGAG 1084
QY 1021 CAGCTGCGGCGCTCTTCTCTACTCAGCTCTCTGAGGCGCGCAAGCTGAGGCTGCGAGG 1080
Db 1085 CAGCTGCGGCGCTCTTCTCTACTCAGCTCTCTGAGGCGCGCAAGCTGAGGCTGCGAGG 1144

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QY 1141 CCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTGGGAAC 1200
Db 1205 CCGCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTTCTGAGCTGCTGGGAAC 1264
QY 1201 CAGCGCAGTGGCCCTACGGGGTGTCTCTCAAGACCACTGCGCGCTGCGAGCTGGGTC 1260
Db 1265 CAGCGCAGTGGCCCTACGGGGTGTCTCTCAAGACCACTGCGCGCTGCGAGCTGGGTC 1324
QY 1261 ACCCCAGCAGCCGCTGTCTGTCGCCGGGAGAGGCCCAAGGCTCTGTGGCGGCCCGAG 1320
Db 1325 ACCCCAGCAGCCGCTGTCTGTCGCCGGGAGAGGCCCAAGGCTCTGTGGCGGCCCGAG 1384
QY 1321 GAGGAGGACACAGACCCCGCTGCTGCTGTCAGCTGCTCCGACAGCAGCAGCCCTGG 1380
Db 1385 GAGGAGGACACAGACCCCGCTGCTGCTGTCAGCTGCTCCGACAGCAGCAGCCCTGG 1444
QY 1381 CAGGTGTACGGCTTCGTGGCGGGCTGCTGCTGCGCGGCTGCTGCGCCCTCTGGGCG 1440
Db 1445 CAGGTGTACGGCTTCGTGGCGGGCTGCTGCTGCGCGGCTGCTGCGCCCTCTGGGCG 1504
QY 1441 TCCAGGCAACAAGAACCGCGCTTCTCAAGAACCAAGAAATTCTCTCTGGGGAAG 1500
Db 1505 TCCAGGCAACAAGAACCGCGCTTCTCAAGAACCAAGAAATTCTCTCTGGGGAAG 1564
QY 1501 CATGCCAAGCTCTGCTGAGGAGCTGACCTGGAAGATGAGCGTGGGGAAGCTGGCTTGG 1560
Db 1565 CATGCCAAGCTCTGCTGAGGAGCTGACCTGGAAGATGAGCGTGGGGAAGCTGGCTTGG 1624
QY 1561 CTGCGCAGGAGCCCGAGGGGTGGCTGTGTTCCGAGCCGACAGACACCTGCTGAGGAG 1620
Db 1625 CTGCGCAGGAGCCCGAGGGGTGGCTGTGTTCCGAGCCGACAGACACCTGCTGAGGAG 1684
QY 1621 ATCTGGCCAAAGTCTCTGCACTGCTGATGATGTGTACGTGCTGAGCTGCTCAGTCT 1680
Db 1685 ATCTGGCCAAAGTCTCTGCACTGCTGATGATGTGTACGTGCTGAGCTGCTCAGTCT 1744
QY 1681 TTCTTTATGTACCGAGACCAAGCTTTCAAAAGAACAGGCTTTTCTACCGGAAGAT 1740
Db 1745 TTCTTTATGTACCGAGACCAAGCTTTCAAAAGAACAGGCTTTTCTACCGGAAGAT 1804
QY 1741 GTCTGAGCAAGTGTCAAAAGCATTTGAATGAGACAGCACTTGAAGGGTGCAGTGG 1800
Db 1805 GTCTGAGCAAGTGTCAAAAGCATTTGAATGAGACAGCACTTGAAGGGTGCAGTGG 1864
QY 1801 GAGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCTGTGACGTCC 1860
Db 1865 GAGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCTGTGACGTCC 1924
QY 1861 AGACTCGCTTCAATCCCCAAGCCTGACGGGCTGGCGGATTTGTAACATGACTACGTC 1920
Db 1925 AGACTCGCTTCAATCCCCAAGCCTGACGGGCTGGCGGATTTGTAACATGACTACGTC 1984
QY 1921 GTGGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAG 1980
Db 1985 GTGGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAG 2044
QY 1981 GCACTGTTCAAGCTGTCAACTACAGAGGGGGCGGGCCCGGCTCTCTGGCGGCTCT 2040
Db 2045 GCACTGTTCAAGCTGTCAACTACAGAGGGGGCGGGCCCGGCTCTCTGGCGGCTCT 2104
QY 2041 GTGCTGGGCTGGAAGATATCCACAGGGCTGGCGCACTTGTGCTGCTGCTGGCGG 2100
Db 2105 GTGCTGGGCTGGAAGATATCCACAGGGCTGGCGCACTTGTGCTGCTGCTGGCGG 2164
QY 2101 CAGGACCCGCGCTGAGCTGTACTTGTCAAGGTGATGACGGCGCTACGACACC 2160
Db 2165 CAGGACCCGCGCTGAGCTGTACTTGTCAAGGTGATGACGGCGCTACGACACC 2224
QY 2161 ATCCCCCAGGACAGGCTACGAGGTCAATCGCCAGCATCAAAACCCAGAACAGTAC 2220

Db 2225 ATCCCCCAGGACAGGCTCAAGGAGTCAATCGCCAGCATCAAAACCCAGAACAGTAC 2284
QY 2221 TGGCTGCGTGGTATGCGCGGTGCCAGAGGCCGCCCATGGGCAAGCTCCGCAAGGCTTC 2280
Db 2285 TGGCTGCGTGGTATGCGCGGTGCCAGAGGCCGCCCATGGGCAAGCTCCGCAAGGCTTC 2344
QY 2281 AAGAGCCACGTCTCTACTTGAACAGACCTCCAGCCGTAATGCGACAGTTCGTGCTCAC 2340
Db 2345 AAGAGCCACGTCTCTACTTGAACAGACCTCCAGCCGTAATGCGACAGTTCGTGCTCAC 2404
QY 2341 CTGAGGAGACCAAGCCCGCTGAGGGATGCGCTGCTATCGAGCAGAGCTCTCCCTGAAT 2400
Db 2405 CTGAGGAGACCAAGCCCGCTGAGGGATGCGCTGCTATCGAGCAGAGCTCTCCCTGAAT 2464
QY 2401 GAGGCCAGCAGTGGCTCTTTCAGCGTCTTCTACGCTTCAATGTCACCAAGCGCTGGC 2460
Db 2465 GAGGCCAGCAGTGGCTCTTTCAGCGTCTTCTACGCTTCAATGTCACCAAGCGCTGGC 2524
QY 2461 ATCAGGGGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCCGCAGAGGCTCCATCTCCACG 2520
Db 2525 ATCAGGGGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCCGCAGAGGCTCCATCTCCACG 2584
QY 2521 CTGCTCTGAGCCTGTGTACCGGCGACATGAGAACAAAGCTGTTGCGGGATTCGGCGG 2580
Db 2585 CTGCTCTGAGCCTGTGTACCGGCGACATGAGAACAAAGCTGTTGCGGGATTCGGCGG 2644
QY 2581 GACGGGCTGCTCTGCGTTTGTGTGATGATTTCTGTTGTGACACCTCAACCTCAC 2640
Db 2645 GACGGGCTGCTCTGCGTTTGTGTGATGATTTCTGTTGTGACACCTCAACCTCAC 2704
QY 2641 GCGAAACCTTCTCTAGAACCTCTGTCAGAGTCTCTGATGATGCTGCTGCTGTAAC 2700
Db 2705 GCGAAACCTTCTCTAGAACCTCTGTCAGAGTCTCTGATGATGCTGCTGCTGTAAC 2764
QY 2701 TTGCGGAAGACAGTGTGAACCTTCCCTGTAGAAAGACAGGCGCTGGTGCAAGCTTTT 2760
Db 2765 TTGCGGAAGACAGTGTGAACCTTCCCTGTAGAAAGACAGGCGCTGGTGCAAGCTTTT 2824
QY 2761 GTTCAGATGCGGCCCAAGGCTATTCCTGTGTGCGGCTGCTGTGATACCCGAGAC 2820
Db 2825 GTTCAGATGCGGCCCAAGGCTATTCCTGTGTGCGGCTGCTGTGATACCCGAGAC 2884
QY 2821 CTGAGGTGCAAGCGACTACTCCAGCTATGCGCGGACCTCCATCAGAGCAAGTCTCAC 2880
Db 2885 CTGAGGTGCAAGCGACTACTCCAGCTATGCGCGGACCTCCATCAGAGCAAGTCTCAC 2944
QY 2881 TTCAACCGCGCTTCAAGGCTGGAAGAACATGCGTGCAGAACTTTTGGGGTCTTGCGG 2940
Db 2945 TTCAACCGCGCTTCAAGGCTGGAAGAACATGCGTGCAGAACTTTTGGGGTCTTGCGG 3004
QY 2941 CTGAAGTGCAGAGCTGTTTCTGATTTGAGGTGAACAGCCTCCAGACGCTGACACC 3000
Db 3005 CTGAAGTGCAGAGCTGTTTCTGATTTGAGGTGAACAGCCTCCAGACGCTGACACC 3064
QY 3001 AACATCTACAGATCTCTGCTGAGCGCTACAGGTTTCAAGCATGTGTGCTGACGTC 3060
Db 3065 AACATCTACAGATCTCTGCTGAGCGCTACAGGTTTCAAGCATGTGTGCTGACGTC 3124
QY 3061 CCATTTCAATCAAGTGTGAAGAACCCACATTTTCTGCGGCTCATCTGACACG 3120
Db 3125 CCATTTCAATCAAGTGTGAAGAACCCACATTTTCTGCGGCTCATCTGACACG 3184
QY 3121 GCCTCCCTGCTACTCATCTCTGAAGCCAGAACGCAAGGATGTGCTGGGGCCAG 3180
Db 3185 GCCTCCCTGCTACTCATCTCTGAAGCCAGAACGCAAGGATGTGCTGGGGCCAG 3244
QY 3181 GCGCGCGCGGCTCTGCGCTCGAGGGCGCTGAGTGGTGTGCCAACAGCATTCCTG 3240
Db 3245 GCGCGCGCGGCTCTGCGCTCGAGGGCGCTGAGTGGTGTGCCAACAGCATTCCTG 3304
QY 3241 CTCAAGTGAATGACACCGTGTCACTAGTGCACCTCTGGGGTCACTCAGGACAGCC 3300

Db 3305 CTCAAGCTGACTGACACCGTGTACCTACGTGCACTCCTGGGTGCACTCAGACAGCC 3364
Qy 3301 CAGACGAGCTGAGTCGGAAGCTCCCGGGAGACGCTGACTGCTGAGAGCCGAGCC 3360
Db 3365 CAGACGAGCTGAGTCGGAAGCTCCCGGGAGACGCTGACTGCTGAGAGCCGAGCC 3424
Qy 3361 AACCCGCACTGCTCAGACTTCAAGACCATCTGACTGATGAGCCACC 3411
Db 3425 AACCCGCACTGCTCAGACTTCAAGACCATCTGACTGATGAGCCACC 3475

RESULT 3
PCT-US01-15774-3
Sequence 3, Application PC/TUS0115774
GENERAL INFORMATION:
APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Brett P. Monia
APPLICANT: William Gaarde
APPLICANT: Susan M. Freiler
APPLICANT: Edward V. Wanciewicz
TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
FILE REFERENCE: ISPH-0568
CURRENT FILING DATE: PCT/US01/15774
PRIOR APPLICATION NUMBER: 2001-05-15
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 108
SEQ ID NO 3
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56) ... (3454)
PCT-US01-15774-3

Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCGATGCGCGCGCTCCCGCTGCGGAGCGCTGCTCCCTGCTGCGCAGCCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGGAGCGCTGCTCCCTGCTGCGCAGCCACTACCGC 112
Qy 61 GAGGTGCTGCGCTGCGCAGCTTCTGCTGCGCGCTGCGGAGCGCTGCGGAGCGCTG 120
Db 113 GAGGTGCTGCGCTGCGCAGCTTCTGCTGCGCGCTGCGGAGCGCTGCGGAGCGCTG 172
Qy 121 CAGCGCGGGGAGCCCGCGGCTTTCGCGCGCTGCTGCGGAGCGCTGCTGCTGCTGCG 180
Db 173 CAGCGCGGGGAGCCCGCGGCTTTCGCGCGCTGCTGCGGAGCGCTGCTGCTGCG 232
Qy 181 TGGGACGACG 240
Db 233 TGGGACGACG 292
Qy 241 CTGGTGGCGCGAGTGTGCAAGAGGCTGTGCAAGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGGTGGCGCGAGTGTGCAAGAGGCTGTGCAAGCGCGCGCGCGCGCGCGCGCGCG 352
Qy 301 GGGCTTGGCGCTGCTGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GGGCTTGGCGCTGCTGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
Qy 361 CGCAGCTACCTGCGCAACAGCGGTGACCGAGCACTGCGGAGGAGCGCGCGCGCG 420
Db 413 CGCAGCTACCTGCGCAACAGCGGTGACCGAGCACTGCGGAGGAGCGCGCGCGCG 472
Qy 421 CTGCTGCG 480
Db 473 CTGCTGCG 532
Qy 481 GTGCTGTGCTGCCAGCTGCGCTACCGAGGTGTGCGGCGCGCGCGCTGTACAGCTCG 540

Db 533 GTGCTGTGCTGCCAGCTGCGCTTACCGAGTGTGCGGCGCGCGCGCTGTACAGCTCG 592
Qy 541 GCTGCCTCAGGCG 600
Db 593 GCTGCCTCAGGCG 652
Qy 601 GAAAGGCGCTGGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAAAGGCGCTGGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 712
Qy 661 GGTGCGAGAGCG 720
Db 713 GGTGCGAGAGCG 772
Qy 721 GGTGCGAGAGCG 780
Db 773 GGTGCGAGAGCG 832
Qy 781 GGCAGGAGCGGTGACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 840
Db 833 GGCAGGAGCGGTGACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 892
Qy 841 GAAAGGCGCGCTTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 893 GAAAGGCGCGCTTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 952
Qy 901 GGCAGGAGCGGTGACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 960
Db 953 GGCAGGAGCGGTGACCGAGTACCGGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 1012
Qy 961 CCTGTCCCGCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGACA 1020
Db 1013 CCTGTCCCGCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAAGCGACA 1072
Qy 1021 CAGCTGCGCGCGCTTCTCTACTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1073 CAGCTGCGCGCGCTTCTCTACTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1132
Qy 1081 CTGCTGAGACCACTTCTCTGCTTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1140
Db 1133 CTGCTGAGACCACTTCTCTGCTTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1192
Qy 1141 CCG 1200
Db 1193 CCG 1252
Qy 1201 CAGCGCGAGTGCCTTACGCGGTGTCTCTCAAGCGCGCGCGCGCGCGCGCGCG 1260
Db 1253 CAGCGCGAGTGCCTTACGCGGTGTCTCTCAAGCGCGCGCGCGCGCGCGCGCG 1312
Qy 1261 ACCCGAGAGCGCGGTGTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320
Db 1313 ACCCGAGAGCGCGGTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1372
Qy 1321 GAGGAGGACACAGACCGCGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1380
Db 1373 GAGGAGGACACAGACCGCGGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1432
Qy 1381 CAGGTGTACGGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1440
Db 1433 CAGGTGTACGGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1492
Qy 1441 TCCAGGACACAGACCGCGGTTCCTCAAGGACACCAAGAGTTCACTCCCTGGG 1500
Db 1493 TCCAGGACACAGACCGCGGTTCCTCAAGGACACCAAGAGTTCACTCCCTGGG 1552
Qy 1501 CATGCCAGCTTCTGCTGCAAGAGCTGACGTGAAGATGAGCGTGGGAGTGGCGCT 1560
Db 1553 CATGCCAGCTTCTGCTGCAAGAGCTGACGTGAAGATGAGCGTGGGAGTGGCGCT 1612
Qy 1561 CTGCGAGAGCGCGCGGTGTGCTGTCTCCGCGCGCGCGCGCGCGCGCGCGCGCG 1620

Db 1613 CTGCGAGAGAGCCAGGGTGGCTGTGTCCGGCCGAGAGCACCGTCTGGCTGAGAG 1672
QY 1621 ATCTGGCCAAAGTTCCTGCTGCTGCTGATGATGTGTGCTGCTGCTGCTGCTGCT 1680
Db 1673 ATCTGGCCAAAGTTCCTGCTGCTGCTGATGATGTGTGCTGCTGCTGCTGCTGCT 1732
QY 1681 TTCTTTATGTACGAGAGACGTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGT 1740
Db 1733 TTCTTTATGTACGAGAGACGTTTCAAAAGAACAGGCTCTTTTCTACCGAAGAGT 1792
QY 1741 GTCTGAGCAAGTTGCAAGCAATGGAATCAGACAGCACTTGAAGAGGTGAGCTGCGG 1800
Db 1793 GTCTGAGCAAGTTGCAAGCAATGGAATCAGACAGCACTTGAAGAGGTGAGCTGCGG 1852
QY 1801 GAGCTGTGGAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCCCGCTGCTGAGCTCC 1860
Db 1853 GAGCTGTGGAAGCAGAGGTGAGGAGCATCGGGAAGCCAGGCCCGCTGCTGAGCTCC 1912
QY 1861 AGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCGGATTTGGAACATGGAATACTGTC 1920
Db 1913 AGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGGCGGATTTGGAACATGGAATACTGTC 1972
QY 1921 GTGGAGCCAGAACGTTCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAG 1980
Db 1973 GTGGAGCCAGAACGTTCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGGGTGAAG 2032
QY 1981 GCACTGTTCAGCGTGTCTCACTACGAGCGGGCGCGCGCCCGCTCTGAGGGCGCTCT 2040
Db 2033 GCACTGTTCAGCGTGTCTCACTACGAGCGGGCGCGCGCCCGCTCTGAGGGCGCTCT 2092
QY 2041 GTGCTGGGCTTGAACGATATCCACAGGGCCCTGGCGCACTTGTGCTGCTGCTGCTGCGG 2100
Db 2093 GTGCTGGGCTTGAACGATATCCACAGGGCCCTGGCGCACTTGTGCTGCTGCTGCTGCGG 2152
QY 2101 CAGGACCCCGCCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCTACGACACC 2160
Db 2153 CAGGACCCCGCCCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGCTACGACACC 2212
QY 2161 ATCCCCCAGAGCAGGCTTCAAGAGGTGATGCGCAGCATCATCAAAACCCAGAACAGCTAC 2220
Db 2213 ATCCCCCAGAGCAGGCTTCAAGAGGTGATGCGCAGCATCATCAAAACCCAGAACAGCTAC 2272
QY 2221 TGGCTGCGTGGTATGCGCTGCTGCTCAGAGGGCCCGCATGGGCACTGCGCAAGGCTTC 2280
Db 2273 TGGCTGCGTGGTATGCGCTGCTGCTCAGAGGGCCCGCATGGGCACTGCGCAAGGCTTC 2332
QY 2281 AAGAGCCAGCTCTTCACTTGAACAGACCTTCAGCCGTACATGCGAGAGTTGCTGCTCAC 2340
Db 2333 AAGAGCCAGCTCTTCACTTGAACAGACCTTCAGCCGTACATGCGAGAGTTGCTGCTCAC 2392
QY 2341 CTGAGAGAGACAGCCCGCTGAGGAGTGGCTGCTCATGAGCAGAGCTCTCCCTGAAT 2400
Db 2393 CTGAGAGAGACAGCCCGCTGAGGAGTGGCTGCTCATGAGCAGAGCTCTCCCTGAAT 2452
QY 2401 GAGGCCAGCAGTGGCTCTTGAACGCTCTTCACTGCTTCACTGCGCAACAGCCGTGCGC 2460
Db 2453 GAGGCCAGCAGTGGCTCTTGAACGCTCTTCACTGCTTCACTGCGCAACAGCCGTGCGC 2512
QY 2461 ATCAGGGGCAAGTCTTCACTGCTCAGTGCAGGAGATCCCGCAGGGCTCATCTCTCCAG 2520
Db 2513 ATCAGGGGCAAGTCTTCACTGCTCAGTGCAGGAGATCCCGCAGGGCTCATCTCTCCAG 2572
QY 2521 CTGCTCTGAGCCTGTGCTACGCGCAGATGAGAACAAAGCTGTTGCGGGGATTCGGCGG 2580
Db 2573 CTGCTCTGAGCCTGTGCTACGCGCAGATGAGAACAAAGCTGTTGCGGGGATTCGGCGG 2632
QY 2581 GACGGGCTGCTCTGCTGCTTGTGATGATTTCTTGTGTGACACCTCACTCAACCAAC 2640
Db 2633 GACGGGCTGCTCTGCTGCTTGTGATGATTTCTTGTGTGACACCTCACTCAACCAAC 2692
QY 2641 GCGAAACCTTCTCAGAGACCCCTGTGCGAGGTGCTCCCTGATATGCTGCTGCTGAGAC 2700
Db 2693 GCGAAACCTTCTCAGAGACCCCTGTGCGAGGTGCTCCCTGATATGCTGCTGCTGAGAC 2752

QY 2701 TTGCGAAGACAGTGTGAATTCCTCTGTAGAAGACAGAGCCCTGGGTGACACGGCTTTT 2760
Db 2753 TTGCGAAGACAGTGTGAATTCCTCTGTAGAAGACAGAGCCCTGGGTGACACGGCTTTT 2812
QY 2761 GTTCAATGCGCGCCACCGCTATTCCTCTGTGTGCGGCTGTGCTGATACCGGACCC 2820
Db 2813 GTTCAATGCGCGCCACCGCTATTCCTCTGTGTGCGGCTGTGCTGATACCGGACCC 2872
QY 2821 CTGAGGTGAGAGCGACTACTTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAC 2880
Db 2873 CTGAGGTGAGAGCGACTACTTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGCGCTTCAAGGCTGGAGAGAACATGCGTGCAGAACTCTTTGGGTCTTGGCG 2940
Db 2933 TTCAACCGCGCTTCAAGGCTGGAGAGAACATGCGTGCAGAACTCTTTGGGTCTTGGCG 2992
QY 2941 CTGAAGTGCACAGCCTGTTCTGATTTGCAAGTGAACAGCCTCCAGACGGGTGCAAC 3000
Db 2993 CTGAAGTGCACAGCCTGTTCTGATTTGCAAGTGAACAGCCTCCAGACGGGTGCAAC 3052
QY 3001 AACATCTACAAGATCTCTCTGCTGACAGCGGTACAGGTTTCAACGATGTGTGCTGACACTC 3060
Db 3053 AACATCTACAAGATCTCTCTGCTGACAGCGGTACAGGTTTCAACGATGTGTGCTGACACTC 3112
QY 3061 CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGTGACACAG 3120
Db 3113 CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGTGACACAG 3172
QY 3121 GCTCTCCCTGCTACTCTCATCTCTGAAAGCCAGAAACGCAAGGATGTGCTGCGGCGCCAAAG 3180
Db 3173 GCTCTCCCTGCTACTCTCATCTCTGAAAGCCAGAAACGCAAGGATGTGCTGCGGCGCCAAAG 3232
QY 3181 GGGCGCGCGCGCCCTCTGCGCTCCGAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTG 3240
Db 3233 GGGCGCGCGCGCCCTCTGCGCTCCGAGGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTG 3292
QY 3241 CTCAAGCTGACTGACACCGTGTGCACTACCTAGTGCACCTCTGGGGTCACTCAAGACAGCC 3300
Db 3293 CTCAAGCTGACTGACACCGTGTGCACTACCTAGTGCACCTCTGGGGTCACTCAAGACAGCC 3352
QY 3301 CAGACGAGCTGAGTGGAAAGCTCCCGGGGAGCAGCGTGAATGCTGAGGCGCGAGCC 3360
Db 3353 CAGACGAGCTGAGTGGAAAGCTCCCGGGGAGCAGCGTGAATGCTGAGGCGCGAGCC 3412
QY 3361 AACCCGGCACTGCTCTGAGACTTCAAGACCATCTGAGTATGCGCAACC 3411
Db 3413 AACCCGGCACTGCTCTGAGACTTCAAGACCATCTGAGTATGCGCAACC 3463

RESULT 4
PCT-US02-10421-817
; Sequence 817, Application PC/TUS0210421
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Wang, Tonglong
; APPLICANT: Wang, Siqing
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Gaiger, Alexander
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF CANCER
; FILE REFERENCE: 210121.565PC
; CURRENT APPLICATION NUMBER: PCT/US02/10421
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2959
; SEQ ID NO 817
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10421-817

Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCGC 60
Db 53 GCGATGCCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCGC 112
QY 61 GAGGTGCTGCGCTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAG 120
Db 113 GAGGTGCTGCGCTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGTGCGAG 172
QY 121 CAGCGCGGAGCGCGCGCGCTTTCGCGCGGTGCGAGCGGTGCGAGCGGTGCGAG 180
Db 173 CAGCGCGGAGCGCGCGCGCTTTCGCGCGGTGCGAGCGGTGCGAGCGGTGCGAG 232
QY 181 TGGAGCGAGCGCGCGCGCTTTCGCGCGGTGCGAGCGGTGCGAGCGGTGCGAG 240
Db 233 TGGAGCGAGCGCGCGCGCTTTCGCGCGGTGCGAGCGGTGCGAGCGGTGCGAG 292
QY 241 CTGCTGCGCGAGGTGCTGAGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGT 300
Db 293 CTGCTGCGCGAGGTGCTGAGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGT 352
QY 301 GCGCTGCGCGAGGTGCTGAGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGT 360
Db 353 GCGCTGCGCGAGGTGCTGAGAGCGGTGCGAGCGGTGCGAGCGGTGCGAGCGGT 412
QY 361 CGCAGCTACTGCGCGAGGTGCTGAGAGCGGTGCGAGCGGTGCGAGCGGTGCGAG 420
Db 413 CGCAGCTACTGCGCGAGGTGCTGAGAGCGGTGCGAGCGGTGCGAGCGGTGCGAG 472
QY 421 CTGCTGCGCGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGTGCGAG 480
Db 473 CTGCTGCGCGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGTGCGAG 532
QY 481 GTGCTGCTGCGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGTGCGAG 540
Db 533 GTGCTGCTGCGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGTGCGAG 592
QY 541 GCTGCTGCTGCGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGTGCGAG 600
Db 593 GCTGCTGCTGCGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGTGCGAG 652
QY 601 GAACGGGCTGGAACCATAGCGTCAAGGAGCGGTGCGAGCGGTGCGAGCGGTGCGAG 660
Db 653 GAACGGGCTGGAACCATAGCGTCAAGGAGCGGTGCGAGCGGTGCGAGCGGTGCGAG 712
QY 661 GGTGCGAGAGCGCGCGCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 720
Db 713 GGTGCGAGAGCGCGCGCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 772
QY 721 CGTGGCGCTGCGCGCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 780
Db 773 CGTGGCGCTGCGCGCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 832
QY 781 GGCAGGAGCGGTGGAACCATAGCGTCAAGGAGCGGTGCTGAGAGCGGTGCGAGCGGT 840
Db 833 GGCAGGAGCGGTGGAACCATAGCGTCAAGGAGCGGTGCTGAGAGCGGTGCGAGCGGT 892
QY 841 GAAGAAGCACTCTTTGAGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 900
Db 893 GAAGAAGCACTCTTTGAGAGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 952
QY 901 GGCAGGAGCAACAGCGCGCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 960
Db 953 GGCAGGAGCAACAGCGCGCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 1012
QY 961 CTTTGTCCCGGTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 1020
Db 1013 CTTTGTCCCGGTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 1072
QY 1021 CAGCTGCGCGCTGCTTCTTACTAGCTCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 1080
Db 1073 CAGCTGCGCGCTGCTTCTTACTAGCTCTGAGAGCGGTGCTGAGAGCGGTGCGAGCGGT 1132

QY 1081 CTCGTGAGAGCACTTTTCTGAGTTCAGAGCGGTGATGCAAGGAGCTCCCGCAGGTTG 1140
Db 1133 CTCGTGAGAGCACTTTTCTGAGTTCAGAGCGGTGATGCAAGGAGCTCCCGCAGGTTG 1192
QY 1141 CCGCGCTGCGCGAGCGGTACTGGAATGCGCGCGGTGTTTCTGAGCTGCTTGGAAAC 1200
Db 1193 CCGCGCTGCGCGAGCGGTACTGGAATGCGCGCGGTGTTTCTGAGCTGCTTGGAAAC 1252
QY 1201 CACGCGAGTCCCTTACGAGGTGCTCTCAAGACGACTGCGCGGTGCGAGCTGCGGT 1260
Db 1253 CACGCGAGTCCCTTACGAGGTGCTCTCAAGACGACTGCGCGGTGCGAGCTGCGGT 1312
QY 1261 ACCCGAGAGCGCGGTGCTGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAG 1320
Db 1313 ACCCGAGAGCGCGGTGCTGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCGAG 1372
QY 1321 GAGAGGACACAGACCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGT 1380
Db 1373 GAGAGGACACAGACCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGT 1432
QY 1381 CAGGTGACGCGCTTCTGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAG 1440
Db 1433 CAGGTGACGCGCTTCTGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAG 1492
QY 1441 TCCAGGACACAGACCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGT 1500
Db 1493 TCCAGGACACAGACCGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGT 1552
QY 1501 CATGCCAAGCTCTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAG 1560
Db 1553 CATGCCAAGCTCTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAG 1612
QY 1561 CTGCGCAGAGCGCGAGGCTGCTGAGAGCGGTGCTGAGAGCGGTGCTGAGAGCGGT 1620
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QY 2101 CAGGACCGCGCGCTGAGCTGACTTTGTCAAGGTGATGATGAGCGCGCGCTGAGCAAC 2160
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Db	2213	ATCCCCCAGGACAGGCTCACGGAGGTATCGCCAGCATCATCAAAACCCCAAGAACGTTAC	2272
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Db	2273	TGCGTGCCTCGGTATATGCCGTGCTCCAGAAAGGCCGCCATGGGCAAGTCCGCAAGGCTTC	2332
QY	2281	AAGAGCCACGTCCTACCTTGACAGACCTCCAGCCGTACATGCAAGTTCTGTGCTCAC	2340
Db	2333	AAGAGCCACGTCCTACCTTGACAGACCTCCAGCCGTACATGCAAGTTCTGTGCTCAC	2392
QY	2341	CTGCAGAGAACCAAGCCCGCTGAGGGATGCCGTGTCATCGACAGAGCTCCTCCCTGAAT	2400
Db	2393	CTGCAGAGAACCAAGCCCGCTGAGGGATGCCGTGTCATCGACAGAGCTCCTCCCTGAAT	2452
QY	2401	GAGGCCAGCAGTGGCCCTTTGACGTCCTTCTACGCTTCATGTGCCACCAAGCCGTGGC	2460
Db	2453	GAGGCCAGCAGTGGCCCTTTGACGTCCTTCTACGCTTCATGTGCCACCAAGCCGTGGC	2512
QY	2461	ATCAGGGGCAAGTCCCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCCACG	2520
Db	2513	ATCAGGGGCAAGTCCCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCCATCCTCCACG	2572
QY	2521	CTGCTCTGACGCTGTGCTACGGGACATGAGAACAAAGTCTTGGGGGATTCGGCGG	2580
Db	2573	CTGCTCTGACGCTGTGCTACGGGACATGAGAACAAAGTCTTGGGGGATTCGGCGG	2632
QY	2581	GACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCAC	2640
Db	2633	GACGGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACCTCACCCAC	2692
QY	2641	GCGAAACCTTCCTCAGGACCTGTCGAGGTGTCCCTGAATATGGCTGCGTGGTGAAC	2700
Db	2693	GCGAAACCTTCCTCAGGACCTGTCGAGGTGTCCCTGAATATGGCTGCGTGGTGAAC	2752
QY	2701	TTGCGGAAGACAGTGTGTAATTCCCTGTAGAAACGAGGCCCTGGGTGGCACGGCTTTT	2760
Db	2753	TTGCGGAAGACAGTGTGTAATTCCCTGTAGAAACGAGGCCCTGGGTGGCACGGCTTTT	2812
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Db	2813	GTTCAGATGCCGGCCACGGGCTATTCCCCTGGTGGGCTGCTGTGATACCCGAC	2872
QY	2821	CTGGAAGTGCAGAGCGACTATCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCAC	2880
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QY	2881	TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTGCAGAACTCTTTGGGCTTCGCG	2940
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QY	2941	CTGAAGTGTACAGGCTGTTTCTGATTGTGAGGTGAACAGCCTCCAGACGGTGTGACC	3000
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QY	3061	CCATTTTCATCAGCAAGTTTGAAGAACCACATTTTCTCGCGCTCATCTGTACACG	3120
Db	3113	CCATTTTCATCAGCAAGTTTGAAGAACCACATTTTCTCGCGCTCATCTGTACACG	3172
QY	3121	GCCTCCCTCTGCTACTTCATCCTGAAAGCCAAAGAACGAGGATGTCCGTGGGGCCAAAG	3180
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QY	3181	GGCGCGCGCGGCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGATTTCCTG	3240
Db	3233	GGCGCGCGCGGCTCTGCCCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGATTTCCTG	3292
QY	3241	CTCAAGCTGACTGCACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGGACAGCC	3300

Db 3293 CTCAAGCTGACTGCACACCGTGTCACTACTGCGCACTCCTGGGTCACCTCAGACAGCC 3352

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QY 3361 AACCCGCACTGCCCTCAGACTTCAAGACCATCCTGACTGATGACCAACC 3411

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RESULT 5
PCT-US02

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1 ; Sequence 1, Application PC/TUS0214867
2 ; GENERAL INFORMATION:
3 ; APPLICANT: Geron Corporation
4 ; APPLICANT: Jiang, Xu-Rong
5 ; APPLICANT: Chiu, Choy-pik
6 ; APPLICANT: Harley, Calvin B.
7 ; TITLE OF INVENTION: Treatment for wounds
8 ; FILE REFERENCE: 120/200
9 ; CURRENT APPLICATION NUMBER: PCT/US02/14867
10 ; CURRENT FILING DATE: 2002-05-09
11 ; PRIOR APPLICATION NUMBER: 60/289,903
12 ; PRIOR FILING DATE: 2001-05-09
13 ; NUMBER OF SEQ ID NOS: 2
14 ; SOFTWARE: PatentIn version 3.1
15 ; SEQ ID NO 1
16 ; LENGTH: 4015
17 ;
18 ; TYPE: DNA
19 ;
20 ; ORGANISM: Homo sapiens
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22 ; FEATURE:
23 ;
24 ; NAME/KEY: CDS
25 ; LOCATION: (56)..(3454)
26 ; OTHER INFORMATION:
27 ;
28 PCT-US02-14867-1

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Query Match      100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	173	CA	GC	GC	GC	GC	GA	CC	CC	GC	GC	CT	TT	CC	GC	GC	CT	GT	TG	GC	CC	AG	TG	CC	TG	GT	GT	GC	GC	GC	232		
QY	181	TG	GC	GA	CG	CA	CG	GC	CC	GC	CC	CC	CC	CC	CC	CC	CC	CT	CT	TC	CC	GC	CA	GT	GT	CC	TG	CC	TG	GA	AG	240	
Db	233	TG	GC	GA	CG	CA	CG	GC	CC	GC	CC	CC	CC	CC	CC	CC	CC	CT	CT	TC	CC	GC	CA	GT	GT	CC	TG	CC	TG	GA	AG	292	
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Db	473	CT	GC	TG	CC	GC	GC	CG	TG	GC	GC	GC	GC	GC	GC	GC	GC	CT	GT	TC	CA	CC	TG	CT	GC	CA	CG	CT	TG	CC	GC	CT	532

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QY	781	GGCAGACGCGTGAACCGAGTGAACGTGTCTGTGTGTGTCACTGCGACAGCCCGC	840
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QY	841	GAAGAAGCCACTCTTTGAGAGGTGCGCTCTGTGACAGCGCCCACTCCCAACCATCCGTG	900
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QY	901	GGCGCCAGACACCGCGGGCCCCCATCCACATCGCGGCCACACGTCCTGGGACAG	960
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QY	961	CCTTGTCCCCCGGTGTACGCCAGAACCAAGCACTTCTCTACTCTCTAGAGCGACAAAGAG	1020
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Db	1073	CAGCTGCGGCTCTCTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGCGCTCGAGG	1132
QY	1081	CTCGTGAGAGCATCTTTCTGGGTTCCAGGCCCTGATGCGCAGGACTCCCCCGAGTTG	1140
Db	1133	CTCGTGAGAGCATCTTTCTGGGTTCCAGGCCCTGATGCGCAGGACTCCCCCGAGTTG	1192
QY	1141	CCCCGCTGCCCGACTACTGGCAATGCGGCCCTGTTCTGAGCTGCTTGGGAAC	1200
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QY	1201	CACGCGCAGTGGCCCCCTACGGGGTCTCCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTC	1260
Db	1253	CACGCGCAGTGGCCCCCTACGGGGTCTCCTCAAGACGCACTGCCCCGCTGCGAGCTGCGGTC	1312
QY	1261	ACCCCAAGCAGCCGCTGTCTGTGCCCCGGGAGAAAGCCCCCAAGGCTCTGTGGCGGCCCCGAG	1320
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QY	1321	GAGGAGGACACAGACCCCCCGTGCCTGTGTGAGCTGCTCCGCCACAGACAGAGCCCTTG	1380
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QY	1381	CAGGTGTACGGCTTGTGTGCGGACCTGCTGCGCCGCGCTGTGCCCCCAAGGCTCTTGGGCGC	1440
Db	1433	CAGGTGTACGGCTTGTGTGCGGACCTGCTGCGCCGCGCTGTGCCCCCAAGGCTCTTGGGCGC	1492
QY	1441	TCCAGGACACAAAGACGCGCGCTTCTCTAGGAACACCAAGAGTTCATCTCCCTGGGGAG	1500
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Db	1793	GTCCTGAGCAAGTTGCAAGCATTTGGAATCAGACACACTTGAAGAGGCTGACGTCCGG	1852
QY	1801	GAGCTGTCCGAGACGAGGTCAAGGCAGCATCCGGGAGCCAGGCCCGCCCTGCTGACGTCC	1860
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Db 3413 AACCCGCGACTGCTCTCAGACTTCAAGACCATCTGTGACTGATGGCCACCC 3463
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RESULT 6
PCT-US02-31635-1

Sequence 1, Application PC/TUS0231635

GENERAL INFORMATION:

APPLICANT: Boston University et al.

TITLE OF INVENTION: PREADIPOCYTE CELL STRAINS AND USES THEREFORE

FILE REFERENCE: BUI-011PC

CURRENT APPLICATION NUMBER: PCT/US02/31635

PRIOR FILING DATE: 2002-10-07

PRIOR APPLICATION NUMBER: 60/327650

PRIOR FILING DATE: 2001-10-06

PRIOR APPLICATION NUMBER: 60/327651

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 4015

TYPE: DNA

ORGANISM: Homo sapiens

PCT-US02-31635-1

Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CAGCGGCGGAGCGCGGCGGCTTCCGCGCGGTGCGGAGCGGTGCGGAGCGGTG 180
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QY 601 GAACGGGCTGTGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCG 660
Db 653 GAACGGGCTGTGAACCATAGCGTACAGGAGCGCGCGCGCGCGCGCGCGCG 712
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Db 713 GGTGCGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 772
QY 721 CGTGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 773 CGTGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
QY 781 GGCAGGAGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 833 GGCAGGAGCGCGTGTGAGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
QY 841 GAAGAAGCGACCTTTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 893 GAAGAAGCGACCTTTTGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 952
QY 901 GCGCGCGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 953 GCGCGCGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1012
QY 961 CCTGTGCGCGCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCAGGCGAGAGAG 1020
Db 1013 CCTGTGCGCGCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCAGGCGAGAGAG 1072
QY 1021 CAGCTGCGGCGCTCTTCTACTCAGCTCTGTGAGGCCAGCGCTGAGCGGTGAGAG 1080
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Db	1073	CAGCTGCGCCCTCCTTCTACTCAGCTCTCTGAGGCCAGCTGACTGCGCTCGAGG	1132
QY	1081	CTCGTGAGAACCATCTTCTGAGTTCAGGCCCTGATATGCCAGGACTCCCGCAGTTG	1140
Db	1133	CTCGTGAGAACCATCTTCTGAGTTCAGGCCCTGATATGCCAGGACTCCCGCAGTTG	1192
QY	1141	CCCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGCTGCTGGAAAC	1200
Db	1193	CCCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGCTGCTGGAAAC	1252
QY	1201	CACGCGAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGTTC	1260
Db	1253	CACGCGAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGTTC	1312
QY	1261	ACCCACGACGCCGTGTCTGTGCCCCGGAGAAAGCCCCAGGGCTCTGTGCGGCCCCCGAG	1320
Db	1313	ACCCACGACGCCGTGTCTGTGCCCCGGAGAAAGCCCCAGGGCTCTGTGCGGCCCCCGAG	1372
QY	1321	GAGGAGGACACAGACCCCGGTGCGCTGTGTCAGCTGTCTCCGACGACAGCAGCCCTGG	1380
Db	1373	GAGGAGGACACAGACCCCGGTGCGCTGTGTCAGCTGTCTCCGACGACAGCAGCCCTGG	1432
QY	1381	CAGGTGTACGGCTTCGTGCGGGCTTCCTGCGCCGGGTGTGCCCCCAGGCTCTGGGGC	1440
Db	1433	CAGGTGTACGGCTTCGTGCGGGCTTCCTGCGCCGGGTGTGCCCCCAGGCTCTGGGGC	1492
QY	1441	TCCAGGCAACAACGAACGCCGCTTCTCAGGAACACCAAGATTCTCTCCCTGGGGAAG	1500
Db	1493	TCCAGGCAACAACGAACGCCGCTTCTCAGGAACACCAAGATTCTCTCCCTGGGGAAG	1552
QY	1501	CATGCCAAGCTCTGCTGACGAGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGTTGG	1560
Db	1553	CATGCCAAGCTCTGCTGACGAGAGCTGACGTGAAGATGAGCGTGCAGGACTGCGTTGG	1612
QY	1561	CTGCGCAGGAGCCCAAGGGTTGGCTGTTCGCGCCGACAGACACCGTCTGCTGAGAG	1620
Db	1613	CTGCGCAGGAGCCCAAGGGTTGGCTGTTCGCGCCGACAGACACCGTCTGCTGAGAG	1672
QY	1621	ATCCTGGCCAAGTTCCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGTCAAGTCT	1680
Db	1673	ATCCTGGCCAAGTTCCTGCACTGGCTGATGATGTGTACGTGCTGAGCTGTCAAGTCT	1732
QY	1681	TTCTTTTATGTACGAGAACCAACGTTTCAAAAGAACAGGCTTTTCTACCGAAGAGT	1740
Db	1733	TTCTTTTATGTACGAGAACCAACGTTTCAAAAGAACAGGCTTTTCTACCGAAGAGT	1792
QY	1741	GTCTTGAGCAAGTTGCAAAACATTGGAATCAGACAGCACTTGAAGAGGTCAGTCCGG	1800
Db	1793	GTCTTGAGCAAGTTGCAAAACATTGGAATCAGACAGCACTTGAAGAGGTCAGTCCGG	1852
QY	1801	GAGCTGTCCGAAGCAGAGGTCAAGCAGCATCCGGAAAGCCAGCCCGCCCTGCTACGTCC	1860
Db	1853	GAGCTGTCCGAAGCAGAGGTCAAGCAGCATCCGGAAAGCCAGCCCGCCCTGCTACGTCC	1912
QY	1861	AGACTCCGCTTCAATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGCACTACGTC	1920
Db	1913	AGACTCCGCTTCAATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGCACTACGTC	1972
QY	1921	GTGGGAGCCAGAACGTTTCCGACAGAAAAAGAGGGCCGACGCTCTCACTTCAGAGGTGAAG	1980
Db	1973	GTGGGAGCCAGAACGTTTCCGACAGAAAAAGAGGGCCGACGCTCTCACTTCAGAGGTGAAG	2032
QY	1981	GCACTGTTCAGCGGTGCTCAACTACGAGCGGGCGCGGCCCTCCTCTGGGCGGCTCT	2040
Db	2033	GCACTGTTCAGCGGTGCTCAACTACGAGCGGGCGCGGCCCTCCTCTGGGCGGCTCT	2092
QY	2041	GTGCTGGGCTTGAGCATATTCACAGGGCTTGCGCACTTCGTGCTGCGTGTGCGGGCC	2100
Db	2093	GTGCTGGGCTTGAGCATATTCACAGGGCTTGCGCACTTCGTGCTGCGTGTGCGGGCC	2152
QY	2101	CAGGACCCGCGCCTGAGCTGTACTTTGTCAAGGTGATGTACGGGCGCCTACGACACC	2160

Db	2153	CAGGACCCGCCGCTGAGCTGTACTTTGTTCAGGTGGATGTGACGGGGCGGTACGACACC	2212
QY	2161	ATCCCCCAGGACAGGCTCACGGAGGTGATGCGCAGCATCATCAAACCCAGAAACGTTAC	2220
Db	2213	ATCCCCCAGGACAGGCTCACGGAGGTGATGCGCAGCATCATCAAACCCAGAAACGTTAC	2272
QY	2221	TGCGTGCGTCGGTATGCGGTGGTCCAGAAAGGCCCCATGGGCAAGTCCGCAAGGCTTC	2280
Db	2273	TGCGTGCGTCGGTATGCGGTGGTCCAGAAAGGCCCCATGGGCAAGTCCGCAAGGCTTC	2332
QY	2281	AAGAGCCACGTCCTACCTTGAAGACCTCCAGCCGTACATGCGACAGTTGTTGCTCAC	2340
Db	2333	AAGAGCCACGTCCTACCTTGAAGACCTCCAGCCGTACATGCGACAGTTGTTGCTCAC	2392
QY	2341	CTGAGGAGAGACAGCCCCGCTGAGGGATGCGGTGTCATGAGCAGAGCTCCTCCCTGAAT	2400
Db	2393	CTGAGGAGAGACAGCCCCGCTGAGGGATGCGGTGTCATGAGCAGAGCTCCTCCCTGAAT	2452
QY	2401	GAGGCCAGCAGTGGCTCTTCGACGTCCTTCAAGCTTCATATGTGCCACCAAGCGGTGCGC	2460
Db	2453	GAGGCCAGCAGTGGCTCTTCGACGTCCTTCAAGCTTCATATGTGCCACCAAGCGGTGCGC	2512
QY	2461	ATCAGGGGCAAGTCCCTACGTCCAGTGCCAGGGGATCCCGAGGGCTCCATCCTCCACG	2520
Db	2513	ATCAGGGGCAAGTCCCTACGTCCAGTGCCAGGGGATCCCGAGGGCTCCATCCTCCACG	2572
QY	2521	CTGCTCTGACGCTGTGTCTACGGCGACATGGAACAAGCTGTTTGGGGGAAATTCGGCGG	2580
Db	2573	CTGCTCTGACGCTGTGTCTACGGCGACATGGAACAAGCTGTTTGGGGGAAATTCGGCGG	2632
QY	2581	GACGGGCTGCTCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACTCAACCCAC	2640
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QY	2641	GCGAAAACTTCTCTCAGGAACCCCTGTGCCAGGTGTCCCTGAGTATGGCTGCGTGGTGAAC	2700
Db	2693	GCGAAAACTTCTCTCAGGAACCCCTGTGCCAGGTGTCCCTGAGTATGGCTGCGTGGTGAAC	2752
QY	2701	TTGCGGAAGACAGTGGTGAACCTTCCCTGTGAAGACGAGGCCCTGGGTGGCAAGCTTTT	2760
Db	2753	TTGCGGAAGACAGTGGTGAACCTTCCCTGTGAAGACGAGGCCCTGGGTGGCAAGCTTTT	2812
QY	2761	GTTCAGATGCCGGCCCAAGGCTATTCCCTGTGGTGGGCTGTGCTGGATACCGGACC	2820
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QY	2821	CTGGAGGTGACAGGCACTACTCCAGCTATGCGCGAACCTCCATCAGAGCCAGTCTCAC	2880
Db	2873	CTGGAGGTGACAGGCACTACTCCAGCTATGCGCGAACCTCCATCAGAGCCAGTCTCAC	2932
QY	2881	TTCAACCGCGCTTCAAGGCTGGAGGAACATGCGTGCAGAACTCTTTGGGGTCTTGGG	2940
Db	2933	TTCAACCGCGCTTCAAGGCTGGAGGAACATGCGTGCAGAACTCTTTGGGGTCTTGGG	2992
QY	2941	CTGAAGTGTACAGCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGTTGCAAC	3000
Db	2993	CTGAAGTGTACAGCTGTTTCTGATTTGCAAGTGAACAGCCTCCAGACGTTGCAAC	3052
QY	3001	AACATCTACAAGATCCTCTGCTGACGGCTACAGTTTACGCATGTGTGTGACGCTC	3060
Db	3053	AACATCTACAAGATCCTCTGCTGACGGCTACAGTTTACGCATGTGTGTGACGCTC	3112
QY	3061	CCATTTTATCAGCAAGTTTGAAGAACCACAATTTTCTGCGGTATCTTGACACG	3120
Db	3113	CCATTTTATCAGCAAGTTTGAAGAACCACAATTTTCTGCGGTATCTTGACACG	3172
QY	3121	GCCTCCCTCTGTAATCCATCCTGAAGCCAAAGACGAGGATGTGCTGGGGCCAAAG	3180
Db	3173	GCCTCCCTCTGTAATCCATCCTGAAGCCAAAGACGAGGATGTGCTGGGGCCAAAG	3232
QY	3181	GGGCGCGCGGCTCTGCCCTCCGAGCGGTGACGTGGCTGTGCCACCAAGCATTCCTG	3240
Db	3233	GGGCGCGCGGCTCTGCCCTCCGAGCGGTGACGTGGCTGTGCCACCAAGCATTCCTG	3292

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QY 1681 TTCTTTTATGTACAGGAGAGACCAAGCTTTTCAAAAGAACAGAGCTTTTCTACCGGAAGAGT 1740
Db 1733 TTCTTTTATGTACAGGAGAGACCAAGCTTTTCAAAAGAACAGAGCTTTTCTACCGGAAGAGT 1792
QY 1741 GTCTGAGCAGAGTTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGAGCTGCGG 1800
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QY 1801 GAGCTGTCCGAGAGAGAGTCAAGGAGAGATCGGGAAGCCAGGCGCCCTGCTGAGCTGCTC 1860
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QY 2221 TCGCTGCTGCTGATATGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 2280
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Db 2333 AAGAGCAGCTCTCTACCTTGAAGAGCTCCAGCCGATACATGAGCAGAGTTCGTGCTCAC 2392
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QY 2521 CTGCTCTGAGCCTGTGTACGCGGAGCATGAGAGACAGAGTGTTCGGGGGATTCGCGG 2580
Db 2573 CTGCTCTGAGCCTGTGTACGCGGAGCATGAGAGACAGAGTGTTCGGGGGATTCGCGG 2632
QY 2581 GACGGGCTGCTCTGCGTGTGTGATGATTTCTGTGTGTGATGATGATGATGATGATGAT 2640
Db 2633 GACGGGCTGCTCTGCGTGTGTGATGATTTCTGTGTGTGATGATGATGATGATGATGAT 2692
QY 2641 GCGAAAACTTCTCAGAGACCTGTCCGAGGTGTCCCTGAGTATGGTGTGAGTGAAC 2700
Db 2693 GCGAAAACTTCTCAGAGACCTGTCCGAGGTGTCCCTGAGTATGGTGTGAGTGAAC 2752
QY 2701 TTGCGGAGAGCAGTGTGATGATTTCTCTGTAGAGAGCAGAGGCTTGGGTGAGAGCTTTT 2760
Db 2753 TTGCGGAGAGCAGTGTGATGATTTCTCTGTAGAGAGCAGAGGCTTGGGTGAGAGCTTTT 2812

QY 2761 GTTCAGATGCGGCGCCACAGGCGCTATTTCCCTGTGTGCGGCGCTGTGTGATATCCCGGACC 2820
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QY 2821 CTGAGGTGAGAGGAGTACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACC 2880
Db 2873 CTGAGGTGAGAGGAGTACTACTCCAGCTATGCCCCGAGCCTCCATCAGAGCCAGTCTCACC 2932
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RESULT 8

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; Sequence 1, Application PC/TUS0319844

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

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; TITLE OF INVENTION: Cancer Vaccines Containing Xenogeneic Epitopes of Telomerase Re

; TITLE OF INVENTION: Transcriptase

; FILE REFERENCE: 086/200

; CURRENT APPLICATION NUMBER: PCT/US03/19844

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; PRIOR APPLICATION NUMBER: 60/393,295

; PRIOR FILING DATE: 2002-06-27

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patent version 3.1

; SEQ ID NO 1

; LENGTH: 4015

; TYPE: DNA

; ORGANISM: Homo sapiens

; PCT-US03-19844-1

Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1013 CCTGTGCGCGCGGTGTAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1072
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QY 1621 ATCCTGCGCAAGTCTCTGCACTGCTGATGATGATGATGATGATGATGATGATGAT 1680
Db 1673 ATCCTGCGCAAGTCTCTGCACTGCTGATGATGATGATGATGATGATGATGATGAT 1732
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Db 1733 TTCTTTTATGTACGAGAGACCAAGTTCAGAGAACAGAGCTCTTTTCTACCGGAGAGT 1792
QY 1741 GTCTGAGCAAGTGTGCAAGCATTTGAAATCAGACGACTTGAAGAGGCTGAGCTGCG 1800
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QY 1801 GAGCTGTGCGAGAGCAGGTCAAGGCGAGCTGCGGAGCGAGCGCGCGCGCTGAGCTG 1860
Db 1853 GAGCTGTGCGAGAGCAGGTCAAGGCGAGCTGCGGAGCGAGCGCGCGCGCGCTGAGCTG 1912
QY 1861 AGACTCCGCTTCACTCCCAAGCTGACGCGCGCTGCGCGCGCTGCGCGCGCTGAGCTG 1920
Db 1913 AGACTCCGCTTCACTCCCAAGCTGACGCGCGCTGCGCGCGCTGCGCGCGCTGAGCTG 1972
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Db 2093 GTGCTGCGCGCTGAGCAGATATCCAGAGGCGCTGCGCAGCCTTGTGCTGCGGCGC 2152
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QY 2161 ATCCCGCAGGACAGGCTCAGCGAGGTGATGCGCAGCATGATCAAAACCGAGAACAGTAC 2220

Db	2213	ATCCCCAGGACAGGCTCACGGAGGTGATCGCCAGCATCATCAACCCAGAACACGTAC	2272
QY	2221	TGCGTGCGTCGGTATGCGGTGTGTCAGAAAGCCGCCATGGGCACTCCGCAAGCCTTC	2280
Db	2273	TGCGTGCGTCGGTATGCGGTGTGTCAGAAAGCCGCCATGGGCACTCCGCAAGCCTTC	2332
QY	2281	AAGAGCCAAGTCTCTACTTGAAGACCTCCAGCCGTACATGGACAGTTGCTGCTCAC	2340
Db	2333	AAGAGCCAAGTCTCTACTTGAAGACCTCCAGCCGTACATGGACAGTTGCTGCTCAC	2392
QY	2341	CTGACGAGAGACCAAGCCCGCTGAGGATGCCGTGTCATGAGACAGAGCTCCTCCCTGAAT	2400
Db	2393	CTGACGAGAGACCAAGCCCGCTGAGGATGCCGTGTCATGAGACAGAGCTCCTCCCTGAAT	2452
QY	2401	GAGGCCAGCAGTGGCCTCTTGCACGTCTTCTACGCTTCAATGTGCCACCAAGCCGTGCGC	2460
Db	2453	GAGGCCAGCAGTGGCCTCTTGCACGTCTTCTACGCTTCAATGTGCCACCAAGCCGTGCGC	2512
QY	2461	ATCAGGGGCAAGTCTCTACGTTCAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCTCCAG	2520
Db	2513	ATCAGGGGCAAGTCTCTACGTTCAGTGCACAGGGGATCCCGCAGGGCTCCATCCTCTCCAG	2572
QY	2521	CTGCTCTGCAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGCGGGGATTGCGCGG	2580
Db	2573	CTGCTCTGCAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTGCGGGGATTGCGCGG	2632
QY	2581	GACGGGCTGCTCCTGCGTTTGATGATGATTTCTTGTGTGAACAACCTCAACCTCACCCAC	2640
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QY	2641	GCGAAAAACCTTCTCAGAACCCCTGTCCGAGGTGTCCTGAGTATGGCTGCGTGTGAAC	2700
Db	2693	GCGAAAAACCTTCTCAGAACCCCTGTCCGAGGTGTCCTGAGTATGGCTGCGTGTGAAC	2752
QY	2701	TTCGGAAGACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGCAACGGCTTTT	2760
Db	2753	TTCGGAAGACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGCAACGGCTTTT	2812
QY	2761	GTTCAGATGCCGCCACAGGCCCTATTTCCCTGTGTGCGGCTGTGTCGATACCCGGAAC	2820
Db	2813	GTTCAGATGCCGCCACAGGCCCTATTTCCCTGTGTGCGGCTGTGTCGATACCCGGAAC	2872
QY	2821	CTGAGGTGCAGAGCGACTACCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCAC	2880
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QY	2881	TTCAACCCGCGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGCTTTGGCGG	2940
Db	2933	TTCAACCCGCGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGCTTTGGCGG	2992
QY	2941	CTGAAGTGTCAAGCCCTGTCTTGATTTGCAGGTGAACAGCCCTCCAGACGGTGTGCAAC	3000
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QY	3001	AACATCTACAAGATCTCTCTGCTGCAGGCGTACAGGTTTCAAGCATGTGTGTGCAAGCTC	3060
Db	3053	AACATCTACAAGATCTCTCTGCTGCAGGCGTACAGGTTTCAAGCATGTGTGTGCAAGCTC	3112
QY	3061	CCATTTCATCAGCAAGTTTGAAGAACCACCATTTTCTCGCGTCATCTCTGACAG	3120
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QY	3121	GCCTCCCTGTGCTACTCTCTGCTGAAGAACCACCAAGAACGAGGATGTGCTGGGGCCAAG	3180
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RESULT 9
PCT-US99-06898-1

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; Sequence 1, Application PC/TUS99068988
; GENERAL INFORMATION:
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; APPLICANT: Gaeta, Federico C.A.
; APPLICANT: Geron Corporation

1 TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
2
3 ;
4 TITLE OF INVENTION: Response to a Telomerase Antigen
5 ;

FILE REFERENCE: 015389-003500PC
CURRENT APPLICATION NUMBER: PCT/US99/06898

/ CURRENT FILING DATE: 1999-03-30
 / CURRENT APPLICATION NUMBER: USC 06/011 313
 / CURRENT APPLICATION NUMBER: USC 06/011 313

EARLIER APPLICATION NUMBER: US 08/911,312
EARLIER FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US 08/013,051

;; EARLIER APPLICATION NUMBER: US 08/912,951
; EARLIER FILING DATE: 1997-08-14

! EARLIER APPLICATION NUMBER: US 08/915,503
! EARLIER FILING DATE: 1997-08-14

; EARLIER APPLICATION NUMBER: WO PCT/US97/17618
 ; EARLIER FILING DATE: 1997-10-01

; EARLIER APPLICATION NUMBER: WO PCT/US/178
; EARLIER FILING DATE: 1997-10-01

; EARLIER APPLICATION NUMBER: US 08/974,549
; EARLIER FILING DATE: 1997-11-19

EARLIER APPLICATION NUMBER: US 08/974,584
EARLIER FILING DATE: 1997-11-19

NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentn Ver 2.0

COLLTYPE: 1
SEQ ID NO 1
LENGTH: 4015

LENS: 4013
TYPE: DNA
ORGANISM: Homo sapiens

ORGANISM: HOMO SAPIENS
FEATURE:
NAME/ID: AND

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; NAME/KEY: CDS
; LOCATION: (56) .. (3454)
;

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OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
PCT-US99-06898-1

Query Match 100.0%; Score 3411; DB 1; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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5.3 GCGATGCGGCGGCTCCCCGCTGCCGAGCGCGGCGGCTTCCCTGCTGCGCAGCCACTACCGG 112

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[illegible][illegible]

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Db 173 CAGCGCGGGGA.CCCGGCGGCTTCCGCGCGCTGGTGGCCAGTGCCCTGGTGTGCGTGGCC 232

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27 301 GGCTTCGCGTGTGACCGGGCCCGGGGGCCCCCGAGGCTTACACACAGCGG 360

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QY	421	CTGCTGCGCGCGGTGGGGCGACGACGTGCTGTTCACTGCTGCGACCGTGCCTCTTT	480
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QY	481	GTGCTGTGGGCTCCAGCTGCGCTACCAAGTGTGCGGGCGCGCTGTACCACTCGGC	540
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QY	541	GCTGCCACTCAGGCCCCCGCCCCCGCCACACGCTAGTGGAACCCGAAAGCGCTTGGGATGC	600
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QY	601	GAACGGGCTTGAAACCATAGCGTCAAGGAGGCGCGGGTCCCCCTGGGCTTGCAGCCCCG	660
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QY	721	CGTGCGCTGCCCCCTGAGCCCGAGCGGACGCCCCGTTGGCAGGGGCTTGGGCCCAACCG	780
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QY	781	GGCAGACGCGGTGACCCGAGTGAACCGTGTCTTCTGTGTGTGTCACTGCGACGACCGCC	840
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QY	841	GAAGAAGCCACTCTTTGAGAGGTGCGCTCTCTGCGACGCGCACTCCCAACCATCCGTG	900
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QY	901	GGCGCGCAGCACACGCGGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACAG	960
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QY	961	CCTTGTCCCCCGGTGTACGCGCGAGAACCAAGCACTTCTCTACTCTCTCAGCGGACAGAG	1020
Db	1013	CCTTGTCCCCCGGTGTACGCGCGAGAACCAAGCACTTCTCTACTCTCTCAGCGGACAGAG	1072
QY	1021	CAGCTGCGGGCCCTCCTTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGGAG	1080
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QY	1081	CTCGTGAGAGCACTCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGACAGTTG	1140
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QY	1141	CCCCGCTGCCCCCAGCGCTACTGGCAAAATGCGGCCCTGTCTTCTGAGCTGCTTGGGAAC	1200
Db	1193	CCCCGCTGCCCCCAGCGCTACTGGCAAAATGCGGCCCTGTCTTCTGAGCTGCTTGGGAAC	1252
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QY	1261	ACCCCAAGCAGCCGGGTGTCTGTGCCCCGGAGAAAGCCCCAAGGCTCTGTGCGGCCCCCGAG	1320
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QY	1321	GAGGAGGACACAGACCCCCCGTGCCTGTGTGAGCTGCTCCGACAGCAGACAGCCCTGG	1380
Db	1373	GAGGAGGACACAGACCCCCCGTGCCTGTGTGAGCTGCTCCGACAGCAGACAGCCCTGG	1432
QY	1381	CAGGTGTACGGCTTGTGTGCGGGCTGCTGCGCGGCTGTGCCCCCAGGCTTGTGGGGC	1440

Db	1433	CAGGTGTACGGCTTTCGTGCGGGCCCTGCCTGC	CGCGCTGTGCCCCCAGGCTCTGGGCG	1492
QY	1441	TCGAGGACAACGAACGCCGCTTCTCAGAAACACCA	GAAGTTCACTCCCTGGGGAAG	1500
Db	1493	TTCCAGGCACAACGAACGCCGCTTCTCAGAAACAC	CAAGAAGTTCACTCCCTGGGGAAG	1552
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Db 2693 GCGAAACCTTCTCAGGACCCCTGTCCGAGGTGTCCCTGAGTATGCTGCTGTGAAC 2752
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RESULT 10

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PCT-US99-07097-1
; Sequence 1, Application PC/TUS9907097
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 015389-003310PC
; CURRENT APPLICATION NUMBER: PCT/US99/07097
; CURRENT FILING DATE: 1999-03-31
; EARLIER APPLICATION NUMBER: US 09/052,864
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; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: US 09/128,354
; EARLIER FILING DATE: 1998-08-03
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; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
PCT-US99-07097-1
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Query Match 100.0%; Score 3411; DB 1; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 241 CTGCTGCGCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGCTGCGCGAGTGTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GCGTTGCGCGCTGTGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
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QY 721 CGTGCGGCTCCCGCTGAGCGCGGAGCGAGCGCGCGTGGGAGAGGGTCTGGGCGCACCC 780
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Db 2573 CTGCTCTGACGCTGTGCTACGCGGACGACATGAGAAACAAGCTGTTTGGCGGATTCGGCGG 2632
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RESULT 11

PCT-US99-07160-1
Sequence 1, Application PC/TUS9907160

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APPLICANT: Geron Corporation

TITLE OF INVENTION: Antisense Compositions for Detecting and Inhibiting

TITLE OF INVENTION: Telomerase Reverse Transcriptase

FILE REFERENCE: 015389-003610PC

CURRENT APPLICATION NUMBER: PCT/US99/07160

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NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 4015
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (56)..(3454)
OTHER INFORMATION: human telomerase reverse transcriptase (hTRT)
PCT-US99-07160-1

Query Match 100.0%; Score 3411; DB 1; Length 4015;
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Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2761 GTTCAAGTCCGCGCCACGCGCTATTTCCCTGTGCGCGCTGCTGATACCCGAGAC 2820
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Db	713	GGTGCAGAGGAGGCGCGGGGCGAGTCCAGCCGAAGTCTGCCGTGCCCAAGAGGCCCAAG	772
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Db	893	GAAGAAGCCACCTCTTTGAGAGGTGCGCTCTCTGCGACGCGCCCACTCCCAACCATCCGT	952
QY	901	GGCGGCCAGCACCAACGCGGGCCCCCATCCACATCGCGGCCCAACAGTCCCTGGGACACG	960
Db	953	GGCGGCCAGCACCAACGCGGGCCCCCATCCACATCGCGGCCCAACAGTCCCTGGGACACG	1012
QY	961	CCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGCAAGAG	1020
Db	1013	CCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCTCTACTCTCTCAGGCGCAAGAG	1072
QY	1021	CAGCTGCGGCCCTCTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGG	1080
Db	1073	CAGCTGCGGCCCTCTCTCTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGCTCGAGG	1132
QY	1081	CTCGTGAGACCATCTTTCTGAGTTCAGAGCCCTGATGCCAGGACTCCCCGACAGTTG	1140
Db	1133	CTCGTGAGACCATCTTTCTGAGTTCAGAGCCCTGATGCCAGGACTCCCCGACAGTTG	1192
QY	1141	CCCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTGAGCTGCTTGGAAAC	1200
Db	1193	CCCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTCTTGAGCTGCTTGGAAAC	1252
QY	1201	CACGCGAGTGGCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGTGGGTTC	1260
Db	1253	CACGCGAGTGGCCCTACGGGGTGTCTCTCAAGACGCACTGCCCGCTGCGAGTGGGTTC	1312
QY	1261	ACCCAGCAGCGGTTGTGTGCCCCGGAGAGCCCCAGGGCTCTGTGCGGCCCCCGAG	1320
Db	1313	ACCCAGCAGCGGTTGTGTGCCCCGGAGAGCCCCAGGGCTCTGTGCGGCCCCCGAG	1372
QY	1321	GAGGAGGACACAGACCCCGGTGCGCTGTGACGTGTCGCCAGACACAGACGCCCCTG	1380
Db	1373	GAGGAGGACACAGACCCCGGTGCGCTGTGACGTGTCGCCAGACACAGACGCCCCTG	1432
QY	1381	CAGGTGTACGCTTGTGTGCGGGCTGCTGCGCGCGGTGTGCCCCCAGGCTCTTGGGGC	1440
Db	1433	CAGGTGTACGCTTGTGTGCGGGCTGCTGCGCGCGGTGTGCCCCCAGGCTCTTGGGGC	1492
QY	1441	TCCAGGACACACGACCGCGCTTCTCAGGAACACCAAGAATTATCTCCTTGGGGAAG	1500
Db	1493	TCCAGGACACACGACCGCGCTTCTCAGGAACACCAAGAATTATCTCCTTGGGGAAG	1552
QY	1501	CATGCCAAGCTCTGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGCGGACTTGGCTTGG	1560
Db	1553	CATGCCAAGCTCTGCTGCAAGAGCTGACGTGGAAGATGAGCGTGGCGGACTTGGCTTGG	1612
QY	1561	CTGCCAGAGGCCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGAG	1620
Db	1613	CTGCCAGAGGCCCAGGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCGTGAGAG	1672

QY	1621	ATCCTGGCCCAAGTTCTCTGCACTGGGCTGATGAGTGTGTACGTGCTGCAAGCTGCTCAGGCTCT	1680
Db	1673	ATCCTGGCCCAAGTTCTCTGCACTGGGCTGATGAGTGTGTACGTGCTGCAAGCTGCTCAGGCTCT	1732
QY	1681	TTCTTTTATGTACGGAGAACCAACGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGT	1740
Db	1733	TTCTTTTATGTACGGAGAACCAACGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGT	1792
QY	1741	GTCTGGAGCAAGTGTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTTGACGTGCGG	1800
Db	1793	GTCTGGAGCAAGTGTGCAAAAGCATTTGGAATCAGACAGCACTTGAAGAGGTTGACGTGCGG	1852
QY	1801	GAGCTGTGGAGAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCGCTGTGACGTCC	1860
Db	1853	GAGCTGTGGAGAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCCGCTGTGACGTCC	1912
QY	1861	AGACTCCGCTTCAATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGAACTACGTC	1920
Db	1913	AGACTCCGCTTCAATCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGAACTACGTC	1972
QY	1921	GTGGAGCCAGAACGTTCCGACAGAAAAAGAGGCCAGCGTCTCACCTCGAAGGTTGAAG	1980
Db	1973	GTGGAGCCAGAACGTTCCGACAGAAAAAGAGGCCAGCGTCTCACCTCGAAGGTTGAAG	2032
QY	1981	GCACTGTTCAAGCTGTCTCAACTACGAGCGGCGCGGCCGCCGCTCTCGTGGCGCCTCT	2040
Db	2033	GCACTGTTCAAGCTGTCTCAACTACGAGCGGCGCGGCCGCCGCTCTCGTGGCGCCTCT	2092
QY	2041	GTGCTGGGCTGAGCATATCCACAGGGCTGTGGCGCACCTTGTGTGCTGCGTGTGGGGCC	2100
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QY	2101	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGGTACGACACC	2160
Db	2153	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGTGTGATGTGACGGGCGGTACGACACC	2212
QY	2161	ATCCCCCAGAGACAGGCTCACGAGGTCATCGCCAGCATCATCAAACCCCAAGAACAGTAC	2220
Db	2213	ATCCCCCAGAGACAGGCTCACGAGGTCATCGCCAGCATCATCAAACCCCAAGAACAGTAC	2272
QY	2221	TGCGTGCCTCGGTATGCCGTGTGTCCAGAGGCCGCCCATGAGGCAAGTCCGCAAGGCTTC	2280
Db	2273	TGCGTGCCTCGGTATGCCGTGTGTCCAGAGGCCGCCCATGAGGCAAGTCCGCAAGGCTTC	2332
QY	2281	AAGAGCCACGTTCTTACTTGTACAGACCTTCCAGCCGTACATGCGACAGTTTGTGGCTCAC	2340
Db	2333	AAGAGCCACGTTCTTACTTGTACAGACCTTCCAGCCGTACATGCGACAGTTTGTGGCTCAC	2392
QY	2341	CTGCAGAGAGACCAAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTTCTCCCTGAAT	2400
Db	2393	CTGCAGAGAGACCAAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTTCTCCCTGAAT	2452
QY	2401	GAGGCCAGCAGTGGCCTCTTCGACGTCCTTCTTCTACGCTTCATGTGCCAACAGCCGTGCGC	2460
Db	2453	GAGGCCAGCAGTGGCCTCTTCGACGTCCTTCTTCTACGCTTCATGTGCCAACAGCCGTGCGC	2512
QY	2461	ATCAGGGGGCAAGTCTTACGTCCAGTCCAGGGGAATCCCGCAGGGGCTTCATCTCTCCACG	2520
Db	2513	ATCAGGGGGCAAGTCTTACGTCCAGTCCAGGGGAATCCCGCAGGGGCTTCATCTCTCCACG	2572
QY	2521	CTGCTCTGCAGCGCTGTGCTACGGCGCATGGAGAACAAAGCTGTTTGGGGGGATTGGGCGG	2580
Db	2573	CTGCTCTGCAGCGCTGTGCTACGGCGCATGGAGAACAAAGCTGTTTGGGGGGATTGGGCGG	2632
QY	2581	GACGGGCTGTCTCTGCGTTGGTGTGATTTTCTTGTGTGTGACACCTCAACCTCACCCAC	2640
Db	2633	GACGGGCTGTCTCTGCGTTGGTGTGATTTTCTTGTGTGTGACACCTCAACCTCACCCAC	2692
QY	2641	GCGAAAACTTCTCTCAGGACCTTGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAAC	2700
Db	2693	GCGAAAACTTCTCTCAGGACCTTGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAAC	2752

QY 2701 TTGCGGAGACAGTGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTT 2760
Db 2753 TTGCGGAGACAGTGTGAACCTTCCCTGTAGAGACGAGGCCCTGGGTGGCAGCGCTTTT 2812
QY 2761 GTTCAGATGCGGCGCCACGCGCTTATTTCCCTGTGCGGCGCTGTGTGATACCGCGGACC 2820
Db 2813 GTTCAGATGCGGCGCCACGCGCTTATTTCCCTGTGCGGCGCTGTGTGATACCGCGGACC 2872
QY 2821 CTGAGAGTGACAGAGCGACTACTCCAGCTATGCCGGAACCTCCATCAGAGCGAGTCTCACC 2880
Db 2873 CTGAGAGTGACAGAGCGACTACTCCAGCTATGCCGGAACCTCCATCAGAGCGAGTCTCACC 2932
QY 2881 TTCAACCGCGGCTTCAAGCGCTGGAGAGAACATGCTGCAAACTCTTTGGGGTCTTGCGG 2940
Db 2933 TTCAACCGCGGCTTCAAGCGCTGGAGAGAACATGCTGCAAACTCTTTGGGGTCTTGCGG 2992
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Db 3173 GCCTCCCTCTGCTACTCTCATCTGAAAGCCAGAACGACGAGATGTGCTGGGGCCAAAG 3232
QY 3181 GGGCGCGCGCGCTCTGCGCTCCGAGCGCGTGCAGTGGCTGTGCCAACCAAGCATTTCTG 3240
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Db 3353 CAGACGAGCTGAGTGGGAAGCTCCCGGGGAGACGCTGACTGCCCTGGAGGCGCGCAGCC 3412
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RESULT 13
US-09-052-864-1
Sequence 1, Application US/09052864

GENERAL INFORMATION:
APPLICANT: Morin, Gregg B.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
TITLE OF INVENTION: Variants
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,864
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CLASSIFICATION: 435

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APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
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APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-003300US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (hTERT)"
US-09-052-864-1

Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGATGCGCGCGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCGC 112
QY 61 GAGGTGCTGCGCGTGGCCACGTTGTTGCGGCGCTTGGGGCCCGCAGGCTGGCGGCTGTG 120
Db 113 GAGGTGCTGCGCGTGGCCACGTTGTTGCGGCGCTTGGGGCCCGCAGGCTGGCGGCTGTG 172
QY 121 CAGCGCGGGGAGCGCGCGGCTTCCGCGCGCTGTGGGCCAGTGTGCTGTGCGGCC 180
Db 173 CAGCGCGGGGAGCGCGCGGCTTCCGCGCGCTGTGGGCCAGTGTGCTGTGCGGCC 232
QY 181 TGGGACGACAGCG 240
Db 233 TGGGACGACAGCG 292
QY 241 CTGTTGGCGCGAGTGTGACAGAGGCTGTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGTTGGCGCGAGTGTGACAGAGGCTGTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GGGTTGCGCGCTGTGAGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360

Db 353 GAGCTTCGCGCTGTGACGGGGCCCGGGGGCCCCCGAGGCTTCAACACAGCGTG 412
QY 361 CGCAGCTACCTGCCCCAACACGGTGACCGCACTGCGGGGAGCGGGGGCTGGGGCTG 420
Db 413 CGCAGCTACCTGCCCCAACACGGTGACCGCACTGCGGGGAGCGGGGGCTGGGGCTG 472
QY 421 CTGCTGCGCGCGTGGGCGACGACGTGTGTCTCACTGTGCGACGCTGCGCTCTT 480
Db 473 CTGCTGCGCGCGTGGGCGACGACGTGTGTCTCACTGTGCGACGCTGCGCTCTT 532
QY 481 GTGCTGTGCTCCCACTGCGCTGCGCTGCGCTGCGCGCGCGCTGTAACAGCTGCG 540
Db 533 GTGCTGTGCTCCCACTGCGCTGCGCTGCGCTGCGCGCGCGCTGTAACAGCTGCG 592
QY 541 GCTGCACTCAGGCG 600
Db 593 GCTGCACTCAGGCG 652
QY 601 GAACGGGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
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QY 661 GTGCGAGAGAGCG 720
Db 713 GTGCGAGAGAGCG 772
QY 721 CGTGCGCGCTGCGCGCTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 773 CGTGCGCGCTGCGCGCTGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 832
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Db 833 GGCAGAGCGCGTGAACCGAGTGACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 892
QY 841 GAAGAAGCCACCTTTTGGAGGGGTGCGGTCTGTGCAACCGCGCGCGCGCGCGCG 900
Db 893 GAAGAAGCCACCTTTTGGAGGGGTGCGGTCTGTGCAACCGCGCGCGCGCGCGCG 952
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QY 1021 CAGCTGCGCGCTCTCTCTCTACTAGCTCTCTGAGCGCGCGCGCGCGCGCGCGCG 1080
Db 1073 CAGCTGCGCGCTCTCTCTCTACTAGCTCTCTGAGCGCGCGCGCGCGCGCGCGCG 1132
QY 1081 CTGCTGAGAGCACTTTTCTGGGTTCCAGGCGCTGATGCGCAGGCACTCCCGCAGGTTG 1140
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Db 1253 CAGCGCAGTGCGCGCTTACGGGGTCTCTCAAGACGCACTGCGCGCTGCGAGCTGCGGTC 1312
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Db 1373 GAGGAGACACAGACCGCGCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1432
QY 1381 CAGGTGTACGGCTTGT 1440

Db 1433 CAGGTGTACGGCTTGT 1492
QY 1441 TCCAGGACACACGACCGCGCTTCTCTAGAGAACCAAGAAATTCTCTCTGGGAGAG 1500
Db 1493 TCCAGGACACACGACCGCGCTTCTCTAGAGAACCAAGAAATTCTCTCTGGGAGAG 1552
QY 1501 CATGCCAAGCTCTGCTGTGACAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGGCTTGG 1560
Db 1553 CATGCCAAGCTCTGCTGTGACAGAGCTGACGTGGAAGATGAGCGTGGGAGCTGGCTTGG 1612
QY 1561 CTGCGCAGAGAGCGCGGGGTGGCTGTGTTCGGCGCGCGAGAGCACCGCTCTGCGTGAAGAG 1620
Db 1613 CTGCGCAGAGAGCGCGGGGTGGCTGTGTTCGGCGCGCGAGAGCACCGCTCTGCGTGAAGAG 1672
QY 1621 ATCCTGCGCAAGTTCTCTGCACTGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCT 1680
Db 1673 ATCCTGCGCAAGTTCTCTGCACTGCTGATGATGTGTACGTGCTGAGCTGCTCAGGTCT 1732
QY 1681 TTCTTTTATGTACGAGAGACCAAGTTTGAATGACAGCACTTGAAGAGGTGACGTGCGG 1740
Db 1733 TTCTTTTATGTACGAGAGACCAAGTTTGAATGACAGCACTTGAAGAGGTGACGTGCGG 1792
QY 1741 GTCTGAGCAAGTTGCAAAAGCATTTGGAATGACAGCACTTGAAGAGGTGACGTGCGG 1800
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QY 1861 AGACTCGCGTTATCCCAAGCCTGACGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920
Db 1913 AGACTCGCGTTATCCCAAGCCTGACGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1972
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Db 1973 GTGGAGCCAGACGTTCGCGAGAAAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2032
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QY 2221 TGCGTGCCTGCGTATGCGGTGTGTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 2280
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QY 2281 AAGAGCCACGTCTTACTACTTGAACAGCTTCCAGCGCTACATGCGACAGTTCTGTGCTCAC 2340
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Q	y	121	CAGCGCGGGGACCCGGGGCTTTCGGCGCGCTGTGGCCAGTGCTGGTGTGCGTGCC	180
D	b	173	CAGCGCGGGGACCCGGGGCTTTCGGCGCGCTGTGGCCAGTGCTGGTGTGCGTGCC	232
Q	y	181	TGGAGCCGACGGCGCCCCCGCCCTCTCTTCCGCCAAGTGTCTGTGCTGAAGAG	240
D	b	233	TGGAGCCGACGGCGCCCCCGCCCTCTCTTCCGCCAAGTGTCTGTGCTGAAGAG	292
Q	y	241	CTGGTGGCCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGGAAGACGTGCGCTTC	300
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Q	y	301	GGCTTCGCGCTGCTGGACGGGGCCCGCGGGGCCCCCGAGAGCCTTCAACACAGCGTG	360
D	b	353	GGCTTCGCGCTGCTGGACGGGGCCCGCGGGGCCCCCGAGAGCCTTCAACACAGCGTG	412
Q	y	361	CGCAGCTACCTGCCCCAACACCGGTGACCGGACCACTGCGGGGAGCGGGCGTGGGGCTG	420
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Q	y	421	CTGCTGCGCCGCGTGGGCGACGACGTGTGTTCACTGCTGCGACGCTGCGGCTCTT	480
D	b	473	CTGCTGCGCCGCGTGGGCGACGACGTGTGTTCACTGCTGCGACGCTGCGGCTCTT	532
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D	b	593	GCTGCCACTCAGCCCCCGCCCCGCCACACGCTAGTGAACCCCGAAGCGCTCGGGATGC	652
Q	y	601	GAACCGGCTTGGAAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGCGCTGCCAGCCCCG	660
D	b	653	GAACCGGCTTGGAAACCATAGCGTCAGGGAGGCGGGGTCCCCCTGGCGCTGCCAGCCCCG	712
Q	y	661	GGTGGAGGAGGCGCGGGGCGAGTGCGACCGGAAGTCTGCCGTTGCCAAGAGGCCAGG	720
D	b	713	GGTGGAGGAGGCGCGGGGCGAGTGCGACCGGAAGTCTGCCGTTGCCAAGAGGCCAGG	772
Q	y	721	CGTGGCGCTGCCCTCTAGCCCGAGCGGACGCCCTTGGGCAAGGGCTCTGGGCCACCCG	780
D	b	773	CGTGGCGCTGCCCTCTAGCCCGAGCGGACGCCCTTGGGCAAGGGCTCTGGGCCACCCG	832
Q	y	781	GCGAGGACCGCTGGAACCGAGTGACCGTGGTTTCTGTGTGTGTACCTGCCAGACCCGCC	840
D	b	833	GCGAGGACCGCTGGAACCGAGTGACCGTGGTTTCTGTGTGTGTACCTGCCAGACCCGCC	892
Q	y	841	GAAGAAGCCACTCTTTGAGGGTGGCTCTTGGCACGCGCACTGCCACCATCCGTG	900
D	b	893	GAAGAAGCCACTCTTTGAGGGTGGCTCTTGGCACGCGCACTGCCACCATCCGTG	952
Q	y	901	GCGCGCCAGCACCAACGCGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACG	960
D	b	953	GCGCGCCAGCACCAACGCGGCCCCCATCCACATCGCGGCCACACAGTCCCTGGGACACG	1012
Q	y	961	CCTTGTCCCCCGGTGTACGCGCGAACAAGCACTTCTCTTACTCTCTCAAGCGACAAGAG	1020
D	b	1013	CCTTGTCCCCCGGTGTGTACGCGCGAACAAGCACTTCTCTTACTCTCTCAAGCGACAAGAG	1072
Q	y	1021	CAGCTGCGGCGCTCTCTTCTCTACTCAGCTCTCTGAGGCCAAGCTTGACTGGCGCTCGAGG	1080
D	b	1073	CAGCTGCGGCGCTCTCTTCTCTACTCAGCTCTCTGAGGCCAAGCTTGACTGGCGCTCGAGG	1132
Q	y	1081	CTCGTGAGAGCAATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGCAAGTTG	1140
D	b	1133	CTCGTGAGAGCAATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGCAAGTTG	1192
Q	y	1141	CCCCGCTGCCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGAGCTGCTTGGGAAC	1200
D	b	1193	CCCCGCTGCCCCCAGCGCTACTGGCAATGCGGCCCCCTGTTTCTGAGAGCTGCTTGGGAAC	1252

QY	1201	CACGCGCAGTGC	CCCCCTACGGGGGTGCTCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTC	1260
Db	1253	CACGCGCAGTGC	CCCCCTACGGGGGTGCTCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTC	1312
QY	1261	ACCCCAAGCAGCC	GGGTGTGTGTGTGCCCCGGGAGAAAGCCCCAAGGGCTCTGTGGCGGCCCCCGAG	1320
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QY	1381	CAGGTGTACGGCT	TCGTGTGGGGGCTTGCCCTGCGCGGGCTGTGCCCCCAGGCTCTTGGGGC	1440
Db	1433	CAGGTGTACGGCT	TCGTGTGGGGGCTTGCCCTGCGCGGGCTGTGCCCCCAGGCTCTTGGGGC	1492
QY	1441	TCCAGGACACAA	CGAAGCCGCTTCTCTCAGGAACACCAAGAAAGTTCATCTCCTTGGGGAA	1500
Db	1493	TCCAGGACACAA	CGAAGCCGCTTCTCTCAGGAACACCAAGAAAGTTCATCTCCTTGGGGAA	1552
QY	1501	CATGCCAAGCTCT	CTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTG	1560
Db	1553	CATGCCAAGCTCT	CTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGGCGGACTGCGCTTG	1612
QY	1561	CTGCGCAGGAGCC	CAAGGGTTGGCTGTGTTCGGCCGACAGACACCGCTCTGCGTGAAGAG	1620
Db	1613	CTGCGCAGGAGCC	CAAGGGTTGGCTGTGTTCGGCCGACAGACACCGCTCTGCGTGAAGAG	1672
QY	1621	ATCCTGGCCCAAG	TCTCTGCACTGCGCTGATGATGTGTACGTCTGTCAGCTGCTCAGGTCT	1680
Db	1673	ATCCTGGCCCAAG	TCTCTGCACTGCGCTGATGATGTGTACGTCTGTCAGCTGCTCAGGTCT	1732
QY	1681	TTCTTTTATGTAC	CGAGAACACAGCTTTTCAAAAGAACAGGCTCTTTTCTTCAACGGAAGT	1740
Db	1733	TTCTTTTATGTAC	CGAGAACACAGCTTTTCAAAAGAACAGGCTCTTTTCTTCAACGGAAGT	1792
QY	1741	GTCGTGAGCAAG	TGTCAAAGCATTGGAATCAGACACTTGAAGAGGGTGCAGCTGCGG	1800
Db	1793	GTCGTGAGCAAG	TGTCAAAGCATTGGAATCAGACACTTGAAGAGGGTGCAGCTGCGG	1852
QY	1801	GAGCTGTGGAAG	CAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGGCTGCTGACGTCC	1860
Db	1853	GAGCTGTGGAAG	CAGAGTCAAGCAGCATCGGGAAGCCAGGCCCGGCTGCTGACGTCC	1912
QY	1861	AGACTCCGCTTCA	TCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTC	1920
Db	1913	AGACTCCGCTTCA	TCCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTC	1972
QY	1921	GTEGGAGCCAGAA	CGTTCGCGACAGAAAGAGGGCCGAGCGTCTCACTTCAGAGGTGAAG	1980
Db	1973	GTEGGAGCCAGAA	CGTTCGCGACAGAAAGAGGGCCGAGCGTCTCACTTCAGAGGTGAAG	2032
QY	1981	GCACTGTTCAAG	CTGTCTCACTACGAGCGGGCGGGCGCCCCGGGCTCTTGGGCGCTCT	2040
Db	2033	GCACTGTTCAAG	CTGTCTCACTACGAGCGGGCGGGCGCCCCGGGCTCTTGGGCGCTCT	2092
QY	2041	GTGCTGGGCTTGA	CGATATCCACAGGGCCTGGCGCACTTCTGTGCTGTGCGGTGTGCGGGCC	2100
Db	2093	GTGCTGGGCTTGA	CGATATCCACAGGGCCTGGCGCACTTCTGTGCTGTGCGGTGTGCGGGCC	2152
QY	2101	CAGGACCCGCGCT	GAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACC	2160
Db	2153	CAGGACCCGCGCT	GAGCTGTACTTTGTCAAGGTGATGTGACGGGCGCGTACGACACC	2212
QY	2161	ATCCCCCAGGACA	GAGCTCACCGGAGGTCAATGCCACGATCATCAAAACCCACAGAACACGTAC	2220
Db	2213	ATCCCCCAGGACA	GAGCTCACCGGAGGTCAATGCCACGATCATCAAAACCCACAGAACACGTAC	2272
QY	2221	TGCGTCCGTTCGTA	TGCCGTGTGTCCAGAGGCCCGCCATGGGCAAGTCCGCAAGGCGCTTC	2280
Db	2273	TGCGTCCGTTCGTA	TGCCGTGTGTCCAGAGGCCCGCCATGGGCAAGTCCGCAAGGCGCTTC	2332

QY 2281 AAGAGCCAGTCTCTA CTTGACAGACTTCCAGCCGTACATGCGACAGTTGTTGCTCAC 2340
Db 2333 AAGAGCCAGTCTCTA CTTGACAGACTTCCAGCCGTACATGCGACAGTTGTTGCTCAC 2392
QY 2341 CTGAGAGAGACAGCCCGCTGAGGAGTCCGTGCTATGAGAGAGCTCCTCTGAAT 2400
Db 2393 CTGAGAGAGACAGCCCGCTGAGGAGTCCGTGCTATGAGAGAGCTCCTCTGAAT 2452
QY 2401 GAGGCCAGAGTGGCTCTTTCAGAGTCTTCTA CCGCTTATGTCACACAGCCGCTGCGC 2460
Db 2453 GAGGCCAGAGTGGCTCTTTCAGAGTCTTCTA CCGCTTATGTCACACAGCCGCTGCGC 2512
QY 2461 ATCAGGGGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCCGCAGAGCTCCTCTGACG 2520
Db 2513 ATCAGGGGCAAGTCTTACGTCAGTCCAGTCCAGGGGATCCCGCAGAGCTCCTCTGACG 2572
QY 2521 CTGCTCTGAGCCTGTGTACAGCGGCAATGAGACAAAGCTGTTGCGGGATTGCGCGG 2580
Db 2573 CTGCTCTGAGCCTGTGTACAGCGGCAATGAGACAAAGCTGTTGCGGGATTGCGCGG 2632
QY 2581 GACGGGCTGCTCTGCTGCTTGTGTGATGATTTCTTGTGTGACACCTCAGCTCAGCCAC 2640
Db 2633 GACGGGCTGCTCTGCTGCTTGTGTGATGATTTCTTGTGTGACACCTCAGCTCAGCCAC 2692
QY 2641 GCGAAAACCTTCTCAGAGACCTGTGCGAGGTGTCCTGATATGGCTGCGTGTGAAC 2700
Db 2693 GCGAAAACCTTCTCAGAGACCTGTGCGAGGTGTCCTGATATGGCTGCGTGTGAAC 2752
QY 2701 TTGCGAAGAGAGTGTGTA CTTCCCTGTAGAAGACGAGGCCCTGGGTGACAGGCTTTT 2760
Db 2753 TTGCGAAGAGAGTGTGTA CTTCCCTGTAGAAGACGAGGCCCTGGGTGACAGGCTTTT 2812
QY 2761 GTTCAGATGCGGCGCCACAGCCCTATTCCTGTGTGCGGCTGTGTGATACCCGGAAC 2820
Db 2813 GTTCAGATGCGGCGCCACAGCCCTATTCCTGTGTGCGGCTGTGTGATACCCGGAAC 2872
QY 2821 CTGAGAGTGAAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAAC 2880
Db 2873 CTGAGAGTGAAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAAC 2932
QY 2881 TTCAACCGCGGCTTCAAGGCTGGAGAAATGCGTCGCAAACTCTTGGGGTCTTGGG 2940
Db 2933 TTCAACCGCGGCTTCAAGGCTGGAGAAATGCGTCGCAAACTCTTGGGGTCTTGGG 2992
QY 2941 CTGAAGTGTCAAGCTGTGTTGATTTGCAAGGTGAACAGCTCCAGAGGCTGTGAC 3000
Db 2993 CTGAAGTGTCAAGCTGTGTTGATTTGCAAGGTGAACAGCTCCAGAGGCTGTGAC 3052
QY 3001 AACATCTACAGATCTCTCTGTGCAAGCGTACAGGTTTCAAGCATGTGTGCTGACGTC 3060
Db 3053 AACATCTACAGATCTCTCTGTGCAAGCGTACAGGTTTCAAGCATGTGTGCTGACGTC 3112
QY 3061 CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACAGC 3120
Db 3113 CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGCGTCACTCTGACAGC 3172
QY 3121 GCCTCCCTCTGCTACTCCATCTGAAAGCCCAAGAACGAGGATGTGCTGGGGGCGCAAG 3180
Db 3173 GCCTCCCTCTGCTACTCCATCTGAAAGCCCAAGAACGAGGATGTGCTGGGGGCGCAAG 3232
QY 3181 GGGCGCGCGCGCTCTGCGCTCCGAGGCGGTGCAAGTGGCTGTGCAACCAAGCATTCCTG 3240
Db 3233 GGGCGCGCGCGCTCTGCGCTCCGAGGCGGTGCAAGTGGCTGTGCAACCAAGCATTCCTG 3292
QY 3241 CTCAAGCTGACTGCAACCGGTGTCACTTACGTGCACTCTGCGGGTCACTCAGGACAGCC 3300
Db 3293 CTCAAGCTGACTGCAACCGGTGTCACTTACGTGCACTCTGCGGGTCACTCAGGACAGCC 3352
QY 3301 CAGACGCAAGCTGAGTGGAAAGTCCCGGGGAGACGAGCTGAGTGGCTTGAGGGCGCGAGCC 3360
Db 3353 CAGACGCAAGCTGAGTGGAAAGTCCCGGGGAGACGAGCTGAGTGGCTTGAGGGCGCGAGCC 3412
QY 3361 AACCCGGCACTGCCCTCAGACTTCAAGACCATCTGTGACTGATGGCCACCC 3411

Db 3413 AACCCGGCACTGCCCTCAGACTTCAAGACCATCTGTGACTGATGGCCACCC 3463

RESULT 15
US-09-601-645-10
; Sequence 10, Application us/09601645
; GENERAL INFORMATION:
; APPLICANT: Michael Dahm
; APPLICANT: Robert C. Phelps
; APPLICANT: Carsten Brockmeyer
; TITLE OF INVENTION: Method for the quantitative determination of tumor cells
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/601,645
; PRIOR FILING DATE: 2000-08-04
; PRIOR FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PADAT Sequenzmodul, Version 1.0
; SEQ ID NO 10
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-601-645-10

Query Match 100.0%; Score 3411; DB 25; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGGCTGCGAGCCGTGCGCTCCCTGCTGCGAGCCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGGCTGCGAGCCGTGCGCTCCCTGCTGCGAGCCACTACCGC 112
QY 61 GAGTGTGCGCGCTGCGCACTGTTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCTG 120
Db 113 GAGTGTGCGCGCTGCGCACTGTTGCGCGCGCTGCGCGCGCTGCGCGCGCTGCGCGCTG 172
QY 121 CAGCGCGGGAACCGCGGCTTCCCGCGCGCTGCTGCGCGCGCTGCTGCGCGCGCTGCGCG 180
Db 173 CAGCGCGGGAACCGCGGCTTCCCGCGCGCTGCTGCGCGCGCTGCTGCGCGCGCTGCGCG 232
QY 181 TGGAGCGCAAGCG 240
Db 233 TGGAGCGCAAGCG 292
QY 241 CTGTGCGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGTGCGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GGGTTGCGCGCTGTGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GGGTTGCGCGCTGTGAGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGAGCTACTGCTCCCAACAGGTGACCGCACTGCGGGGAGCGGGGCGTGGGGGCTG 420
Db 413 CGAGCTACTGCTCCCAACAGGTGACCGCACTGCGGGGAGCGGGGCGTGGGGGCTG 472
QY 421 CTGCTGCGCGCGGTGGGCGAGCGAGTGTGTTCACTGCTGCGCAAGCTGCGCGCTTT 480
Db 473 CTGCTGCGCGCGGTGGGCGAGCGAGTGTGTTCACTGCTGCGCAAGCTGCGCGCTTT 532
QY 481 GTGCTGTGAGTCCCAAGTGTGCGCTTACAGGTGTGCGGGCGCGCTGTACAGAGCTCGG 540
Db 533 GTGCTGTGAGTCCCAAGTGTGCGCTTACAGGTGTGCGGGCGCGCTGTACAGAGCTCGG 592
QY 541 GCTGCACTCAGGCG 600
Db 593 GCTGCACTCAGGCG 652
QY 601 GAACGGGCTTGAACCATAGCGTCAAGGAGGCGGGGCTCCCTTGGGCTGCAAGCCCG 660

D	b	653	GAACGGGCGCTGGAAACCATAGCGTCAGGGAGGCCGGGGTCCCGCTGGGCGCTGCAGCCCCG	712
O	y	661	GGTGCAGAGAGGCGCGGGGCGAGTGCACGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGG	720
D	b	713	GGTGCAGAGAGGCGCGGGGCGAGTGCACGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGG	772
O	y	721	CGTGGCGTGCCTCCCTGAGCCGGAGCGGCCGTTGGGCAGGGGTCTGGGCCCAACCCG	780
D	b	773	CGTGGCGTGCCTCCCTGAGCCGGAGCGGCCGTTGGGCAGGGGTCTGGGCCCAACCCG	832
O	y	781	GGCAGGACGCGTGGACCCGAGTGACCGTGGTTCTGTGTGTGTACCTGCCAGACCCGCC	840
D	b	833	GGCAGGACGCGTGGACCCGAGTGACCGTGGTTCTGTGTGTGTGTACCTGCCAGACCCGCC	892
O	y	841	GAAGAAGCCACTCTTTGGAGGGTGCCTCTCTGGCACGCGGCCACTTCCCAACCATCCGTG	900
D	b	893	GAAGAAGCCACTCTTTGGAGGGTGCCTCTCTGGCACGCGGCCACTTCCCAACCATCCGTG	952
O	y	901	GGCGCGCAGACCAACGCGGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACG	960
D	b	953	GGCGCGCAGACCAACGCGGGGCCCCCATCCACATCGCGGCCACCAAGTCCCTGGGACACG	1012
O	y	961	CCTTGTCCCCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAGAG	1020
D	b	1013	CCTTGTCCCCCGGTGTACGCGCGAGACCAAGCACTTCTCTACTCTCAGGGCGACAAGAG	1072
O	y	1021	CAGCTGGGCGCTCTCTCTCTACTCAAGCTCTGAGGCCAGCGCTGACTGGCGCTCGAGG	1080
D	b	1073	CAGCTGGGCGCTCTCTCTCTACTCAAGCTCTGAGGCCAGCGCTGACTGGCGCTCGAGG	1132
O	y	1081	CTCGTGGAGAACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAATCCCGCAGGTTG	1140
D	b	1133	CTCGTGGAGAACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGAATCCCGCAGGTTG	1192
O	y	1141	CCCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGACTGCTTGGGAAC	1200
D	b	1193	CCCCGCTGCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGACTGCTTGGGAAC	1252
O	y	1201	CAGCGCAGTGCCTTACGGGGTCTCTCAAGACGCACTGCCCGCTGCCAGCTGCCGTG	1260
D	b	1253	CAGCGCAGTGCCTTACGGGGTCTCTCAAGACGCACTGCCCGCTGCCAGCTGCCGTG	1312
O	y	1261	ACCCCAAGCAGCCGGTGTCTGTGCCCGGAGAGACCCCAAGGCTCTGTGGCGGCCCCCGAG	1320
D	b	1313	ACCCCAAGCAGCCGGTGTCTGTGCCCGGAGAGACCCCAAGGCTCTGTGGCGGCCCCCGAG	1372
O	y	1321	GAGGAGGACACAGACCCCCCGTGCCTGTGTGACGTGCTCCGCCACACAGCAGCCCTTGG	1380
D	b	1373	GAGGAGGACACAGACCCCCCGTGCCTGTGTGACGTGCTCCGCCACACAGCAGCCCTTGG	1432
O	y	1381	CAGGTGTACGGCTTCTGTGCCGSCCTGCTGCGCGCGGTGTGCCCCCAAGGCTCTGGGGC	1440
D	b	1433	CAGGTGTACGGCTTCTGTGCCGSCCTGCTGCGCGCGGTGTGCCCCCAAGGCTCTGGGGC	1492
O	y	1441	TCCAGGCACAACGAAACGCCGCTTCTCAGGAACCAAGAAATCATCTCCCTGGGGAAAG	1500
D	b	1493	TCCAGGCACAACGAAACGCCGCTTCTCAGGAACCAAGAAATCATCTCCCTGGGGAAAG	1552
O	y	1501	CATGCCAAGCTCTCGCTGACAGAGCTGACGTGGAAGATGAGCGTGGGACTGCGCTTGG	1560
D	b	1553	CATGCCAAGCTCTCGCTGACAGAGCTGACGTGGAAGATGAGCGTGGGACTGCGCTTGG	1612
O	y	1561	CTGCGCAGGAGCCCAAGGGTGGCTGTGTTCCGGCCGACAGCAACCGTCTGCGTGAAGAG	1620
D	b	1613	CTGCGCAGGAGCCCAAGGGTGGCTGTGTTCCGGCCGACAGCAACCGTCTGCGTGAAGAG	1672
O	y	1621	ATCCTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGTC	1680
D	b	1673	ATCCTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCTGAGCTGCTCAGGTC	1732
O	y	1681	TTCTTTATGTACCGAGACCAAGTTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGT	1740

Db	1733	TTCTTTATATGTCACGGAGACCAAGCTTTCAAAGAACAAGGCTTTTCTACCGAAGAGT	1792
QY	1741	GTCTGGAGCAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGACGTGG	1800
Db	1793	GTCTGGAGCAAGTTGCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGACGTGG	1852
QY	1801	GAGCTGTCCGAAGCAGAGGTCAAGCAGCATCCGGAAAGCAAGCCCGCCCTGCTGACGTCC	1860
Db	1853	GAGCTGTCCGAAGCAGAGGTCAAGCAGCATCCGGAAAGCAAGCCCGCCCTGCTGACGTCC	1912
QY	1861	AGACTCCGCTTCATCCCAAGCCTGACGGGCTGGCCGATTTGTGAACATGACTACGTTC	1920
Db	1913	AGACTCCGCTTCATCCCAAGCCTGACGGGCTGGCCGATTTGTGAACATGACTACGTTC	1972
QY	1921	GTGGAGCCAGAACGTTCCCGCAGAGAAAGAAGGGCCCAAGCCTCTCACTCGAGGTTGAAG	1980
Db	1973	GTGGAGCCAGAACGTTCCCGCAGAGAAAGAAGGGCCCAAGCCTCTCACTCGAGGTTGAAG	2032
QY	1981	GCACTGTTCAAGCGTGTCAACTACGAGCCGGCCCGCCCGCCCTCCTGGCCGCTCT	2040
Db	2033	GCACTGTTCAAGCGTGTCTCACTACGAGCCGGCCCGCCCGCCCTCCTGGCCGCTCT	2092
QY	2041	GTCTGGGCGCTTGAACGATATCCACAGGGCCTGGCCGACCTTCGTGCTGCTGTGGGGCC	2100
Db	2093	GTCTGGGCGCTTGAACGATATCCACAGGGCCTGGCCGACCTTCGTGCTGCTGTGGGGCC	2152
QY	2101	CAGAACCCCGCCCTGAGCTGTACTTTGTCAAGTGATGTGACGGGCGCGTACGACACC	2160
Db	2153	CAGAACCCCGCCCTGAGCTGTACTTTGTCAAGTGATGTGACGGGCGCGTACGACACC	2212
QY	2161	ATCCCCCAGGACAGGCTCAACGAGGTATGCGCAGCATCATCAACCCCAAGAACAGTAC	2220
Db	2213	ATCCCCCAGGACAGGCTCAACGAGGTATGCGCAGCATCATCAACCCCAAGAACAGTAC	2272
QY	2221	TGCGTGCCTGGTATGCGGTGTCCAGAAAGCCGCCCATGGGCAAGTCCCGCAAGGCTTC	2280
Db	2273	TGCGTGCCTGGTATGCGGTGTCCAGAAAGCCGCCCATGGGCAAGTCCCGCAAGGCTTC	2332
QY	2281	AAGAGCCACGTCTTACTTGAAGACACTCCAGCCGTACATGCGACAGTTGTTGGCTCAC	2340
Db	2333	AAGAGCCACGTCTTACTTGAAGACACTCCAGCCGTACATGCGACAGTTGTTGGCTCAC	2392
QY	2341	CTGACGAGAGACCAAGCCCGCTGAGGGATGCGGTGATGAGCAGAGCTCCCTCCCTGAAT	2400
Db	2393	CTGACGAGAGACCAAGCCCGCTGAGGGATGCGGTGATGAGCAGAGCTCCCTCCCTGAAT	2452
QY	2401	GAGGCCAGCAGTGGCCTCTTGACGTCTTCTTACGCTTCATGTGCCACCAAGCCGTGGC	2460
Db	2453	GAGGCCAGCAGTGGCCTCTTGACGTCTTCTTACGCTTCATGTGCCACCAAGCCGTGGC	2512
QY	2461	ATCAGGGGCAAGTCCCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACG	2520
Db	2513	ATCAGGGGCAAGTCCCTACGTCCAGTCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACG	2572
QY	2521	CTGCTCTGACGCTGTGTCTACGGCGCATGAGAGAACAGCTGTTTGGGGGATTCGGCGG	2580
Db	2573	CTGCTCTGACGCTGTGTCTACGGCGCATGAGAGAACAGCTGTTTGGGGGATTCGGCGG	2632
QY	2581	GACGGGCTGCTCTGCGTTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC	2640
Db	2633	GACGGGCTGCTCTGCGTTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC	2692
QY	2641	GCGAAAACCTTCTCAGGACCCCTGTCCGAGGTGTCCTGAGTATGGCTGCGGTGTGAAC	2700
Db	2693	GCGAAAACCTTCTCAGGACCCCTGTCCGAGGTGTCCTGAGTATGGCTGCGGTGTGAAC	2752
QY	2701	TTGCGGAAGACAGTGTGTAACCTCCCTGTGAGAGACGAGGCGCTGGGTGGCACGGCTTTT	2760
Db	2753	TTGCGGAAGACAGTGTGTAACCTCCCTGTGAGAGACGAGGCGCTGGGTGGCACGGCTTTT	2812
QY	2761	GTTCAAGATGCGGCGCCCAAGGCTATTTCCCTGTGTGCGGCTGCTGTGATACCCGGAGCC	2820
Db	2813	GTTCAAGATGCGGCGCCCAAGGCTATTTCCCTGTGTGCGGCTGCTGTGATACCCGGAGCC	2872

QY 2821 CTGAGGTGACAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACC 2880
DB 2873 CTGAGGTGACAGAGCGACTACTCCAGCTATGCCCCGACCTCCATCAGAGCCAGTCTCACC 2932
QY 2881 TTCAACCGCGGCTTCAAGGCTGGGAGGAAACATGCGTGGCAAACTCTTTGGGGTCTTGCGG 2940
DB 2933 TTCAACCGCGGCTTCAAGGCTGGGAGGAAACATGCGTGGCAAACTCTTTGGGGTCTTGCGG 2992
QY 2941 CTGAGGTGACAGAGCGCTGTCTGGAATTGCAAGGTGAACAGCCTCCAGAGCGTGTGCAAC 3000
DB 2993 CTGAGGTGACAGAGCGCTGTCTGGAATTGCAAGGTGAACAGCCTCCAGAGCGTGTGCAAC 3052
QY 3001 AACATCTACAAGATCCTCTGCTGCAAGCGGTACAGGTTTCAAGCATGTGTGCTGCAAGCTC 3060
DB 3053 AACATCTACAAGATCCTCTGCTGCAAGCGGTACAGGTTTCAAGCATGTGTGCTGCAAGCTC 3112
QY 3061 CCATTTTCATCAGCAAGTTTGAAGAAACCCACATTTTCTCTGCGCGTCACTCTGACACG 3120
DB 3113 CCATTTTCATCAGCAAGTTTGAAGAAACCCACATTTTCTCTGCGCGTCACTCTGACACG 3172
QY 3121 GCTTCCCTCTGCTACTCCATCTCTGAAAGCCAAAGACGAGGATGTGCTGGGGGCCAAG 3180
DB 3173 GCTTCCCTCTGCTACTCCATCTCTGAAAGCCAAAGACGAGGATGTGCTGGGGGCCAAG 3232
QY 3181 GCGCGCGCGCGCGCTCTGCTCTGCGAGGCGCGTGCAGTGGCTGTGCAAGCATTCCTG 3240
DB 3233 GCGCGCGCGCGCGCTCTGCTCTGCGAGGCGCGTGCAGTGGCTGTGCAAGCATTCCTG 3292
QY 3241 CTCAGCTGACTGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGACAGACC 3300
DB 3293 CTCAGCTGACTGACACCGTGTCACTACGTGCCACTCCTGGGGTCACTCAGACAGACC 3352
QY 3301 CAGACGAGCTGAGTGGAAAGCTCCCGGGAGCAGAGCTGACTGCCCTGAGAGCCGAGACC 3360
DB 3353 CAGACGAGCTGAGTGGAAAGCTCCCGGGAGCAGAGCTGACTGCCCTGAGAGCCGAGACC 3412
QY 3361 AACCCGGCACTGCCCTCAGACTTCAAGAACCATCTGACTGATGGCCACC 3411
DB 3413 AACCCGGCACTGCCCTCAGACTTCAAGAACCATCTGACTGATGGCCACC 3463

Search completed: March 1, 2004, 22:57:54
Job time : 6924.41 secs

QY 66 GCTGCCCTGACCACTTCTGTCGGCGCCCTGGGGCCCCAGGGCTGGCGCTGTGCAGCG 125
DB 167 GCGCGTGCATACCGCGCGCGCGCGAGACAGTCCGCAAGCGCGCGCGCTGCACGG 226
QY 126 CGGGGACCGCGCGCTTTCGCGCGCGCTGTGGCCAGTGCTGTGTGCTGCTGGGA 185
DB 227 CTGGGGCGACGACCGCTTCGCGCGCATGACTTCCAGAGCTCGCATCTCCAGTACGC 286
QY 186 CGCAGCGCGCGCGCGCGCGCGCGCTCTCTCCGCAAGTGTCTGTCTGCAAGAGCTGTG 245
DB 287 CTCCCGCGCGCGCGCGCGCGCGAGCTCGCTTACCTTCCACTCATGCCCCCTGT 346
QY 246 GCGCCGAGTGTGCAGAGGCTGTGCAGCGCGCGCGCGAAGACGT--GCTGCGCTTCGGC 303
DB 347 CGAGCGTTCATCGCGCGCGCGCGCGCGCGCGCTCTCTCCGCGCGCTCTCCGC 406
QY 304 TTGCGCTGTGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTACCAAGAGCTGCGC 363
DB 407 GTCCACCGCGCGCTGTGTCTGTACAGAGTCAACGCGCTTCGCGCGCGAGAGGCC 466
QY 364 AGCTACCTGCGCAACAGGTGACCGAGCACTGCGGGGAGCGCGCGCTGGGCTGTG 423
DB 467 GCGCGCTGTGCGCAACGCGCGCGCGCTTCGCGTTCACAGCGCGCGCGCTCATGCTC 526
QY 424 CTGCGCGCGCTGGCGCAAGCTGTGTCTGTCTGTGCTGTGCTGTGCTGTGCTGTG 472
DB 527 CCGCACATGACGCGTGGCGCGCGCGCTCTCTCGCGAGCTGACCGCGCTGTG 575

RESULT 5
US-10-767-701-30024

; Sequence 30024, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30024
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 9848339
US-10-767-701-30024

Query Match 1.6%; Score 53.2; DB 6; Length 522;
Best Local Similarity 49.4%; Pred. No. 0.0033;
Matches 167; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

QY 63 GGTGCTGCGCTGCGCACTTCTGTGCGCGCGCTGGGGCCCCAGGGCTGGCGCTGTGCA 122
DB 56 GAGCGCGTGTGCGCTGCGCGCGCGCTGTGCGCGCGCGCGAGGGCGGGGTGCACGCGG 115
QY 123 GCGCGGAGCGCGCG--GCTTTCGCGCGCTGTGTGCGCGAGTGTGCTGTGCTGTGCG 179
DB 116 GCGCGCGCGCGCTGTCTCCCTACGCGCGCGAGCTGTGCGCGCGCGCTGTGCGCGCG 175
QY 180 CTGGAGCAGCGCGCGCGCGCGCGCGCGCTCTCTTCGCGAGTGTCTGTGCTGAAGA 239
DB 176 GCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGTGCGCGCG 235
QY 240 GCTGTGTGCTT 299
DB 236 CATGCGTGG 295
QY 300 CGGCTTGTGCGCTGTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 359
DB 296 CGACCTGCGCAAGCGAT 355

QY 360 GCGCAGTACTGCGCCACACAGGTGACCGAGCGCACTGC 397
DB 356 GCTCTGAGCTCTCCCGACCTTTGTGATGACGAGAGGC 393

RESULT 6
US-10-767-701-8805

; Sequence 8805, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 8805
; LENGTH: 667
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56975_1
US-10-767-701-8805

Query Match 1.6%; Score 53.2; DB 6; Length 667;
Best Local Similarity 45.0%; Pred. No. 0.0035;
Matches 199; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

QY 67 CTGCGCGTGGCCACCTTCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
DB 23 CTCTCTGTATGCGCATTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 82
QY 127 GGGAGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
DB 83 CACCAACCGCGCTCTCTCACTCCACTTCCACCGCGCGCGCGCGCGCGCGCGCGCG 142
QY 187 GCAGCG 246
DB 143 GCGTGGCG 202
QY 247 GCGCGAGTGTGCGAGAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 306
DB 203 CCG 262
QY 307 GCGCTGTGAGCG 366
DB 263 GCG 322
QY 367 TACCTGCCAACAAGGTGACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 426
DB 323 GCG 382
QY 427 GCGCGCGTGGCGCGAGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 486
DB 383 CG 442
QY 487 GTGCTCCAGCTGCGCGCTACC 508
DB 443 CTTCGCGTGGCG 464

RESULT 7

US-10-767-701-4466

; Sequence 4466, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4466
; LENGTH: 580
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS80039_1
US-10-767-701-4466

Query Match 1.5%; Score 52.6; DB 6; Length 580;
Best Local Similarity 54.9%; Pred. No. 0.0046;
Matches 128; Conservative 0; Mismatches 99; Indels 6; Gaps 1;

QY 7 CCGCGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCGGAGCGACTACCGGAGTG 66
Db 165 CCGCGCGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCGGAGCGACTACCGGAGTG 224
QY 67 CTGCGCGTGGACACTTCTGCGGCGCGCTGGGGCCCCAGGAGCTGGCGCTGTGACAGCG 126
Db 225 GCGCGCGCGTGGCGGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 284
QY 127 GGGGACC-----CGGCGCGCTTCCCGCGCGCTGTGCGGCGCGCGCGCGCGCGCG 180
Db 285 TCG 344
QY 181 TGGGACGACG 233
Db 345 GTGCG 397

RESULT 8

US-10-767-701-12235/C

; Sequence 12235, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12235
; LENGTH: 1165
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS24569_1
US-10-767-701-12235

Query Match 1.5%; Score 51.2; DB 6; Length 1165;
Best Local Similarity 50.4%; Pred. No. 0.011;
Matches 125; Conservative 0; Mismatches 123; Indels 0; Gaps 0;

QY 23 GCCGAGCGGTGCGCTCCCTGCTGCGAGCACTACCGGAGTGCTGCGGCGCACT 82
Db 591 GCTTGGGAGCGCGCGCTGCTTACCTTGGCGGAGGCTTGGGCTTGGCGCGG 532
QY 83 TCGTGGCGCGCTGGGGCCCCAGGAGCTGGCGGCTGTGACGCGCGGAGACCGCGCGCTT 142
Db 531 TCTTGGCGCGCTGGGCTGCTTGGCGGCTGGCGGCGCGCGCTTGGCGCGGAG 472
QY 143 TCCGCGCGTGTGGCGCGAGTGCCTGTGTGCGTGCCTGGAGCGACGCGCGCGCGCG 202
Db 471 GCGCGCGGTGACCGGCGAGCTTGAACGAGTCTTCACTCTGTCACTTCCCGCGCGG 412
QY 203 CCGCGCGCTCTCCCGCGAGGTGTCTGCTGAAGAGAGTGTGGCGCGGAGTGTGACGA 262
Db 411 CGAGCTTCTTCACTGCGAGGTCACTGCTTGGCGAGAGTGTGGGAGAGCTTGGCGCG 352

QY 263 GGCTGTGC 270
Db 351 GCTTCTCC 344

RESULT 9

US-10-767-701-2473

; Sequence 2473, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 2473
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(570)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS41826_1
US-10-767-701-2473

Query Match 1.5%; Score 51; DB 6; Length 570;
Best Local Similarity 50.4%; Pred. No. 0.01;
Matches 207; Conservative 0; Mismatches 195; Indels 9; Gaps 3;

QY 88 CCGCGCGTGGGCGCGCGCGAGGCTGCGGCTGTGACGCGCGGAGACCGCGGCTTCCGC 147
Db 19 CGCGCGCTCCG 77
QY 148 GCGCTGTGCGCGAGTGCCTGTGTGCGTGCCTGTGAGCGACGCGCGCGCGCGCGCG 207
Db 78 GGGGCGCGCGCGCTCCCG 137
QY 208 CCCTCCTTCCGCGAGGTGTCTGCTGCTGAAGAGTGTGCGCGCGCGCGCGCGCGCGCG 267
Db 138 CCG 197
QY 268 TCGGAGCGCGCGCGCGAGAGAGTGTGCTGCGCTTCCGCTTCCGCTGCTGAGCGGCGCG 327
Db 198 CACGCGCGCGCTTGGCG 257
QY 328 GGGGCG 387
Db 258 CGCGCGCGCTTGGCG 310
QY 388 GACGCACTGCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 447
Db 311 CGCGCGCGCGCTTGGCG 369
QY 448 CTGTTCACTGCTGTGCG 498
Db 370 CCGGACCG 420

RESULT 10

US-10-767-701-8767

; Sequence 8767, Application US/10767701
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 8767
LENGTH: 1215
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS56207_1
US-10-767-701-8767

Query Match 1.5%; Score 51; DB 6; Length 1215;
Best Local Similarity 48.4%; Pred. No. 0.013;
Matches 170; Conservative 0; Mismatches 180; Indels 1; Gaps 1;

QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGAGCCACTACCG 60
DB 33 GCGCACCCCTCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 92
QY 61 GAGTGTGCGCTGCGACAGTCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCTG 120
DB 93 CGCCCCCG 152
QY 121 CAGCGCGGAGCGCGCGCGCTTCCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCG 180
DB 153 CTCCCCCG 212
QY 181 TGGAGCGACG 240
DB 213 GCGGTGCG 272
QY 241 CTGTGCG 300
DB 273 CACGTGCG 332
QY 301 GCGTTCG 351
DB 333 -TCTCCGCGCTCGCTCC 382

RESULT 11
US-10-767-701-1482
Sequence 1482, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 1482
LENGTH: 963
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS25355_1
US-10-767-701-1482

Query Match 1.5%; Score 50.8; DB 6; Length 963;
Best Local Similarity 46.5%; Pred. No. 0.013;
Matches 200; Conservative 0; Mismatches 227; Indels 3; Gaps 1;

QY 16 CCGCGCTGCGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 75
DB 108 CTCTGTTCCGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAC 167
QY 76 GCCAGTTCGTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG--GGGAC 132
DB 168 GACG 227

QY 133 CCGCGCGCTTCCCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
DB 228 TGCG 287
QY 193 CCGCCCCCG 252
DB 288 GCGGAGCG 347
QY 253 GTGCTGACAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 312
DB 348 CTCTACACCGAGTCCCG 407
QY 313 CTGACG 372
DB 408 CGGTGCGGAGCTGCG 467
QY 373 CCCACACGCTGACCG 432
DB 468 CGCGCGACGCTGCG 527
QY 433 GTGGCGGACG 442
DB 528 CACGCGCTCG 537

RESULT 12
US-10-767-701-18773
Sequence 18773, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 18773
LENGTH: 571
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: LIB3478-056-Q6-K1-H7
US-10-767-701-18773

Query Match 1.5%; Score 50.4; DB 6; Length 571;
Best Local Similarity 54.3%; Pred. No. 0.014;
Matches 102; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 90 GCGCTGCG 149
DB 194 GCGGTGCG 253
QY 150 GCTGTGCG 209
DB 254 GCTGAGGAGGTGTGCG 313
QY 210 CTCCTCCCG 269
DB 314 CTCTCCCG 373
QY 270 CGAGCGCG 277
DB 374 TGAGCGAG 381

RESULT 13
US-10-767-701-10516/c
Sequence 10516, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 10516
LENGTH: 572
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1663_1
US-10-767-701-10516

Query Match 1.5%; Score 50.4; DB 6; Length 572;
Best Local Similarity 46.6%; Pred. No. 0.014;
Matches 194; Conservative 0; Mismatches 221; Indels 1; Gaps 1;

QY 120 GCAGCGGAGGACCGCGGCTTCCGCGCTGTGAGCCAGTGTGTGCGCC 179
DB 521 GCGCGGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 462
QY 180 CTGGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 239
DB 461 GCGCGCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 402
QY 240 GCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 299
DB 401 GCAGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 342
QY 300 CGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359
DB 341 GGGCTTGACG-TGCGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCG 283
QY 360 GCGGAGTACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 419
DB 282 GCGCGCGGAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 223
QY 420 GCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
DB 222 ACTGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 163
QY 480 TGT 535
DB 162 CCAGCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 107

RESULT 14

US-10-767-701-11623
Sequence 11623, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 11623
LENGTH: 584
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS70322_1
US-10-767-701-11623

Query Match 1.5%; Score 50.4; DB 6; Length 584;
Best Local Similarity 47.0%; Pred. No. 0.014;
Matches 156; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

QY 67 CTGCGCTGCGCAGCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 126
DB 236 CTGCGGAGCTGTGAGCGCTGTGAGAGCGCGCGCGCGCGCGCGCG 295
QY 127 GGGGACCGCGCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186
DB 296 CTGCTAAGCGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCG 355
QY 187 GCAGCG 246
DB 356 TCCGACCGCGCGCGCTACCGCAGCGCGCGCGCGCGCGCGCGCG 415
QY 247 GCGGAGTGTGAGAGCGCTGTGCGAGCGCGCGCGCGCGCGCGCG 306
DB 416 GCGCGGAGGTGAGAGCTGTGTCCGCGCTGTGAGAGCGCGCGCG 475
QY 307 GCGCTGTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 366
DB 476 GCGGAGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 535
QY 367 TACCTGCCAACAAGGTGACCGCAGCGACTGCG 398
DB 536 CAGCTGCCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 567

RESULT 15

US-10-767-701-14885
Sequence 14885, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14885
LENGTH: 1854
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS810_1
US-10-767-701-14885

Query Match 1.5%; Score 50.4; DB 6; Length 1854;
Best Local Similarity 43.0%; Pred. No. 0.019;
Matches 356; Conservative 0; Mismatches 466; Indels 6; Gaps 2;

QY 134 CGCGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 193
DB 947 CGCGGTGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1006
QY 194 CG 253
DB 1007 GCGCGGAGCAGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1066
QY 254 TGCTCAGAGGTGTGCGAGCGG--GCGCGAAGAGCTGTGCGCGCG 311
DB 1067 CGCGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1126
QY 312 GCTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 371
DB 1127 GCTGCTGCTTACTCTTCAAGCGCGCGCGCGCGCGCGCGCGCGCG 1186
QY 372 GCGCAACAGGTGACCGCAGCTGTGCGCGCGCGCGCGCGCGCGCG 431
DB 1187 CG 1246
QY 432 CGTGGGCGAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491

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Page 7

Dp 1247 GGGCGCCGACGCCCCGGCGCGCCCCCGCTCGCCGAGCGGGCGGAGGGCCGGCCCCGGCGCGC 1306

QY 492 TCCCAAGCTCGCCTTACCAAGTGTGCGGGCCGGCCGCTGTACCAAGCTCGGCGCTGCCACTCA 551

Dp 1307 GGGCGGGGGCCCCCAACGGCTTCCCGCCCCCTCCGGGGTACG---CGTGGCCCCGGGCGC 1362

QY 552 GGGCCCCGGCCCCCGCCACACGCTTAGTGGACCCCGAAGGCGCTCTGGGATGCGAACGGGCGTG 611

Dp 1363 CGCGCCGCGCGCGCGCGCGCTTAGCGCGCACGCGGGGCGCGGGGGGGGGGGGGCGCGC 1422

QY 612 GAACCATAGCGTCAAGGAGGCGCGGGGTCCCCCTGGGCGCTGCCAGCCCCGGGTGCCAGGAG 671

Dp 1423 GCGGGCGCGCGGACCGGCGCCCTTCCCTCCCGCGCGGGCGCGCGCGCGCTCGGCGCACCGC 1482

QY 672 GCGCGGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCAAGAGCCCAAGGCGTGGCGCTGC 731

Dp 1483 CGCGCCGCGGAGGGGGCCAGCGCGCCGACCCGATACTGCCCCGGCCGGAGCGGGCTGCGC 1542

QY 732 CCCTGAGCCGGAGCGCGACGCCGTTGGGCAAGGGTCTTGGGCCCCAACCCGGGCAAGACGCG 791

Dp 1543 CGCGCGCTCCAGCCCCCTGCGCGGCCCAAGGCGGGCCCCCGGACCCCTGAGCGCCCCGGGGGG 1602

QY 792 TGGACCGAGTGACCGTGGTTTCTGTGTGTACCTTGGCCAGACCCGCGCGAAGAGCCAC 851

Dp 1603 CGCGCGGACGCGCGCGAAGCTGCGCCTCCCCCGACCAAGGCCACCCCGCGCCTGCTTCCAC 1662

QY 852 CTCTTTGAGAGGTGCGCTCTTGGCACGCGCCACTGCCACCCATCCGTGGGCGCGCCAGCA 911

Dp 1663 CCCCACACCGCGCCCCCACCCCTCTCCGCGCTCACTTTCACCTCCACATGCCCCGCCCC 1722

QY 912 CCAAGCGGGCCCCCCCATTCACATCGCGGCCAACCAAGTCCCTGGGACAC 959

Dp 1723 CACTACCGCGACACCATTCACCTTCGCGCACACCCCGGACCGCGGGCCCC 1770

Search completed: March 1, 2004, 23:56:47
Job time : 51.0927 secs

Search completed: March 1, 2004, 23:56:47
Job time : 51.0927 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 29, 2004, 17:50:03 ; Search time 5405.32 Seconds
(without alignments)
18844.394 Million cell updates/sec

Title: US-09-424-686F-11
Perfect score: 3411
Sequence: 1 gcgatgcgcgcgcctcccg.....tcctgactgatgcccacc 3411

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1584	46.4	1826	29	AY407349	Homo sapi
2	1308.6	38.4	1584	29	AY407350	Pan trogl
3	911.4	26.7	1835	29	AY407351	Mus muscu
4	806	23.6	925	12	BM453198	AGENCOURT

5	500.2	14.7	851	13	BU702370	UI-M-FIO-
6	445	13.0	492	12	BM824748 <th>X-EST0096</th>	X-EST0096
7	419	12.3	851	12	BG917907 <th>602820830</th>	602820830
8	385.8	11.3	389	9	AA281296 <th>AA281296 zt08902.r</th>	AA281296 zt08902.r
9	341.8	10.0	688	14	CF531121 <th>CF531121 UI-M-FY0-</th>	CF531121 UI-M-FY0-
10	336	9.9	649	14	CF531069 <th>CF531069 UI-M-FY0-</th>	CF531069 UI-M-FY0-
11	317.8	9.3	664	13	BQ258274 <th>BQ258274 NISC_kp11</th>	BQ258274 NISC_kp11
12	313.2	9.2	599	10	BB618671 <th>BB618671 BB618671</th>	BB618671 BB618671
13	282	8.3	614	10	BB651920 <th>BB651920 BB651920</th>	BB651920 BB651920
14	267	7.8	866	10	BE371943 <th>BE371943 601217728</th>	BE371943 601217728
15	252.2	7.4	715	10	BE396925 <th>BE396925 601290610</th>	BE396925 601290610
16	249.6	7.3	409	9	AA311750 <th>AA311750 EST182469</th>	AA311750 EST182469
17	248.8	7.3	679	10	BE396606 <th>BE396606 601289077</th>	BE396606 601289077
18	243.2	7.1	649	10	BE514070 <th>BE514070 601316376</th>	BE514070 601316376
19	243	7.1	610	10	BE514188 <th>BE514188 601316376</th>	BE514188 601316376
20	214	6.3	344	14	CF531258 <th>CF531258 UI-M-FY0-</th>	CF531258 UI-M-FY0-
21	208.6	6.1	779	10	BE268183 <th>BE268183 601125261</th>	BE268183 601125261
22	203.8	6.0	336	13	BY775178 <th>BY775178 BY775178</th>	BY775178 BY775178
23	203.2	6.0	343	13	BY783093 <th>BY783093 BY783093</th>	BY783093 BY783093
24	200.6	5.9	326	13	BY784804 <th>BY784804 BY784804</th>	BY784804 BY784804
25	192.2	5.6	326	13	BY149368 <th>BY149368 BY149368</th>	BY149368 BY149368
26	189.2	5.5	753	13	BU452535 <th>BU452535 603767927</th>	BU452535 603767927
27	182.6	5.4	347	10	AW244516 <th>AW244516 BR-END068</th>	AW244516 BR-END068
28	180.2	5.3	880	13	BU377259 <th>BU377259 603811228</th>	BU377259 603811228
29	167.6	4.9	775	12	BI388013 <th>BI388013 BFL26_002</th>	BI388013 BFL26_002
30	165	4.8	712	13	BX886589 <th>BX886589 BX886589</th>	BX886589 BX886589
31	154.8	4.5	696	13	BU139751 <th>BU139751 603134527</th>	BU139751 603134527
32	150.4	4.4	668	14	CA380121 <th>CA380121 659344 NC</th>	CA380121 659344 NC
33	132	3.9	641	28	AZ972318 <th>AZ972318 2M0246F07</th>	AZ972318 2M0246F07
34	128.8	3.8	875	13	BU122597 <th>BU122597 603148441</th>	BU122597 603148441
35	123.8	3.6	813	12	BG198331 <th>BG198331 RST17589</th>	BG198331 RST17589
36	116.8	3.4	632	14	CA353864 <th>CA353864 625469 NC</th>	CA353864 625469 NC
37	115.8	3.4	732	13	BX889962 <th>BX889962 BX889962</th>	BX889962 BX889962
38	114.8	3.4	654	13	BX882610 <th>BX882610 BX882610</th>	BX882610 BX882610
39	114.8	3.4	739	13	BX315053 <th>BX315053 BX315053</th>	BX315053 BX315053
40	113.4	3.3	568	13	BX521269 <th>BX521269 BX521269</th>	BX521269 BX521269
41	111.8	3.3	534	10	AW318894 <th>AW318894 um09a02.y</th>	AW318894 um09a02.y
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Homo sapiens TERT gene, VIRUAL TRANSCRIPT, partial sequence.
ACCESSION AY407349
VERSION AY407349.1 GI:39763320
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE
Infering nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,

Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

Location/Qualifiers

Source

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ORIGIN /locus_tag="HCM2861"

Query Match

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Best Local Similarity 86.7%; Pred. No. 3.2e-246;

Matches 1584; Conservative 0; Mismatches 242; Indels 0; Gaps 0;

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DEFINITION Pan troglodytes TERT gene, VIRtual TRANSCRIPT, partial sequence,
ACCESSION genomic survey sequence.
VERSION AY407350
KEYWORDS AY407350.1 GI:39763321
SOURCE GSS.
ORGANISM Pan troglodytes (chimpanzee)
REFERENCE Pan troglodytes
AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1584)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Fierliera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1584)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Fierliera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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Best Local Similarity 83.1%; Pred. No. 1.2e-201;
Matches 1317; Conservative 0; Mismatches 267; Indels 0; Gaps 0;
QY 1577 GGGTGGCTGTGTTCCGGCCGAGACACCGTCTGCTGAGAGATCCGGCAAGTTCC 1636
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LOCUS	AY407351
DEFINITION	Mus musculus TERT gene, VIRTUAL TRANSCRIPT, partial sequence, GSS 15-DEC-2003
	1835 bp DNA linear

ACCESSION	AY407351	
VERSION	AY407351.1	GI:39763322
KEYWORDS	GSS.	
SOURCE	Mus musculus	(house mouse)
ORGANISM	Mus musculus	

REFERENCE
1 (bases 1 to 1835)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)

TITLE Direct Submission
SUBMITTED (16-NOV-2003) **CELESTRA GENOMICS, 45 WEST GULF DRIVE**

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES	Location/Qualifiers
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Matches 1188; Conservative	0;	Mismatches 638;	Indels 9;	Gaps 3

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JOURNAL COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

FEATURES

source

Seq primer: PYX-5.

Location/Qualifiers

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/note="Organ: Brain; Vector: PYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Heming Chin, Ph.D., Program coordinator."

ORIGIN

Query Match 14.7%; Score 500.2; DB 13; Length 851;
Best Local Similarity 75.1%; Pred. No. 7.6e-71;
Matches 638; Conservative 0; Mismatches 206; Indels 6; Gaps 1;

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OY 2504 GCTCCATCTCTCCAGCGCTGCTGTCAGCGCTGTGCTACGCGGACATGAGAGCAAGCTGT 2563
DB 301 GCTCCAGCTATCCACCCTGCTGTCAGTCTGTGTTTCGAGAGACATGAGAGCAAGCTGT 360
OY 2564 TTGGCGGGATTCGGCGGAGCGGGGCTGCTCCTGCGTTGGTGGATGATTTCTTGTGTGA 2623
DB 361 TTGCTGAGGTGACAGCGGAGTGGTGTCTTTACGTTTGTGATGACTTCTGTGTGTGA 420
```

```
OY 2624 CACCTCACTCACCACCGGAAACCTTCTCAGGACCCCTGTGTCGAGGTGTCCTGAGT 2683
DB 421 CGCCTCACTTGGACCAAGCAAAACCTTCTCAGACACCCCTGTGTCATGCGGTCCTGAGT 480
OY 2684 ATGGCTGCGTGTGAAGTCTGCGGAGAGACAGTGTGAAGTCTTCTGTAGAAGACGAGGCC 2743
DB 481 ATGGGTGATGATAAAGTCTGAGAGAGACAGTGTGAAGTCTTCTGTGAGCCTGTGATCCC 540
OY 2744 TGGGTGACGCGCTTTTGTTCAGATGCGCGCCACGCGCTAATTCCTGTGCGGCTGC 2803
DB 541 TGGTGTGAGAGCTCCATACAGCTGCTGCTCAGTGCCTGTTTCCCTGTGTGCTTGC 600
OY 2804 TGCTGATACCCGAGACCCCTGAGGTGACAGAGCGACTACTCAGCTATGCCCCGACCTCA 2863
DB 601 TGCTGACACTCAGACTTTGAGGTGTTCTGTGACTACTCAGGTTATGCCAGACCTCAA 660
OY 2864 TCAGAGCAGTCTCACCCTTCAACCGCGCTTCAAGGCTGGAGAGAACATGCGTCAAC 2923
DB 661 TTAAGACAGCTCACCCTTCCAGAGTCTTTCANAGCTGGAGAACATGCGGAACANGC 720
OY 2924 TCTTTGGGCTCTTGGCGCTGAAGTGTACAGAGCTGTCTGTGATTTGACAGGTGAACGCC 2983
DB 721 TCCTGTGCTTCTTGGCGGTGAAGTGTACAGGCTCTATTTCTGAGACTTGACAGGTGAACGCC 780
OY 2984 TCAGAGCGTGTGACACCAACATCTCAAGATCTCTGCTGACAGCGGTACAGGTTTCAAG 3043
DB 781 TCAGAGCGTGTGACATCAATATATACAGATCTTCTGCTTCANAGCTACAGGTTTCAAG 840
OY 3044 CATGTGTGCT 3053
DB 841 CATGTGTGAT 850
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RESULT 6
BM824748 492 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0096335 S22SNUL6n1 Homo sapiens cDNA clone S22SNUL6n1-99-E07
DEFINITION 5', mRNA sequence.

ACCESSION BM824748.1 GI:19181161
VERSION BM824748
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 99 row: E column: 07
High quality sequence stop: 492.

FEATURES

source

1. 492
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNUL6n1-99-E07"
/sex="F"
/tissue_type="Ascites"
/cell_type="Lymphoblast-like"
/cell_line="SNU-16"
/lab_host="DH10B"
/clone_lib="S22SNUL6n1"
/note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;

Site_2: NCBI; The S2SNU16 library was contributed by the Soares laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780.

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 445; DB 12; Length 492;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2716 GTGAACCTCCCTGTAGAGACGAGGCCCTGGTGGACAGGCTTTGTTGATGATGCCGCC 2775
DB 1 GTGAACCTCCCTGTAGAGACGAGGCCCTGGTGGACAGGCTTTGTTGATGATGCCGCC 60
QY 2776 CACGGCCTATTCCTCCCTGGTGGCCTGCTGCTGATACCCCGACCTGGAGGTGACAGC 2835
DB 61 CACGGCCTATTCCTCCCTGGTGGCCTGCTGCTGATACCCCGACCTGGAGGTGACAGC 120
QY 2836 GACTACTCCAGCTATGCCCCGAGCCTCCATCAGACCCAGTCTCACTTCAACCGCGCTTC 2895
DB 121 GACTACTCCAGCTATGCCCCGAGCCTCCATCAGACCCAGTCTCACTTCAACCGCGCTTC 180
QY 2896 AAGGCTGGAGGACATGCTGCGAACTCTTTGGGGTCTTGGCGGTGAAGTGTACAGC 2955
DB 181 AAGGCTGGAGGACATGCTGCGAACTCTTTGGGGTCTTGGCGGTGAAGTGTACAGC 240
QY 2956 CTGTTCTGATTTGAGGTGACAGCCTCCAGACGGGTGTGACCAACATCTACAGATC 3015
DB 241 CTGTTCTGATTTGAGGTGACAGCCTCCAGACGGGTGTGACCAACATCTACAGATC 300
QY 3016 CTCCTGTGACGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTTTCATCAGCA 3075
DB 301 CTCCTGTGACGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTTTCATCAGCA 360
QY 3076 GTTTGGAAGAACCCCACTTTTCTGCGCGTCTCTGACACGGCCTCCCTGTCTAC 3135
DB 361 GTTTGGAAGAACCCCACTTTTCTGCGCGTCTCTGACACGGCCTCCCTGTCTAC 420
QY 3136 TCCATCTCTGAAGCCAGAACGCGAG 3160
DB 421 TCCATCTCTGAAGCCAGAACGCGAG 445

RESULT 7

BG917907

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

602820830F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4949887 5',
trna sequence.
BG917907
BG917907.1 GI:14298383
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 851)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10903 row: K column: 08

FEATURES High quality sequence stop: 753.
Location/Qualifiers

Source

1..851

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4949887"

/sex="female, virgin"

/tissue_type="infiltrating ductal carcinoma"

/dev_stage="5 months"

/lab_host="DH10B"

/clone_id="NCI_CGAP_Mam6"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies, Inc. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Query Match

Best Local Similarity 71.9%; Score 419; DB 12; Length 851;
Matches 579; Conservative 0; Mismatches 215; Indels 11; Gaps 2;

QY 2599 TTGGTGGATGATTTCTTTGTTGGTGAACACCTCACTCAACCAAGCAAACTTCTCAGG 2658
DB 38 TTGGTGGATGATTTCTTTGTTGGTGAACACCTCACTCAACCAAGCAAACTTCTCAGG 97
QY 2659 ACCCTGTCGAGGTGTCCTCCCTGAGTATGCTGCTGCTGTAACCTTGGGAGACAGTGTG 2718
DB 98 ACCCTGTCGAGGTGTCCTCCCTGAGTATGCTGCTGCTGTAACCTTGGGAGACAGTGTG 157
QY 2719 AACTTCCCTGTAGAGACGAGGCCCTGGTGGACAGGCTTTGTTGATGATGCCGCCAC 2778
DB 158 AACTTCCCTGTAGAGACGAGGCCCTGGTGGACAGGCTTTGTTGATGATGCCGCCAC 217
QY 2779 GGCCTATTCCTCCCTGGTGGCCTGCTGCTGATACCCGAGCCTGGAGGTGACAGCGAC 2838
DB 218 TGCCTGTTCCCTGGTGGTGGCTGCTGCTGATACCCGAGCCTGGAGGTGATCTGTGAC 277
QY 2839 TACTCAGCTATGCCCCGAGCCTCCATCAGACCCAGTCTACCTTCAACCGCGCTTCAAG 2898
DB 278 TACTCAGCTATGCCCCGAGCCTCCATCAGACCCAGTCTACCTTCAACCGCGCTTCAAA 337
QY 2899 GCTGGAGGACATGCTGCGAACTCTTTGGGGTCTTGGCGGTGAAGTGTACAGCCTG 2958
DB 338 GCTGGAGGACATGCTGCGAACTCTTCTGCGGTCTTGGCGGTGAAGTGTACAGCCTG 397
QY 2959 TTTCTGATTTGAGGTGACAGCCTCCAGACGGGTGTGACCAACATCTACAAGATCCTC 3018
DB 398 TTTCTGATTTGAGGTGACAGCCTCCAGACGGGTGTGACCAACATCTACAAGATCCTC 457
QY 3019 CTGCTGACGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTTTCATCAGCAAGT 3078
DB 458 CTGCTGACGGCGTACAGGTTTCAAGCATGTGTGCTGACGCTCCATTTTCATCAGCAAGT 517
QY 3079 TGAAGAACCCCACTTTTCTGCGCGTCTCTGACACGGCCTCCCTGTCTACTCC 3138
DB 518 AGGAAGAACCTCACTTTCTTCTGCGCATCTCTCAGCCAGCATCTGCTGTATGCT 577
QY 3139 ATCTGAAGCCAGAACGAGGATGCTGCTGGGGCCAAAGGGCGCGCCCTCTG 3198
DB 578 ATCTGAAGCCAGAACGAGGATGCTGCTGGGGCCAAAGGGCGCGCCCTCTG 627
QY 3199 CCTCCGAGGCGTGCAGTGTGCTGCTGCAACAGCATTCCT-GCTCAAGCTGACTGACA 3257
DB 628 TCTCCTGAAGCCAGCATTTGCTGCTGCTGCAACAGCATTCCTGCTGCTGCTCA 687
QY 3258 CCGTGTACCTACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3317
DB 688 TCTGTCTATCAAAATGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
QY 3318 GAAGCTCCCGGAGCAGAGCTGACTGCTCTGAGGCGCGCAACCCGCACTGCTGCTGCTG 3377

Db 748 GAAGTCGAGAGGCGACATGACCATGCTTACAGCTGACGTGACCCAGACCTAAGAC 807

QY 3378 AGACTCAAGACCATCTTGACTGA 3402

Db 808 AGACTTCAGAGCATTGGAGCTAA 832

RESULT 8

AA281296 389 bp mRNA linear EST 14-AUG-1997

LOCUS zt08g02.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712562 5',

DEFINITION mRNA sequence.

ACCESSION AA281296

VERSION AA281296.1 GI:1924194

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS 1 (bases 1 to 389)

TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-r@mail.nih.gov

THIS CLONE IS AVAILABLE ROYALTY-FREE THROUGH LNL; CONTACT THE IMAGE CONSORTIUM (info@image.lnl.gov) FOR FURTHER INFORMATION.

INSERT LENGTH: 2187 Std Error: 0.00

SEQ PRIMER: -28ml3 rev2 ET from Amersham

HIGH QUALITY SEQUENCE STOP: 385.

FEATURES

source

1. 389

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:712562"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/clone_lib="NCI CGAP GCB1"

/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Altman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer (5'-TGTACCAATCTGAGTGGAGCGCGCCCTCATTTTCTTTT-3', 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 11.3%; Score 385.8; DB 9; Length 389;

Best Local Similarity 99.5%; Pred. No. 1.9e-52;

Matches 387; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1627 GCCAAGTTCCTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAGTCTTTCTTT 1686

Db 1 GCCAAGTTCCTGCACTGGCTGATGAGTGTGACGTGCTGAGCTGCTCAGTCTTTCTTT 60

QY 1687 TATGTCACGAGACCAAGCTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 1746

Db 61 TATGTCACGAGACCAAGCTTCAAAAGACAGGCTCTTTTCTACCGGAAGAGTGTCTGG 120

QY 1747 AGCAAGTTCGAAGCATTTGAATCAGACACACTTGAAGAGGCTGCAAGCTGCGGAGCTG 1806

Db 121 AGCAAGTTCGAAGCATTTGAATCAGACACACTTGAAGAGGCTGCAAGCTGCGGAGCTG 180

QY 1807 TCGAAGCAGAGGTCAAGCAGATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTC 1866

Db 181 TCGAAGCAGAGGTCAAGCAGATCGGGAAGCCAGGCCCGCTGCTGACGTCCAGACTC 240

QY 1867 CGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGAATCAGTCTGGGA 1926

Db 241 CGCTTCATCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGAATCAGTCTGGGA 300

QY 1927 GCCAAGCTTCGCGAGAGAAAAGAGGCGGAGCGCTCTCAGCTGAGGGTGAAGCACTG 1986

Db 301 GCCAAGCTTCGCGAGAGAAAAGAGGCGGAGCGCTCTCAGCTGAGGGTGAAGCACTG 360

QY 1987 TTCAGCGTGTCAACTACGAGCGGCGCG 2015

Db 361 TTCAGCGTGTCAACTACGAGCGGCGCG 389

RESULT 9

CF531121 688 bp mRNA linear EST 12-SEP-2003

LOCUS UI-M-FY0-CGP-m-21-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone

DEFINITION IMAGE:30355988 5', mRNA sequence.

ACCESSION CF531121

VERSION CF531121.1 GI:34583085

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 688)

TITLE NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-r@mail.nih.gov

TISSUE PROCUREMENT: Dr. Jim Lin, University of Iowa

CDNA LIBRARY PREPARATION: Dr. M. Bento Soares, University of Iowa

CDNA LIBRARY ARRAYED BY: Dr. M. Bento Soares, University of Iowa

DNA SEQUENCING BY: Dr. M. Bento Soares, University of Iowa

CLONE DISTRIBUTION: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>

THIS CLONE WAS CONTRIBUTED BY THE BRAIN MOLECULAR ANATOMY PROJECT (BMAP)

Seq primer: PYX-5.

FEATURES

source

1. 688

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/strain="C57BL/6"

/clone="IMAGE:30355988"

/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phase resistant)"

/clone_lib="NIH_BMAP_FY0"

/note="Organ: Brain; Vector: pYX-Aac; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Aac vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 10.0%; Score 341.8; DB 14; Length 688;

Best Local Similarity 74.3%; Pred. No. 3.1e-45;

Matches 430; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY	2	CGATGCCGCGGGCTCCCCGCTGCCGAGCCGTGGCGCTCCCTGCTGCCAGCCACTACCGCG	61
Db	77	CAATGACCCCGCGCTCCTCGTTGCCCGCGGTGGCTCTCTGCTGCCAGCCGATACCGGG	136
QY	62	AGGTGCTGCCCGCTGGCCACGTTCCGTGCGCGCCCTGGGGCCCCAGGCGTGGCGGCTGTGC	121
Db	137	AGGTGTGCGCCGCTGGCAACCTTTGTGCGCGCCCTGGGGCCCCGAGGGCAGCGGGCTTGTGC	196
QY	122	AGCGCGGGGACCCCGCGGCTTTCCGCGCGCTGTGTGCCCAAGTCCCTGTTGTGCGTGCCCT	181
Db	197	AACTCGGGGACCCGGAAGATCTACCGCACTTTGGTTGCCCAATGCTAGTGTGCAATGCACT	256
QY	182	GGGACGCCACGGCGCGCCCCCGCGCCCTCTCTCCGCCAGGTGTCTGCTGAAGAGC	241
Db	257	GGGGCTCACAGCCTCCACCTGCCGACTTTCCTTCCACCAGTGTCAATCCCTGAAGAAGC	316
QY	242	TGCTGCGCCCGAGTGTCTGCAGAGCGTGTGCGAGCGCGCGCGAAGAACTGTCTGGCCTTCG	301
Db	317	TGCTGCGCCAGGGTGTGCAGAGACTGTGCGAGCGCAACGAGAGAACTGTCTGGCTTTTG	376
QY	302	GCTTCGCGCTGTGACGCGGGCGCGCGGGGGCCCCCGAGGCGCTTCAACCAACGCGTGC	361
Db	377	GCTTTGAGCTGCTTAACGAGGCGCAGAGCGGGCCTCCCATGCGCTTCACTAGTAGCGTGC	436
QY	362	GCACTACTTGCCCCAACACAGGTGACCAACGCACTGCCGGGGAGCGGGCGTGGGGGCTGC	421
Db	437	GTAAGTACTTGCCCCAACACTGTTATTGAGACCCTGCGTGTCAAGTGTGATGATGCTAC	496
QY	422	TGCTGCGCGCGGTGGGGCGACGAGTGTGTTCACTGCTGTCACCGTGCAGCGCTCTTTG	481
Db	497	TGTTGAGCCGAGTGGGGCGACGACCTGTCTGTCTACTGCTGGCACACTGTGTCTTTATC	556
QY	482	TGCTGTGGCTCCCAAGCTGCGCTTACCAAGTGTGCGGGCGCGCGCTGTATCAAGCTCGCG	541
Db	557	TTCTGTGCGCCCCCAGCTGTGCTTACCAAGGGGAGATGGCCANGAGCGTCTAAACCCCTCA	616
QY	542	CTGCCACTCAGGCGCGCGCGCGCCGACACGCTAGTGAC	580
Db	617	TTCTTACTCAGCANCCTCCAGCCTTAATTGACTGGGGCC	655

RESULT	10
CF531069	
LOCUS	
DEFINITION	
UI-M-FY0-CGP-C-19-0-UI.r1 NIH BMAP_FY0 Mus musculus CDNA clone IMAGE:30355746 5', mRNA sequence.	649 bp mRNA linear EST 12-SEP-2003

ACCESSION	CF531069
VERSION	CF531069.1
	GI:34583033

SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE

TITLE

COMMENT

FEATURE

807
808
809

/strain="C57BL/6"
 /db_xref="taxon:10090"
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 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bonaïdo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is AGCAGACACAG. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

Query Match	9.9%;	Score 336;	DB 14;	Length 649;
Best Local Similarity	77.9%;	Pred. NO. 2.7e-44;		
Matches 405;	Conservative 0;	Mismatches 115;	Indels 0;	Gaps 0;

QY	2	CGATGCCGCGCGCTCCCCGCTGCCGAGCCGTCGCTCCCTGCTGCCGACCACTACCGCG	61
Db	40	CAATGACCCGCGCTCTCGTTGCCCGCGGTGCGCTCTCTGCTGCCGACCGAATACCGGG	99
QY	62	AGGTGCTGCCGCTGGCCACAGTTCGTGCGGCGCTTGGGGCCCCAGGGGCTGGCGGCTGTGC	121
Db	100	AGGTGTGCGCGCTGGCAACCTTTGTGCGCGCTTGGGGCCCCGAGGGCAGGCGGCTTGTGC	159
QY	122	AGCGCGGGAGACCCGGCGGCTTTCCGCGCGCTGTGGCCCACTGCTGTGTGCGTGCCT	181
Db	160	AACCCGGGAGACCCGAAGATCTACCGCACTTTGGTTGCCCAATGCTAGTGTGATGCACT	219
QY	182	GGGACGCACGCGCGCGCCCCCGCGCGCCCCCTCTCTCCGCGAGGTGTCCTGCTGAAGAGC	241
Db	220	GGGGCTACAGCCTCCACCTGCGGACCTTCTCTCCACCGAGTGTATCCCTGAAGAAGC	279
QY	242	TGTTGCCCCGAGTGTGTCAGAGAGCTGTGCGAGCGCGCGGAAGAACTGTGCGCTTGC	301
Db	280	TGTTGCGCAGGGTTGTGCAGAGACTCTGCGAGCGCAACGAGAAACGTGTGCGCTTTG	339
QY	302	GCTTGCAGCTGCTGGAACGGGCGCGCGGGGGCCCCCGGAGCCTTCAACCAACAGCGTGC	361
Db	340	GCTTTGAGCTGCTTAACGAGGCCAGAGCGGGGCTCCCATGTGCTTCACTAGTAGCGTGC	399
QY	362	GCAGCTACTGCCCCAACACACGCGTACCGACCACTGCGGGGGAGCGGGGCGTGGGGGCTGC	421
Db	400	GTAGCTACTTGGCCCCAACACTGTTAATTGAGACCCCTGCGTGTCAGTGGTGCATGATGCTAC	459
QY	422	TGCTGCCGCGCGTGGGGCGAGCAGCGTGTGTTCAACCTGTGCGACCGCTGCGCGCTCTTG	481
Db	460	TGTTGAGCCGAGTGGGGCGACGACCACTGTGTGTTCACTGTGCGACACTGTGCTCTTATC	519
QY	482	TGCTGTGGCTTCCAGCTGCGCTTACCAAGTGTGCGGGCC	521
Db	520	TTCTGTGCGCGCCCAAGCTGTGCTTACCGAGGGAGATGGCC	559

RESULT 11
 BQ258274
 LOCUS
 DEFINITION
 BQ258274 664 bp
 NISC kp11904.q3 Baker mouse embryo e7.5 Mus musculus CDNA clone
 IMAGE:5409222, mRNA sequence.
 BQ258274
 ACCESSION
 VERSION
 BQ258274.1 GI:20459030
 KEYWORDS
 EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 664)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: J. Baker (Stanford University)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
info@image.lnl.gov
MGI:1845958
Plate: L1AM12043 row: N column: 7
Seq primer: Sp6 primer.
Location/Qualifiers
1..664
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:5409222"
/tissue_type="embryo, late gastrula"
/dev_stage="embryo, 7.5 dpc"
/lab_host="XLI-Blue"
/clone_lib="Baker mouse embryo e7.5"
/note="Vector: pCS105; Site 1: NotI; Site 2: SalI; cDNA
made by oligo-dt priming. Directionally cloned into
SalI/NotI sites using the following 5' adaptor:
5'-TCGACCCAGCGCTCCG-3'. Size-selected for average insert
size 1.8-1.9 kb. Library constructed by J. Baker (Stanford
University)."

FEATURES

source

Query Match 9.3%; Score 317.8; DB 13; Length 664;
Best Local Similarity 68.3%; Pred. No. 2.4e-41;
Matches 479; Conservative 0; Mismatches 177; Indels 45; Gaps 1;
ORIGIN
1056 GCCCAGCCTGAGTGGCGCTCGAGAGCTGTGAGAGCATTCTTGGGTCCAGGCCCTG 1115
Db 9 GCCTAAGTGAAGTGGGCGCAGAGAGTGTGAGATCATCTTCTGGGCTCAAGGCTTAG 68
QY 1116 GATGCCAGGAGTCCCGCAGAGTGGCGCTGCGCCAGGCGCTACTGGCAATGCGGCC 1175
Db 69 GACATCAGAGCACTCTGCAAGAGACACCGTCTATCGCGTCACTAGGAGATGCGGCC 128
QY 1176 CCTGTTTCTGAGAGTGTGGAACCAAGCGGAGTGGCGCTCAAGGGGTGCTCTCAAGAC 1235
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RESULT 12

BB618671

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BB618671 599 bp mRNA linear EST 26-OCT-2001
BB618671 RIKEN full-length enriched, 8 days embryo Mus musculus
CDNA clone 5730412M20 5', mRNA sequence.
BB618671 GI:16458173
EST.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 599)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

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FEATURES

source

Location/Qualifiers
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/organism="Mus musculus"
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/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 100.0 Second strand cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGATTTCTCGAGTTAATTAATATCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified Bluescript KS(+) after bulk excision from Lambda Flc I. Cloning sites, 5' end: Sali; 3' end: BamHI."

ORIGIN

Query Match 9.2%; Score 313.2; DB 10; Length 599;
Best Local Similarity 77.8%; Pred. No. 1.3e-40;
Matches 378; Conservative 0; Mismatches 108; Indels 0; Gaps 0;

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RESULT 13

BB651920

LOCUS

DEFINITION

BB651920 RIKEN full-length enriched, ES cells Mus musculus cDNA

clone C330020G14 5', mRNA sequence.

BB651920

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2001)

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Fax: 81-45-503-9216

Email: genome-res@gsr.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>

Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

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genes. Genome Res. 10 (10), 1617-1630 (2000)

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Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.

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10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

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Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

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Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, K.,

Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and

Hayashizaki, Y.

Computational Analysis of Full-length Mouse cDNAs Compared with

Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for

further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers
1. 614
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C330020G14"
/cell_type="ES cells"
/lab_host="SOLR"
/clone_lib="RIKEN full-length enriched, ES cells"
/note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINTL at: image.lnl.gov

Plate: L1CM294 row: c column: 03
High quality sequence stop: 634.

FEATURES

Source

1. 715

Location/Qualifiers

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3621050"

/tissue_type="Burkitt lymphoma"

/lab_host="DH10B (phage-resistant)"

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/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match

Best Local Similarity 7.4%; Score 252.2; DB 10; Length 715;

Matches 307; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

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QY 3301 CAGACGAGCTGAGTGGAAAGCTCCCGGGGACGAGCTGACTGCTGCTGAGAGCGCGAC 3360
Db 3353 CAGACGAGCTGAGTGGAAAGCTCCCGGGGACGAGCTGACTGCTGAGAGCGCGAC 3412
QY 3361 AACCCGCGACTGCTCTCAGACTTCAAGACATCTGACTGATGGCCACC 3411
Db 3413 AACCCGCGACTGCTCTCAGACTTCAAGACATCTGACTGATGGCCACC 3463

RESULT 2
US-09-990-080-1
; Sequence 1, Application US/09990080
; Patent No. US20020102686A1
; GENERAL INFORMATION:
; APPLICANT: Morin, Gregg B.
; APPLICANT: Geron Corporation
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit Variants
; FILE REFERENCE: 018/258c
; CURRENT APPLICATION NUMBER: US/09/990,080
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 09/052,864
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT) cDNA
US-09-990-080-1

Query Match 100.0%; Score 3411; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CAGCGCGGGAACCGCGCGCTTCCCGCGCGCTGCTGCGCGCGCGCGCGCGCGCTG 180
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QY 241 CTGCTGCGCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
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Db	773	CGTGGCGCTGCCCTTGAAGCCCGAGCGGACGCCCGTTGGGCAGAGGGTCTGGGCCACCCG	832
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Db	1073	CAGCTGCGGCCCTCTCTCTACTCAAGCTCTGTAGGCCACGCTGACTGGCGTCGAGG	1132
QY	1081	CTCGTGAGACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGAGTTG	1140
Db	1133	CTCGTGAGACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGGACTCCCCGAGTTG	1192
QY	1141	CCCCGCTGCCCCCAGCGCTACTGGCAATGCGGCCCTGTTCTGAGCTGCTTGGGAAC	1200
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Db	1253	CACGCGCAGTGCCCCCTACGGGGTCTCCTCAAGACGCACCTGCCGCTGCCAGCTGCCGTC	1312
QY	1261	ACCCCGACGAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCCAGGGCTCTGTGGCGCCCCGAG	1320
Db	1313	ACCCCGACGAGCCGGTGTCTGTGCCCCGGGAGAAGCCCCCAGGGCTCTGTGGCGCCCCGAG	1372
QY	1321	GAGGAGGACACAGACCCCGCTGCGCTGTGTGACGCTGCTCCGCCACAGACAGACGCCCTGG	1380
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QY	1381	CAGGTGTACGGCTTGTGTGCGGGGCTGCTGCTGCGCGCGCTGGTGCCCCCAGGGCTCTGGGGG	1440
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Db 2993 CTGAAGTGTACAGCTGTTTCTGATTTGACGTTGACAGCTTCCAGACGCTGTGACC 3052
QY 3001 AACATCTACAAGATCCTCTGCTGACGCGGTACAGTTTCAAGCATGTGTGCTGACGTC 3060
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Db 3413 AACCCGCACTGCTCCCTCAGACTTCAAGACCATCTGACTGATGCGCACCC 3463

RESULT 3

US-09-843-676-224

Sequence 224, Application US/09843676

Patent No. US20020164786A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Linsner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: NO. US20020164786A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/843,676

FILING DATE: 26-Apr-2001

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTRT"
/note= "human telomerase reverse
transcriptase (hTRT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-09-843-676-224

Query Match 100.0%; Score 3411; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCGCGTCCCTGCTGCGAGCCACTACCGC 60
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QY 61 GAGTGTGCGCGCTGCGACGTTGTGCGCGCGCGCTGGGCGCCAGGCTGGCGCTGTG 120
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Db 233 TGGAGCGACG 292
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RESULT 4

US-09-953-052-1

; Sequence 1, Application US/09953052
; Patent No. US20020173476A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Antisense Compositions for Detecting and
Inhibiting Telomerase Reverse Transcriptase
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953, 052

FILING DATE: 14-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,919
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/974,549
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/974,584
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 015389-003600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "human telomerase reverse
transcriptase (htrr)"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-953-052-1
Query Match 100.0%; Score 3411; DB 9; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 593 GCTGCCACTCAGGCG 652
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RESULT 5

US-10-053-758-224
; Sequence 224, Application US/10053758
; Publication No. US20030032075A1

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APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.

Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030032075A1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US/08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US/08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US/08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
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; INFORMATION FOR SEQ ID NO: 224:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4015 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..3454
; OTHER INFORMATION: /product= "hTERT"
; /note= "human telomerase reverse
; transcriptase (hTERT) catalytic protein
; component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-053-758-224
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	533	GTGCTGTGCTGCCAGCTGCGCCTAACAGGTGTGCGGGCGCGCCTGTACCAAGCTCGGC	592
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QY	781	GGCAGGACGCGTGGACCCGAGTGAACCGTGTTCTGTGTGTGTCACTGCGCAAGACCCGCC	840
Db	833	GGCAGGACGCGTGGACCCGAGTGAACCGTGTTCTGTGTGTGTCACTGCGCAAGACCCGCC	892
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Db	893	GAAGAAGCCACCTCTTTGGAGGGTGCCTCTCTGGCAACGCCCACTCCACCCATCCGTG	952
QY	901	GGCGCCAGCACCAAGCGGGCCCCCATTCACATCGCGGCCACACAGTCCCTGGACACG	960
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QY	1021	CAGCTGCGGCCCTCCTTCTACTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGTCGAGG	1080
Db	1073	CAGCTGCGGCCCTCCTTCTACTACTCAGCTCTCTGAGGCCAGCCTGACTGGCGTCGAGG	1132
QY	1081	CTCGTGAGAGCCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGAGGTTG	1140
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QY	1441	TCCAGGACACAGACCGCCGCTTCTCCTCAGGAACACCAAGAGTTCTATCTCCCTGGGGAAG	1500
Db	1493	TCCAGGACACAGACCGCCGCTTCTCCTCAGGAACACCAAGAGTTCTATCTCCCTGGGGAAG	1552
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QY	1741	GTCCTGAGCAAGTTGCCAAAGCATTGGAATCAGACGCACTTGAAGAGGGTGCAGCTCGG	1800
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QY	1801	GAGCTGTGCGAAGCAGAGGTGAGGAGCATGCGGAAAGCCAGGCCCGCCCTGCTGACGTCC	1860
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QY	1861	AGACTCCGCTTCATCCCAAGCCTGACGGGCTGCGCCGATTGTGAACATGGACTACGTC	1920
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QY	1921	GTGGAGCCAGAACGTTCCGACAGAAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAG	1980
Db	1973	GTGGAGCCAGAACGTTCCGACAGAAAAAGGGCCGAGCGTCTCACCTCGAGGGTGAAG	2032
QY	1981	GCACTGTTACGCGTGCTCAACTACGAGCGGGCGCGCCCGGCTCTCTGGCGCTCT	2040
Db	2033	GCACTGTTACGCGTGCTCAACTACGAGCGGGCGCGCCCGGCTCTCTGGCGCTCT	2092
QY	2041	GTGCTGGGCTGAGCAGATATCCACAGGGCTGGCGCACCTTGTGCTGCGTGTGCGGGCC	2100
Db	2093	GTGCTGGGCTGAGCAGATATCCACAGGGCTGGCGCACCTTGTGCTGCGTGTGCGGGCC	2152
QY	2101	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACC	2160
Db	2153	CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGACGGGCGGTACGACACC	2212
QY	2161	ATCCCCCAGGACAGGCTCACGGAAGTCAATCCGACGATCATCAAAACCCAGAACACGTAC	2220
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QY	2221	TGCGTGCCTCGGTATGCCGTGTCAGAAAGCCCGCCATGGGCACTGCCGCAAGCCCTTC	2280
Db	2273	TGCGTGCCTCGGTATGCCGTGTCAGAAAGCCCGCCATGGGCACTGCCGCAAGCCCTTC	2332
QY	2281	AAGAGCCACGTTCTTACTTGTACAGACTCCAGCCGTACATGCGACAGTTCTGTGCTCAC	2340
Db	2333	AAGAGCCACGTTCTTACTTGTGTACAGACTCCAGCCGTACATGCGACAGTTCTGTGCTCAC	2392
QY	2341	CTGCAAGAGACCAAGCCCGCTGAGGGATGCCGTGCTCATGAGCAGAGCTCTCCCTGAAT	2400
Db	2393	CTGCAAGAGACCAAGCCCGCTGAGGGATGCCGTGCTCATGAGCAGAGCTCTCCCTGAAT	2452

QY 2401 GAGGCCAGAGTGGCTCTTCGACGTCTTCTACGCTTCATGTGCAACACGCCGTGCGC 2460
DB 2453 GAGGCCAGAGTGGCTCTTCGACGTCTTCTACGCTTCATGTGCAACACGCCGTGCGC 2512
QY 2461 ATCAGGGCAAGTCCCTACGTCAGTGCAGGGGATCCCGCAGGGGCTCCATCTCTCCACG 2520
DB 2513 ATCAGGGCAAGTCCCTACGTCAGTGCAGGGGATCCCGCAGGGGCTCCATCTCTCCACG 2572
QY 2521 CTGCTCTGAGCTGTGTCTACGCGGACATGGAACAAGCTGTTGGGGGATTCGCGG 2580
DB 2573 CTGCTCTGAGCTGTGTCTACGCGGACATGGAACAAGCTGTTGGGGGATTCGCGG 2632
QY 2581 GACGGGCTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACTCACCAC 2640
DB 2633 GACGGGCTGCTCTGCGTTTGGTGGATGATTTCTTGTGTGACACCTCACTCACCAC 2692
QY 2641 GCGAAAACCTTCTCAGGACCCCTGTCCGAGGTGTCCCTGAGTATGCTGCTGTAAC 2700
DB 2693 GCGAAAACCTTCTCAGGACCCCTGTCCGAGGTGTCCCTGAGTATGCTGCTGTAAC 2752
QY 2701 TTGCGGAGAGACAGTGTGTAATCTCCCTGTAGAGAAGAGAGGCCCTGGGTCAGCTTTT 2760
DB 2753 TTGCGGAGAGACAGTGTGTAATCTCCCTGTAGAGAAGAGAGGCCCTGGGTCAGCTTTT 2812
QY 2761 GTTCAGATGCGCGCCCAAGGCTATTCCTCTGTGCGGCTGCTGCTGATACCCGAGAC 2820
DB 2813 GTTCAGATGCGCGCCCAAGGCTATTCCTCTGTGCGGCTGCTGCTGATACCCGAGAC 2872
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DB 2873 CTGAGAGTGCAGAGCGCACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCCGCGCTTCAAGGCTGGAGAGAACATGCGTCGCAAACTCTTTGGGCTTTCGG 2940
DB 2933 TTCAACCCGCGCTTCAAGGCTGGAGAGAACATGCGTCGCAAACTCTTTGGGCTTTCGG 2992
QY 2941 CTGAAGTGTACAGCGCTTCTCTGATTTGAGGTGAAACAGGCTCCAGAGCGTGTGCA 3000
DB 2993 CTGAAGTGTACAGCGCTTCTCTGATTTGAGGTGAAACAGGCTCCAGAGCGTGTGCA 3052
QY 3001 AACATCTACAGATCTCTCTGCTGAGGCGTACAGTTTCAAGCATGTGTGCTGAGCTC 3060
DB 3053 AACATCTACAGATCTCTCTGCTGAGGCGTACAGTTTCAAGCATGTGTGCTGAGCTC 3112
QY 3061 CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTTGACAG 3120
DB 3113 CCATTTTCATCAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTTGACAG 3172
QY 3121 GCCTCCCTCTGCTACTCTCATCTGAAAGCAAGACAGAGATGTGCTGGGGGCAAG 3180
DB 3173 GCCTCCCTCTGCTACTCTCATCTGAAAGCAAGACAGAGATGTGCTGGGGGCAAG 3232
QY 3181 GGGCGCGCGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATCTCTG 3240
DB 3233 GGGCGCGCGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATCTCTG 3292
QY 3241 CTCAAGCTGACTGACACCGGTGCTACCTGACCTCTGAGGCTCACTCAGAGACGCC 3300
DB 3293 CTCAAGCTGACTGACACCGGTGCTACCTGACCTCTGAGGCTCACTCAGAGACGCC 3352
QY 3301 CAGAGCAGCTGAGTCCGAGAGCTCCGCGGAGAGAGCTGACTGCTGAGAGCGCGAGCC 3360
DB 3353 CAGAGCAGCTGAGTCCGAGAGCTCCGCGGAGAGAGCTGACTGCTGAGAGCGCGAGCC 3412
QY 3361 AACCCGCACTGCGCTCAGACTTCAAGACCATCTGAGTGAATGGCCACCC 3411
DB 3413 AACCCGCACTGCGCTCAGACTTCAAGACCATCTGAGTGAATGGCCACCC 3463

RESULT 6

US-10-208-243-1
; Sequence 1, Application US/10208243
; Publication No. US20030044394A1

GENERAL INFORMATION:
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: Methods and Compositions for Eliciting an Immune
; FILE REFERENCE: 015389-003500PC
; CURRENT APPLICATION NUMBER: US/10/208,243
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/675,321
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/112,006
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: WO PCT/US99/06898
; PRIOR FILING DATE: 1999-03-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (56)..(3454)
; OTHER INFORMATION: human telomerase reverse transcriptase (hTERT)
US-10-208-243-1

Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGGAGCGGCTGCGCTCCCTGTCGCAAGCACTACCGC 60
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QY 61 GAGTGTGCTGCGCGTGCACAGTGTGCGGCGCTGCGGAGCGGCTGCGGCTGCGGCTG 120
DB 113 GAGTGTGCTGCGCGTGCACAGTGTGCGGCGCTGCGGAGCGGCTGCGGCTGCGGCTG 172
QY 121 CAGCGCGGAGCGCGCGCTTCCGCGCGCTGCTGCGGAGCGGCTGCGGCTGCGGCTG 180
DB 173 CAGCGCGGAGCGCGCGCTTCCGCGCGCTGCTGCGGAGCGGCTGCGGCTGCGGCTG 232
QY 181 TGGAGCAGAGCG 240
DB 233 TGGAGCAGAGCG 292
QY 241 CTGTGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 300
DB 293 CTGTGCGCGAGTGTGTCAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GGCTTCCGCGCTGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
DB 353 GGCTTCCGCGCTGTGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGCAGCTACTGCG 420
DB 413 CGCAGCTACTGCG 472
QY 421 CTGCTGCGCGCGCGTGGGCGAGCGAGTGTGTTCACTGCTGCGCACTGCGCGCTTT 480
DB 473 CTGCTGCGCGCGCGTGGGCGAGCGAGTGTGTTCACTGCTGCGCACTGCGCGCTTT 532
QY 481 GTGCTGTGCTCCCAAGTGTGCGCGCTTCAAGTGTGCGGCGCGCGCGCGCGCGCG 540
DB 533 GTGCTGTGCTCCCAAGTGTGCGCGCTTCAAGTGTGCGGCGCGCGCGCGCGCGCG 592
QY 541 GCTGCACTAGCG 600
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QY 601 GAACGGGCGCTGGAACCATAGCGTCAAGGAGCGCGGCGCTGCGGCTGCGGCGCGCG 660
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QY 661 GGTGAGAGAGCGCGGGGAGTGCACCGCAAGTCTGCCGTTGCCCAAGAGGCCCGAG 720
Db 713 GGTGAGAGAGCGCGGGGAGTGCACCGCAAGTCTGCCGTTGCCCAAGAGGCCCGAG 772
QY 721 CGTGGCGTGCCTTGAAGCGCGGAGCGCCGTTGGGCAAGGGTCTTGGGCCCGAG 780
Db 773 CGTGGCGTGCCTTGAAGCGCGGAGCGCCGTTGGGCAAGGGTCTTGGGCCCGAG 832
QY 781 GGCAGAGCGGTGACCGAGTGAACCGTGGTTTCTGTGTGTGTACCTGCGAGACCGCC 840
Db 833 GGCAGAGCGGTGACCGAGTGAACCGTGGTTTCTGTGTGTGTACCTGCGAGACCGCC 892
QY 841 GAAGAAGCCACTCTTTTGAAGGTGCGCTCTTGGCAAGCGCGCACTCCACCCATCCGT 900
Db 893 GAAGAAGCCACTCTTTTGAAGGTGCGCTCTTGGCAAGCGCGCACTCCACCCATCCGT 952
QY 901 GGCAGAGCG 960
Db 953 GGCAGAGCG 1012
QY 961 CCTGTCCCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAGAG 1020
Db 1013 CCTGTCCCGGTGTACCGCGAGACCAAGCACTTCTCTACTCTCTCAGGCGACAGAG 1072
QY 1021 CAGCTGCGCGCGCTCTCTCTACTACTAGCTCTTGAGGCCAGCGCTGAAGCTCGGAG 1080
Db 1073 CAGCTGCGCGCGCTCTCTCTACTACTAGCTCTTGAGGCCAGCGCTGAAGCTCGGAG 1132
QY 1081 CTGCTGAGACCATTTTCTGAGTTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTG 1140
Db 1133 CTGCTGAGACCATTTTCTGAGTTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTG 1192
QY 1141 CCG 1200
Db 1193 CCG 1252
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QY 1261 ACCCGAGAGCGCGGTGTCTGTGCGCGGAGAGCGCGCGCTGTGTGCGCGCGCGAG 1320
Db 1313 ACCCGAGAGCGCGGTGTCTGTGCGCGGAGAGCGCGCGCTGTGTGCGCGCGCGAG 1372
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QY 1861 AGACTCCGCTTCACTCCCAAGCTGAAGGCTGCGCGCGCTGCTGAGCTGAGCTGAGT 1920
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QY 1921 GTGAGCGCAAGACGTTCCGCAAGAAAGAGGCGCGCGCGCTGCTGAGCTGAGT 1980
Db 1973 GTGAGCGCAAGACGTTCCGCAAGAAAGAGGCGCGCGCGCTGCTGAGCTGAGT 2032
QY 1981 GCACTGTTCAAGCTGCTCACTACAGCGCGCGCGCGCGCGCGCTGCTGAGCTGAGT 2040
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QY 2221 TGGGTGCTGTGATATGCGGTGTGCAAGAGCGCGCGCGCGCGCGCTGCTGAGCT 2280
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QY 2281 AAGAGCAGCTCTACTACCTTGAAGACCTCCAGCGCTATGAGACAGCTTCTGCTGCTAC 2340
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QY 2461 ATCAGGCGCAAGTCTTCAAGCTTCAAGGATGCGGATGCGGAGCTTCTCTGCTGAC 2520
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Db 2633 GACGGCTGCTCTGCTGCTTGTGATGATTTCTTGTGTGACACCTCACTCACCCAC 2692
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Db 2993 CTGAAGTGTACAGCCTGTTTCTGGATTGCAAGTGAACAGCCTCCAGACGGTGTGACC 3052
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Db 3413 AACCCGCACTGCGCTCAGACTTCAAGACCATCTGACTGATGGCCACC 3463

RESULT 7
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Sequence 224, Application US/10054295
Publication No. US20030044953A1

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: No. US20030044953A1el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/054,295

FILING DATE: 18-Jan-2002

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/854,050

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-295-224

Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGCGAGCGGTGCGCTCCCTGCTGCGCGAGCCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGCGAGCGGTGCGCTCCCTGCTGCGCGAGCCACTACCGC 112
QY 61 GAGGTGCTGCGCGTGGCCACGTTGTTGGGCGCGCTGGGGCCCCAGGGCTGGCGTGTG 120
Db 113 GAGGTGCTGCGCGTGGCCACGTTGTTGGGCGCGCTGGGGCCCCAGGGCTGGCGTGTG 172
QY 121 CAGCGCGGGGAGCGCGCGGCTTTCGCGCGCTGTTGGCCAGTGTGCTGCTGCTGCTG 180
Db 173 CAGCGCGGGGAGCGCGCGGCTTTCGCGCGCTGTTGGCCAGTGTGCTGCTGCTGCTG 232
QY 181 TGGAGCGACGCGCGCGCGCGCGCGCTTCCGCGAGGTGTCTGCTGCTGAAGAG 240
Db 233 TGGAGCGACGCGCGCGCGCGCGCGCTTCCGCGAGGTGTCTGCTGCTGAAGAG 292
QY 241 CTGTTGCGCGAGTGTGAGAGGCTGTGAGAGCGCGCGCGAGAGAGTGTGCTGCTGCT 300
Db 293 CTGTTGCGCGAGTGTGAGAGGCTGTGAGAGCGCGCGCGAGAGAGTGTGCTGCTGCT 352
QY 301 GCGTTGCGCGTGTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 353 GCGTTGCGCGTGTGAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 412
QY 361 CGAGCTACTGCGCGCAACAGGTGACGCACTGCGGGGAGCGGGGCGTGGGGCTG 420
Db 413 CGAGCTACTGCGCGCAACAGGTGACGCACTGCGGGGAGCGGGGCGTGGGGCTG 472
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Db 533 GTGCTGTTGCTCCAGCTGCGCTACAGGTGTGCGGGCGCGCGCTGTACAGCTGCG 592
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Db 593 GCTGCCACTGAGCGCGCGCGCGCGCGCGCTAGTGACCCCGAGAGCGTGTGGATGC 652

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QY	661	GGTCCGAGGAGGCGCGGGGCGAGTGCCAGCCGGAAGTCTGCCGTTGCCCAAGAGGCCCAGG	720
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Db	773	CGTGGCGCTGCCCCCTGAGCCGGAGCGGAGCCGCCGTTGGGCAAGGGGTCTGGGCCCAACCCG	832
QY	781	GGCAGGACCGCTGGACCCGAGTGAACCGTGTTCTGTGTGTGTCACTTGCAGAACCCGCC	840
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QY	841	GAAGAAACCACCTCTTTTGAAGGTGCGCTCTTGAGCAGCGGCCACTGCCACCTCCGT	900
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QY	901	GGCCCCAGCACCAACGCGGGCCCCCATCCATCCATCGCGGCCACACGTCCCTGGACACG	960
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QY	961	CCTTGTCCTCCCGGTGTAACGCCGAGAACCAAGCACTTCCTCTACTCTCAAGCGACAAGAG	1020
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QY	1021	CAGCTGCGGCTCTCTCTCTACTCACTCTCTGAGGCCAGCCTGACTGCGCTCGAGG	1080
Db	1073	CAGCTGCGGCTCTCTCTCTACTCACTCTCTGAGGCCAGCCTGACTGCGCTCGAGG	1132
QY	1081	CTCGTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCCGAGGTTG	1140
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Db	1253	CACGCGAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTC	1312
QY	1261	ACCCAGCAGCGCGGTGTCTGTGCCCGGAGAGAGCCCCAGGGCTCTGTGGCGGCCCCGAG	1320
Db	1313	ACCCAGCAGCGCGGTGTCTGTGCCCGGAGAGAGCCCCAGGGCTCTGTGGCGGCCCCGAG	1372
QY	1321	GAGGAGGACACAGACCCCCCGTCCGTGTCAGCTGTCCGCCAGACACAGAGCCCCCTGG	1380
Db	1373	GAGGAGGACACAGACCCCCCGTCCGTGTCAGCTGTCCGCCAGACACAGAGCCCCCTGG	1432
QY	1381	CAGGTGTACGGCTTCTGTGCGGGCTGCTTGCGCCGGCTGTGTGCCCAAGGCTCTGGGGC	1440
Db	1433	CAGGTGTACGGCTTCTGTGCGGGCTGCTTGCGCCGGCTGTGTGCCCAAGGCTCTGGGGC	1492
QY	1441	TCCAGGACACAACGAGCGCCGCTTCTCAGGAACACCAAGAACTCATCTCCCTGGGGAAG	1500
Db	1493	TCCAGGACACAACGAGCGCCGCTTCTCAGGAACACCAAGAACTCATCTCCCTGGGGAAG	1552
QY	1501	CATGCCAAGCTCTCGCTGCAGAGACTGAAGTGAAGATGAGCGTCCGGGACTGCGCTTGG	1560
Db	1553	CATGCCAAGCTCTCGCTGCAGAGACTGAAGTGAAGATGAGCGTCCGGGACTGCGCTTGG	1612
QY	1561	CTGCGCAGGAGGCCAAGGGTGTGTGTTCGGGCCAGAGACCGTCTGCGTGAAGAG	1620
Db	1613	CTGCGCAGGAGGCCAAGGGTGTGTGTTCGGGCCAGAGACCGTCTGCGTGAAGAG	1672
QY	1621	ATCCTGGCCAAAGTTCCTGCACTGCTGATGAGTGTGTACGTCTGTCAAGCTGCTCAGGTCT	1680
Db	1673	ATCCTGGCCAAAGTTCCTGCACTGCTGATGAGTGTGTACGTCTGTCAAGCTGCTCAGGTCT	1732

QY	1681	TTCTTTTATGTCAACGGAGACCAACGTTTCAAAGAACAAGGCTCTTTTCTACCGGAAGAGT	1740
Db	1733	TTCTTTTATGTCAACGGAGACCAACGTTTCAAAGAACAAGGCTCTTTTCTACCGGAAGAGT	1792
QY	1741	GTCTGGAGCAAGTTGCCAAGAAGCATTTGGAATCACAAGCACTTGAAGAGGGTGACGTCCG	1800
Db	1793	GTCTGGAGCAAGTTGCCAAGAAGCATTTGGAATCACAAGCACTTGAAGAGGGTGACGTCCG	1852
QY	1801	GAGCTGTCCGAGAGAGAGGTCAGGCAGCATCGGGAAAGCCAGGCCCGCCCTGCTGACGTCC	1860
Db	1853	GAGCTGTCCGAGAGAGAGGTCAGGCAGCATCGGGAAAGCCAGGCCCGCCCTGCTGACGTCC	1912
QY	1861	AGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGSACTACGTC	1920
Db	1913	AGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGSACTACGTC	1972
QY	1921	GTEGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAG	1980
Db	1973	GTEGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAG	2032
QY	1981	GCACTGTTACGCTGCTCAACTACGACGGGCGCGGCCCGCCCTCCTGGGCGCCTCT	2040
Db	2033	GCACTGTTACGCTGCTCAACTACGACGGGCGCGGCCCGCCCTCCTGGGCGCCTCT	2092
QY	2041	GTGCTGGGCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCC	2100
Db	2093	GTGCTGGGCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCTGTGCGGGCC	2152
QY	2101	CAGGACCCGCGCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACC	2160
Db	2153	CAGGACCCGCGCCTGAGCTGTACTTTGTCAAGTGGATGTGACGGGCGCGTACGACACC	2212
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Db	2213	ATCCCCCAGAGACAGGCTCACGGAGGTCAATCGCCAGCATCATCAAACCCCAAGAACGTAAC	2272
QY	2221	TGCGTGCCTCGGTATGCGGTGTGTCCAGAAAGGCCGCCCATGGGCAAGTCCGCAAGGCTTC	2280
Db	2273	TGCGTGCCTCGGTATGCGGTGTGTCCAGAAAGGCCGCCCATGGGCAAGTCCGCAAGGCTTC	2332
QY	2281	AAGAGCCAAGTCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAATTGCTGGCTCAC	2340
Db	2333	AAGAGCCAAGTCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAATTGCTGGCTCAC	2392
QY	2341	CTGCAGGAGACCAAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCTCCCTGAAT	2400
Db	2393	CTGCAGGAGACCAAGCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCTCTCCCTGAAT	2452
QY	2401	GAGGCCAGCAGTGGCTCTTCGACGCTTCCTTACGCTTCACTCATGTGACCAACAGCCGTGCGC	2460
Db	2453	GAGGCCAGCAGTGGCTCTTCGACGCTTCCTTACGCTTCACTCATGTGACCAACAGCCGTGCGC	2512
QY	2461	ATCAGGGGCAAGTCTTACGTCAGTGCCAGTGCCAGGGGATCCCGAGGGCTCCATCTCTCCACG	2520
Db	2513	ATCAGGGGCAAGTCTTACGTCAGTGCCAGTGCCAGGGGATCCCGAGGGCTCCATCTCTCCACG	2572
QY	2521	CTGCTCTGACGCTGTGCTACGCGGACATGAGAACAAGCTGTTTTCGGGGGATTCGGCGG	2580
Db	2573	CTGCTCTGACGCTGTGCTACGCGGACATGAGAACAAGCTGTTTTCGGGGGATTCGGCGG	2632
QY	2581	GACGGGCTGCTCTGCGGTTTGGTGATGATTTCTTGTGTGACACCTCACTCACCCAC	2640
Db	2633	GACGGGCTGCTCTGCGGTTTGGTGATGATTTCTTGTGTGACACCTCACTCACCCAC	2692
QY	2641	GCGAAAACCTTCTCAGGACCCCTGTCCGAGGTTGTCCTGAGTATGGCTGCGTGTGAAC	2700
Db	2693	GCGAAAACCTTCTCAGGACCCCTGTCCGAGGTTGTCCTGAGTATGGCTGCGTGTGAAC	2752
QY	2701	TTGCGGAGAGACAGTGGTGAACCTTCCCTGTAGAGAAGAGGCGCCCTGGGTGCAACGGCTTTT	2760
Db	2753	TTGCGGAGAGACAGTGGTGAACCTTCCCTGTAGAGAAGAGGCGCCCTGGGTGCAACGGCTTTT	2812
QY	2761	GTTACAGATCCCGGCCCAAGGCTATTCCCTGTGTGCGGCTGTGCTGTGAATACCCGGAAC	2820

Db 2813 GTTCAGATGCGGCGCCACGCGCTATTCCTCCCTGTGCGGCTGTGCTGATACCCGACCC 2872
QY 2821 CTGAGGTGACAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAC 2880
Db 2873 CTGAGGTGACAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGCGGCTTCAAGGCTGGAGAACATGCGTCCAACTCTTTGGGCTTTGCGG 2940
Db 2933 TTCAACCGCGGCTTCAAGGCTGGAGAACATGCGTCCAACTCTTTGGGCTTTGCGG 2992
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Db 2993 CTGAAGTGTACAGCGCTGTCTTCTGATTTGCAAGTGAACAGCGCTCCAGACGCTGTCAC 3052
QY 3001 AACATCTACAGATCTCTCTGCTGACGCGGTACAGGTTTCAAGCATGTGTGCTGACGCTC 3060
Db 3053 AACATCTACAGATCTCTCTGCTGACGCGGTACAGGTTTCAAGCATGTGTGCTGACGCTC 3112
QY 3061 CCATTTCATCAGCAAGTTTGAAGAACCCCAATTCTTCTGCGGTCTCTGACAGC 3120
Db 3113 CCATTTCATCAGCAAGTTTGAAGAACCCCAATTCTTCTGCGGTCTCTGACAGC 3172
QY 3121 GCCTCCCTCTGCTACTCTCATCTGAAAGCAAGACGACGAGGATGTGCTGGGGGCCAAG 3180
Db 3173 GCCTCCCTCTGCTACTCTCATCTGAAAGCAAGACGACGAGGATGTGCTGGGGGCCAAG 3232
QY 3181 GGGCGCGCGCGCTCTGCGCTCCGAGGCGGTGACGTGGCTGTGTCACCAAGCATCTCTG 3240
Db 3233 GGGCGCGCGCGCTCTGCGCTCCGAGGCGGTGACGTGGCTGTGTCACCAAGCATCTCTG 3292
QY 3241 CTCAAGCTGACTGACACACCGGTGTCACCTGACCTCTGCGGTCTACTCAGACAGCC 3300
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QY 3301 CAGACGAGCTGAGTGGAGAGCTCCCGGGAGACGACGCTGACCTGCGCTGGAGCGCGACCC 3360
Db 3353 CAGACGAGCTGAGTGGAGAGCTCCCGGGAGACGACGCTGACCTGCGCTGGAGCGCGACCC 3412
QY 3361 AACCCGCGACTGCGCTCAGACTTCAAGACCATCTGACTGATGAGCCACCC 3411
Db 3413 AACCCGCGACTGCGCTCAGACTTCAAGACCATCTGACTGATGAGCCACCC 3463

RESULT 8
US-10-054-611-224
; Sequence 224, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1 Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
/note= "human telomerase reverse
transcriptase (hTERT) catalytic protein
component"
; SEQUENCE DESCRIPTION: SEQ ID NO: 224:
US-10-054-611-224
Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGATGCGCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGC 60
Db 53 GCGATGCGCGCGCTCCCGCTGCGGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGC 112
QY 61 GAGTGTGCGCGCTGCGCAGCTTGTGCGCGCGCTGCGCGCGCGCGCGCGCTGCG 120
Db 113 GAGTGTGCGCGCTGCGCAGCTTGTGCGCGCGCTGCGCGCGCGCGCGCGCTGCG 172
QY 121 CAGCGCGCGCGCGCGCGCTTCCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCG 180
Db 173 CAGCGCGCGCGCGCGCGCTTCCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCG 232
QY 181 TGGAGCGACG 240
Db 233 TGGAGCGACG 292
QY 241 CTGTGCGCGCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 300
Db 293 CTGTGCGCGCGAGTGTGACAGAGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCG 352
QY 301 GCGTTCGCGCTGTGACG 360
Db 353 GCGTTCGCGCTGTGACG 412
QY 361 CGCAGCTACTGCGCGCAACACAGGTGACGACGCACTGCGCGCGCGCGCGCGCGCGCG 420
Db 413 CGCAGCTACTGCGCGCAACACAGGTGACGACGCACTGCGCGCGCGCGCGCGCGCGCG 472
QY 421 CTGTGCGCGCGGTGCGCGACGACGCTGTGTTCACTGCTGCGACGCTGCGCGCTTT 480
Db 473 CTGTGCGCGCGGTGCGCGACGACGCTGTGTTCACTGCTGCGACGCTGCGCGCTTT 532
QY 481 GTGCTGTGCTCCAGCTGCGCTTACAGGTGTGCGCGCGCGCGCGCGCGCTGTAC 540
Db 533 GTGCTGTGCTCCAGCTGCGCTTACAGGTGTGCGCGCGCGCGCGCGCTGTAC 592

QY	541	GCTGCCACTCAGGCCCCCGCCCCCGCCACACGCTAGTGGACCCCGGAAGCGTCTGGATGC	600
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QY	601	GAACGGGCTTGGAACTATAGCGTCAAGGAGGCCCGGGGTCCCCCTGGGGCTTCCAGCCCCG	660
Db	653	GAACGGGCTTGGAACTATAGCGTCAAGGAGGCCCGGGGTCCCCCTGGGGCTTCCAGCCCCG	712
QY	661	GGTGGAGAGGAGCGCGGGGGGSCAGTGGCCAGCCGGAAGTCTGCCGTTGCCCAAGAGGCCAAG	720
Db	713	GGTGGAGAGGAGCGCGGGGGGSCAGTGGCCAGCCGGAAGTCTGCCGTTGCCCAAGAGGCCAAG	772
QY	721	CGTGGCGCTGCCCTTGAAGCCCGAGCCGAGCCGCCGTTGGGCAAGGGTCTGGGGCCACCCG	780
Db	773	CGTGGCGCTGCCCTTGAAGCCCGAGCCGAGCCGCCGTTGGGCAAGGGTCTGGGGCCACCCG	832
QY	781	GGCAGGACCGCTGGACCCGAGTGAACCGTGGTTTCTGTGTGTGTCACTGGCCAGACCCGCC	840
Db	833	GGCAGGACCGCTGGACCCGAGTGAACCGTGGTTTCTGTGTGTGTCACTGGCCAGACCCGCC	892
QY	841	GAAGAAGCCACTCTTTTGGAGGGTGGCTCTCTGGCAGCGGCCACTGCCACCCATCCGTG	900
Db	893	GAAGAAGCCACTCTTTTGGAGGGTGGCTCTCTGGCAGCGGCCACTGCCACCCATCCGTG	952
QY	901	GGCGCCAGCACCAACGCGGGCCCCCATCCATCCATCGCGGCCACCAAGTCCCTGGGACACG	960
Db	953	GGCGCCAGCACCAACGCGGGCCCCCATCCATCCATCGCGGCCACCAAGTCCCTGGGACACG	1012
QY	961	CCTGTCCCCCGGTGTACCGCCGAGACCAAGCACTTCCCTCTACTCTCTCAGGCGACAAGAG	1020
Db	1013	CCTGTCCCCCGGTGTACCGCCGAGACCAAGCACTTCCCTCTACTCTCTCAGGCGACAAGAG	1072
QY	1021	CAGCTGCGGCTCTCTCTCTACTCAAGTCTCTGAGGCCAGCTGAAGTGGCGCTGGAGG	1080
Db	1073	CAGCTGCGGCTCTCTCTCTACTCAAGTCTCTGAGGCCAGCTGAAGTGGCGCTGGAGG	1132
QY	1081	CTCGTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTG	1140
Db	1133	CTCGTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTG	1192
QY	1141	CCCCGCTGCCCCAGCGCTACTGSCAAATGCGGCCCTGTCTTCTGAGCTGCTTGGAAAC	1200
Db	1193	CCCCGCTGCCCCAGCGCTACTGSCAAATGCGGCCCTGTCTTCTGAGCTGCTTGGAAAC	1252
QY	1201	CACGCGAGTGGCCCTACGGGGTCTCTCAAGACGACATGCCCGCTGCGAGCTGCGGTG	1260
Db	1253	CACGCGAGTGGCCCTACGGGGTCTCTCAAGACGACATGCCCGCTGCGAGCTGCGGTG	1312
QY	1261	ACCCAGCAGCGGTGTCTGTGCCGGGAGAGGCCCAAGGCTCTGTGGCGGGCCCCGAG	1320
Db	1313	ACCCAGCAGCGGTGTCTGTGCCGGGAGAGGCCCAAGGCTCTGTGGCGGGCCCCGAG	1372
QY	1321	GAGGAGGACACAGACCCCGCTGCTGTGACGCTGCTCCGACGACACAGCAGCCCTTG	1380
Db	1373	GAGGAGGACACAGACCCCGCTGCTGTGACGCTGCTCCGACGACACAGCAGCCCTTG	1432
QY	1381	CAGGTGTACGGCTTCTGTGCCGGCTGCTGCGCGGGCTGTGCCCCCAAGGCTCTGGGGC	1440
Db	1433	CAGGTGTACGGCTTCTGTGCCGGCTGCTGCGCGGGCTGTGCCCCCAAGGCTCTGGGGC	1492
QY	1441	TCCAGGACACAAGACGCGCTTCTCAGGAACCAAGAAATTCTCTCCCTGGGGAAG	1500
Db	1493	TCCAGGACACAAGACGCGCTTCTCAGGAACCAAGAAATTCTCTCCCTGGGGAAG	1552
QY	1501	CATGCCAAGCTCTCGCTGCAAGAGCTGACGTGGAAGATGAAGCTGGGGACTGCCCTTG	1560
Db	1553	CATGCCAAGCTCTCGCTGCAAGAGCTGACGTGGAAGATGAAGCTGGGGACTGCCCTTG	1612
QY	1561	CTGCGCAGGAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCTGAGAG	1620
Db	1613	CTGCGCAGGAGCCCAAGGGTTGGCTGTGTTCCGGCCGACAGACACCGTCTGCTGAGAG	1672

QY	1621	ATCCTGGCCAAAGTTCCCTGCACTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTCT	1680
Db	1673	ATCCTGGCCAAAGTTCCCTGCACTGGCTGATGAGTGTGTACGTGTCGAGCTGCTCAGGCTCT	1732
QY	1681	TTCTTTTATGTCAACGAGACCAACGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGT	1740
Db	1733	TTCTTTTATGTCAACGAGACCAACGTTTCAAAAAGAACAGGCTCTTTTCTACCGGAAGAGT	1792
QY	1741	GTCTGGAGCAAGTTGCAAAAGCATTTGGATTCAGACGCACTTGAAAGAGGGTGCAGCTCCGG	1800
Db	1793	GTCTGGAGCAAGTTGCAAAAGCATTTGGATTCAGACGCACTTGAAAGAGGGTGCAGCTCCGG	1852
QY	1801	GAGCTGTCCGGAAGCAAGAGTCAAGGACGATCCGGGAAGCCAGGCCCCGCTGCTGACGTCC	1860
Db	1853	GAGCTGTCCGGAAGCAAGAGTCAAGGACGATCCGGGAAGCCAGGCCCCGCTGCTGACGTCC	1912
QY	1861	AGACTCCGCTTCATCCCCCAAGCCTGACGGGCTCCGGCCGATTTGTGAACATGGACTACGTC	1920
Db	1913	AGACTCCGCTTCATCCCCCAAGCCTGACGGGCTCCGGCCGATTTGTGAACATGGACTACGTC	1972
QY	1921	GTGGGAAGCCAGAACGTTCCCGCAGAGAAAAGAGGGCCGAGCGCTCACTCCAGAGGTGAAG	1980
Db	1973	GTGGGAAGCCAGAACGTTCCCGCAGAGAAAAGAGGGCCGAGCGCTCACTCCAGAGGTGAAG	2032
QY	1981	GCACTGTTCAGCGCTGCTCAACTACGAGCGGGCCGGCGCCCCGCTCCTGGGCGCCTCT	2040
Db	2033	GCACTGTTCAGCGCTGCTCAACTACGAGCGGGCCGGCGCCCCGCTCCTGGGCGCCTCT	2092
QY	2041	GTGCTGGGCTTGAGACGATATCCACAGGGCCCTGGCGCACCTTCGTGCTGCTGTGCGGGCC	2100
Db	2093	GTGCTGGGCTTGAGACGATATCCACAGGGCCCTGGCGCACCTTCGTGCTGCTGTGCGGGCC	2152
QY	2101	CAGGACCCGCGCCTGAGCTGTACTTTGTTCAGAGTGGATGTGAACGGGCGCGCTACGACACC	2160
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QY	2161	ATCCCCCAGGACAGGCTCACGGAGGTCAATCCGCCAGCATCATCAAAACCCCAAGAACACGTAC	2220
Db	2213	ATCCCCCAGGACAGGCTCACGGAGGTCAATCCGCCAGCATCATCAAAACCCCAAGAACACGTAC	2272
QY	2221	TGCGTGCGTCCGATATGCCGTGTGTCCAGAAAGCCGCCATATGGGCAACGTCCGCAAGCCCTTC	2280
Db	2273	TGCGTGCGTCCGATATGCCGTGTGTCCAGAAAGCCGCCATATGGGCAACGTCCGCAAGCCCTTC	2332
QY	2281	AAGAGCCACGCTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGGCTCAC	2340
Db	2333	AAGAGCCACGCTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCTGGCTCAC	2392
QY	2341	CTGCAGGAGACCAAGCCCCGCTGAGGGATGCCGTGCTCATCGACAGAGCTCTCCCTGAAT	2400
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QY	2461	ATCAGGGGCAAGTCTTAAGTCCAGTCCCAAGGGAGATCCCCGACAGGCTCCATCTCTCCACG	2520
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QY	2521	CTGCTCTGCAGCCTGTGCTACGGCGACATGAGAAACAAGCTGTTTGGCGGGGATTCGGCGG	2580
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QY	2581	GACGGGCTGCTCTGCGTTTGGTGGATGATTTCTTGTGGTGACACTCACTCAACCCAC	2640
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QY	2641	GCGAAAACCTTCTCAGGAACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAAC	2700
Db	2693	GCGAAAACCTTCTCAGGAACCCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGTGAAC	2752
QY	2701	TTGCCGAAGACAGTGTGTAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGACACGGCTTTT	2760

Db 2753 TTGCGGAGACAGTGTGAACCTTCCCTGTGAAGACGAGGCCCTGGGTGGACCGCTTTT 2812
QY 2761 GTTCAGATGCGGCGCCACGGCCCTATTCCCTGTGTGGCGCTGTGTGATACCCGAC 2820
Db 2813 GTTCAGATGCGGCGCCACGGCCCTATTCCCTGTGTGGCGCTGTGTGATACCCGAC 2872
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QY 3361 AACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3411
Db 3413 AACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3463

RESULT 9

US-10-105-963-1

; Sequence 1, Application US/10105963

; Publication No. US2003006818A1

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

; APPLICANT: Deming, Chris

; APPLICANT: Clark, A. John

; APPLICANT: Schiff, J. Michael

; TITLE OF INVENTION: Animal Tissue with Carbohydrate Antigens Compatible for Human

; TITLE OF INVENTION: Transplantation and a Carbohydrate Determinant Selection System

; TITLE OF INVENTION: Recombination

; FILE REFERENCE: 731/002

; CURRENT APPLICATION NUMBER: US/10/105,963

; CURRENT FILING DATE: 2002-03-21

; PRIOR APPLICATION NUMBER: US 60/277,811

; PRIOR FILING DATE: 2001-03-21

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: Patent version 3.1

; SEQ ID NO 1

; LENGTH: 4015

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

LOCATION: (56) .. (3454)
OTHER INFORMATION:
US-10-105-963-1

Query Match 100.0%; Score 3411; DB 14; Length 4015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 113 GAGGTGCTGCGCTGCGGAGCGGTGCGGAGCGGTGCGGAGCGGTGCGGAGCGGTG 172
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Db 173 CAGCGCGGAGCGCGCGCGCTTCCGCGCGCTGCTGCGGAGCGGTGCGGAGCGGTG 232
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QY 781 GGCAGGAGCGGTGAGCGGAGTACCGTGTGTTCTGTGTGTGTGTGTGTGTGTGTGT 840
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QY 841 GAAGAAGCACTCTTTGAGGAGGCGCTCTCTGCGACGCGCGCACTCCACCATCCGTG 900
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QY 2041 GTGCTGGCCTGACGATATCCACAGGGCTGCGCACTTCTGCTGCTGTGCGGCGC 2100

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QY	961	CCTTGTCCTCCCGGTGTACCGCCGAGACCAAGCACTTCTCTACTCTCAGGCGACAAGAG	1020
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Db	1133	CTCGTGAGAACCATCTTTCTGGGTTCCAGGCCCTGATGCCAGGACTCCCGCAGGTTG	1192
QY	1141	CCCCGCTGCCCCAGCGCTACTGCGAATGCGGCCCTGTTCTGAGCTGCTTGGGAAC	1200
Db	1193	CCCCGCTGCCCCAGCGCTACTGCGAATGCGGCCCTGTTCTGAGCTGCTTGGGAAC	1252
QY	1201	CACGCGCAGTGCCCCCTACGGGTTGCTCCTCAGACGCACCTGCCGCTGCCAGCTGCCGT	1260
Db	1253	CACGCGCAGTGCCCCCTACGGGTTGCTCCTCAGACGCACCTGCCGCTGCCAGCTGCCGT	1312
QY	1261	ACCCCAAGCAGCCGGTGTCTGTGCCCCGGAGAAAGCCCCAGGGCTCTGTGGCGCCCCGAG	1320
Db	1313	ACCCCAAGCAGCCGGTGTCTGTGCCCCGGAGAAAGCCCCAGGGCTCTGTGGCGCCCCGAG	1372
QY	1321	GAGGAGGACACAGACCCCCCGTGCCTGTGTGACAGCTGCTCCGCGACACACAGACGCCCTTG	1380
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QY	1381	CAGGTGTACGGCTTCTGTGCGGGCTGCCTGCGCGGCTGTGTGCCCCCAGGCTCTGGGGC	1440
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QY	1441	TCCAGGCAACAAGAACGCGCTTCTCAGGAACACCAAGATTCACTCCCTGGGGAAG	1500
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RESULT 11

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TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.30

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4015 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 56..3454
OTHER INFORMATION: /product= "hTERT"
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transcriptase (hTERT) catalytic protein
component"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-044-539-1

Query Match 100.0%; Score 3411; DB 14; Length 4015;

Best Local Similarity 100.0%; Pred. No. 0; Matches 3411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1681 TTCTTTTATGTACGAGAGACCAAGTTTCAAAAGACAGGCTTTTCTACCGGAAGAGT 1740
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QY 1741 GTCTGAGCAGAGTTGCAAGCATTGGAATCAGACAGCACTTGAAGAGGCTGACGTCGG 1800
Db 1793 GTCTGAGCAGAGTTGCAAGCATTGGAATCAGACAGCACTTGAAGAGGCTGACGTCGG 1852

QY 1801 GAGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCTCTGACGTCC 1860
Db 1853 GAGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCTCTGACGTCC 1912
QY 1861 AGACTCCGCTTATCCCAAGCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTG 1920
Db 1913 AGACTCCGCTTATCCCAAGCTGACGGGCTGCGGCCGATTTGTGAACATGACTACGTG 1972
QY 1921 GTGGAGCCAGAAAGTTCGCGCAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAG 1980
Db 1973 GTGGAGCCAGAAAGTTCGCGCAGAAAGAGGGCCGAGCGTCTCACTCGAGGGTGAAG 2032
QY 1981 GCACTGTTCAAGCTGTCTCACTCAAGCGGGCGCGGCCCGCTCTCTGGGCGCTCT 2040
Db 2033 GCACTGTTCAAGCTGTCTCACTCAAGCGGGCGCGGCCCGCTCTCTGGGCGCTCT 2092
QY 2041 GTGCTGGGCTGGAACGATATCCACAGGGCTTGCGGCACTTCTGCTGCTGTGCGGCGC 2100
Db 2093 GTGCTGGGCTGGAACGATATCCACAGGGCTTGCGGCACTTCTGCTGCTGTGCGGCGC 2152
QY 2101 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGCGGCGCTACGACACC 2160
Db 2153 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGCGGCGCTACGACACC 2212
QY 2161 ATCCCCAGCAAGGCTCAAGGAGTCAATGCGGACGATCAAAACCCAGAAACAGTAC 2220
Db 2213 ATCCCCAGCAAGGCTCAAGGAGTCAATGCGGAGTCAATCAAAACCCAGAAACAGTAC 2272
QY 2221 TGCGTGGCTGGTATGCGCTGTGTCCAGAAAGCCGCCATGGGCAAGTCCGCAAGGCTTC 2280
Db 2273 TGCGTGGCTGGTATGCGCTGTGTCCAGAAAGCCGCCATGGGCAAGTCCGCAAGGCTTC 2332
QY 2281 AAGAGCCAGTCTTACTACTTGAAGACCTCCAGCCGTTACATGCGACAGTTCGTGGCTAC 2340
Db 2333 AAGAGCCAGTCTTACTACTTGAAGACCTCCAGCCGTTACATGCGACAGTTCGTGGCTAC 2392
QY 2341 CTGCAAGAGACCAAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCTCTCTGAAT 2400
Db 2393 CTGCAAGAGACCAAGCCCGCTGAGGAGTGCCTGCTCATGAGCAGAGCTCTCTCTGAAT 2452
QY 2401 GAGGCAAGAGTGGCTCTTTCAGAGTCTTCTCAAGCTTCAATGTGCCACCAAGCCGTGGC 2460
Db 2453 GAGGCAAGAGTGGCTCTTTCAGAGTCTTCTCAAGCTTCAATGTGCCACCAAGCCGTGGC 2512
QY 2461 ATCAGGGCAAGTCTTACTAGTGCAGGAGTCCCGAGGGCTCCATCTCTCCACAG 2520
Db 2513 ATCAGGGCAAGTCTTACTAGTGCAGGAGTCCCGAGGGCTCCATCTCTCCACAG 2572
QY 2521 CTGCTGCAAGCTGTGTACGCGGACATGAGAAACAAGCTGTTGCGGGGATTCGGCGG 2580
Db 2573 CTGCTGCAAGCTGTGTGTACGCGGACATGAGAAACAAGCTGTTGCGGGGATTCGGCGG 2632
QY 2581 GACGGCTGCTCTGCGTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC 2640
Db 2633 GACGGCTGCTCTGCGTTGGTGTGATGATTTCTTGTGTGACACCTCACTCAACCCAC 2692
QY 2641 GCGAAACCTTCTCAGGACCTGTGTCGAGGTGCTCGAGTATGCGTGGTGAAC 2700
Db 2693 GCGAAACCTTCTCAGGACCTGTGTCGAGGTGCTCGAGTATGCGTGGTGAAC 2752
QY 2701 TTGCGGAGACAGTGTGTAATTCCTGTAGAAGACGAGGCCCTGGGTGCAAGGCTTTT 2760
Db 2753 TTGCGGAGACAGTGTGTAATTCCTGTAGAAGACGAGGCCCTGGGTGCAAGGCTTTT 2812
QY 2761 GTTCAAGTCCGCGCCACGCGCTATTCCTGTGTGCGGCTGCTGTGATACCCGAGC 2820
Db 2813 GTTCAAGTCCGCGCCACGCGCTATTCCTGTGTGCGGCTGCTGTGATACCCGAGC 2872
QY 2821 CTGAGGTGACAGGCACTTCCAGCTATGCGCGGACCTTCATCAGAGCCAGTCTCAC 2880
Db 2873 CTGAGGTGACAGGCACTTCCAGCTATGCGCGGACCTTCATCAGAGCCAGTCTCAC 2932
QY 2881 TTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCTGCAAACTCTTTGGGCTTGGCG 2940

Db 2933 TTCAACCGCGCTTCAAGGCTGGAGGAACATGCGCAACTCTTGGGGTCTTGCGG 2992
QY 2941 CTGAAGTGTACAGCGCTGTTCTTGATTTGAGGTGAACAGCGCTCCAGACGCTGTGACAC 3000
Db 2993 CTGAAGTGTACAGCGCTGTTCTTGATTTGAGGTGAACAGCGCTCCAGACGCTGTGACAC 3052
QY 3001 AACATCTACAGATCTCTCTGCTGAGAGCGTACAGTTTCAAGCATGTGTGTCAGCTC 3060
Db 3053 AACATCTACAGATCTCTCTGCTGAGAGCGTACAGTTTCAAGCATGTGTGTCAGCTC 3112
QY 3061 CCATTTCATCAGCAAGTTTGAAGAACCACCAATTTTCTCTGCGGCTATCTTGACACG 3120
Db 3113 CCATTTCATCAGCAAGTTTGAAGAACCACCAATTTTCTCTGCGGCTATCTTGACACG 3172
QY 3121 GCCTCCCTCTGCTACTCCATCTGAAAGCCAGAAACGAGGATGTGCTGGGGCCAG 3180
Db 3173 GCCTCCCTCTGCTACTCCATCTGAAAGCCAGAAACGAGGATGTGCTGGGGCCAG 3232
QY 3181 GGGCGCGCGCGCGCTGCTGCTCCGAGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTG 3240
Db 3233 GGGCGCGCGCGCGCTGCTGCTCCGAGCGCGTGCAGTGGCTGTGCCACCAAGCATTCCTG 3292
QY 3241 CTCAAGCTGACTCGACACCGGTGTACCTACGTGCCACTCTCTGGGGTCACTCAGAGACAGCC 3300
Db 3293 CTCAAGCTGACTCGACACCGGTGTACCTACGTGCCACTCTCTGGGGTCACTCAGAGACAGCC 3352
QY 3301 CAGACGAGCTGAGTGGAGAGCTCCCGGGGAGAGCGCTGACTGCTGGAAGCGCGCAGCC 3360
Db 3353 CAGACGAGCTGAGTGGAGAGCTCCCGGGGAGAGCGCTGACTGCTGGAAGCGCGCAGCC 3412
QY 3361 AACCCGCGACTGCGCTCAGACTTCAAGACCATCTGTGACTGATGAGCCACCC 3411
Db 3413 AACCCGCGACTGCGCTCAGACTTCAAGACCATCTGTGACTGATGAGCCACCC 3463

RESULT 12
US-10-385-882-1
; Sequence 1, Application US/10385882
; Publication No. US20030232409A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF MINNESOTA
; APPLICANT: FARIS, James
; APPLICANT: FOSTER, Douglas
; APPLICANT: O'GRADY, Scott
; TITLE OF INVENTION: IMMORTAL PORCINE CELLS
; FILE REFERENCE: 110.01700101
; CURRENT APPLICATION NUMBER: US/10/385,882
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 60/363,129
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 4027
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding telomerase reverse transcriptase
US-10-385-882-1

Query Match 99.9%; Score 3407.8; DB 15; Length 4027;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3409; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGATGCGCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCCG 60
Db 54 GCGATGCGCGCGCTCCCGCTGCGAGCGGTGCGCTCCCTGCTGCGCAGCCACTACCCG 113
QY 61 GAGGTGCTGCGCGCTGCGCAGCTTCTGCGGGCGCGCTGCGGGCCAGAGGCTGCGGGCTGTG 120
Db 114 GAGGTGCTGCGCGCTGCGCAGCTTCTGCGGGCGCGCTGCGGGCCAGAGGCTGCGGGCTGTG 173

QY 121 CAGCGCGGGGACCCCGCGGCTTTCCGCGCGCTGTGCGCCAGTGACCTGTGCTGCGCC 180
Db 174 CAGCGCGGGGACCCCGCGGCTTTCCGCGCGCTGTGCGCCAGTGACCTGTGCTGCGCC 233
QY 181 TGGAGCAGCAGCG 240
Db 234 TGGAGCAGCAGCG 293
QY 241 CTGTGCGCGCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 294 CTGTGCGCGCGAGTGTGAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 353
QY 301 GCGTTGCGCGCTGTGAGCG 360
Db 354 GCGTTGCGCGCTGTGAGCG 413
QY 361 CGCAGCTACTGCGCCCAACAGGTGACCGAGCGACTGCGGGGAGCGGGCGGTGGGGCTG 420
Db 414 CGCAGCTACTGCGCCCAACAGGTGACCGAGCGACTGCGGGGAGCGGGCGGTGGGGCTG 473
QY 421 CTGCTGCGCGCGGTGGCGAGCAGCGTGTGTTCACTGCTGCGCAGCTGCGCGCTTT 480
Db 474 CTGCTGCGCGCGGTGGCGAGCAGCGTGTGTTCACTGCTGCGCAGCTGCGCGCTTT 533
QY 481 GTGCTGTGCTGCCAGCTGCGCGCTACCGAGTGTGCGGGCGCGCGCGCGCGCGCGCG 540
Db 534 GTGCTGTGCTGCCAGCTGCGCGCTACCGAGTGTGCGGGCGCGCGCGCGCGCGCGCG 593
QY 541 GCTGCCACTCAGGCG 600
Db 594 GCTGCCACTCAGGCG 653
QY 601 GAAAGGCGCTGGAACCATAGCGTACGAGAGCGCGGGTCCCTGCGCGCTGCGAGCCCG 660
Db 654 GAAAGGCGCTGGAACCATAGCGTACGAGAGCGCGGGTCCCTGCGCGCTGCGAGCCCG 713
QY 661 GGTGCGAGGAGCG 720
Db 714 GGTGCGAGGAGCG 773
QY 721 CGTGCGCGCTGCGCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 774 CGTGCGCGCTGCGCGCTGAGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 833
QY 781 GGCAGGACCGGTGAGCCGAGTACCGGTGTTCTGTGTGTGTCACCTGCGAGACCGCG 840
Db 834 GGCAGGACCGGTGAGCCGAGTACCGGTGTTCTGTGTGTGTCACCTGCGAGACCGCG 893
QY 841 GAAGAAGCAGCTTTTGAAGGCTGCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 894 GAAGAAGCAGCTTTTGAAGGCTGCTCTGCGACGCGCGCGCGCGCGCGCGCGCGCGCG 953
QY 901 GGCAGGACGAGCAGCG 960
Db 954 GGCAGGACGAGCAGCG 1013
QY 961 CCTGTCCCGCGGTGACGCGCGAGCAGCAAGCACTTCTCTACTCTCTCAAGCGACAAGAG 1020
Db 1014 CCTGTCCCGCGGTGACGCGCGAGCAGCAAGCACTTCTCTACTCTCTCAAGCGACAAGAG 1073
QY 1021 CAGCTGCGCGCGCTCTCTCTACTCTCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1074 CAGCTGCGCGCGCTCTCTCTACTCTCTCTGAGGCGCGCGCGCGCGCGCGCGCGCGCG 1133
QY 1081 CTGTGAGAGCACTTTCTGTGGTTCAAGCGCGCTGATGCGAGGAACTCCCGCAGGTG 1140
Db 1134 CTGTGAGAGCACTTTCTGTGGTTCAAGCGCGCTGATGCGAGGAACTCCCGCAGGTG 1193
QY 1141 CCGCGCTGCGCGCGCGCGCTACTGCGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
Db 1194 CCGCGCTGCGCGCGCGCGCGCTACTGCGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCG 1253
QY 1201 CAGCGAGTGCCTTACGCGGTGCTCTCAAGAGCAGCACTGCGCGCTGCGAGCTGCGGT 1260

Db 1254 CACGCGACGTGCTTACCGGGTGTCTCTCAAGACGACCTGCGCTGCGAGCTGGGCTC 1313
QY 1261 ACCCCAGACGCGGTGTGTGTGCCCCGAGAGAGCCCCAGGGCTGTGGCGGCCCCGAG 1320
Db 1314 ACCCCAGACGCGGTGTGTGTGCCCCGAGAGAGCCCCAGGGCTGTGGCGGCCCCGAG 1373
QY 1321 GAGGAGACACAGACCCCCGCTGCTGTGAGCTGTCTCCGACACAGACAGCCCCCTGG 1380
Db 1374 GAGGAGACACAGACCCCCGCTGCTGTGAGCTGTCTCCGACACAGACAGCCCCCTGG 1433
QY 1381 CAGGTGTACGCTTCTGTGCGGCGCTGCGCGCTGCGCGCTGTGCCCCCAGGCTCTGGGGC 1440
Db 1434 CAGGTGTACGCTTCTGTGCGGCGCTGCGCGCTGCGCGCTGTGCCCCCAGGCTCTGGGGC 1493
QY 1441 TCCAGGACACAGACCGCGCTTCTCTAGGAACACCAAGATTCTCTCCCTGGGGAAG 1500
Db 1494 TCCAGGACACAGACCGCGCTTCTCTAGGAACACCAAGATTCTCTCCCTGGGGAAG 1553
QY 1501 CATGCCAAGCTCTCGCTGACGAGAGCTGACGTGGAAAGATGAGCGTGGGGACTGCGCTTG 1560
Db 1554 CATGCCAAGCTCTCGCTGACGAGAGCTGACGTGGAAAGATGAGCGTGGGGACTGCGCTTG 1613
QY 1561 CTGCGCAGAGACCCAGGGGTGTGTGTCTCCGCGCAGACACCGCTCTGCTGTAGAGAG 1620
Db 1614 CTGCGCAGAGACCCAGGGGTGTGTGTCTCCGCGCAGACACCGCTCTGCTGTAGAGAG 1673
QY 1621 ATCTGCGCAAGTCTCTGACACTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1680
Db 1674 ATCTGCGCAAGTCTCTGACACTGCTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1733
QY 1681 TTCTTTTATGTCAACGAGACACCGTTTCAAAAGACAGGCTTTTCTACCGGAAGAT 1740
Db 1734 TTCTTTTATGTCAACGAGACACCGTTTCAAAAGACAGGCTTTTCTACCGGAAGAT 1793
QY 1741 GTCTGAGCAAGTGTCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGCAGTGGG 1800
Db 1794 GTCTGAGCAAGTGTCAAAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGCAGTGGG 1853
QY 1801 GAGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGCCCTGCTGACGTCC 1860
Db 1854 GAGCTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGCCCTGCTGACGTCC 1913
QY 1861 AGACTCCGCTTATCCCCAAGCCTGAAGGCTGCGGCGCAATTGTGAACATGACTACGTCC 1920
Db 1914 AGACTCCGCTTATCCCCAAGCCTGAAGGCTGCGGCGCAATTGTGAACATGACTACGTCC 1973
QY 1921 GTGAGCCAGAAAGTTCGCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAG 1980
Db 1974 GTGAGCCAGAAAGTTCGCGAGAGAAAGAGGGCCGAGCGTCTACCTCGAGGGTGAAG 2033
QY 1981 GCACCTGTGAGCGTGTCACTACGAGCGGGCGCGCGCGCGCTCTCTGCGGCGCTCT 2040
Db 2034 GCACCTGTGAGCGTGTCACTACGAGCGGGCGCGCGCGCGCTCTCTGCGGCGCTCT 2093
QY 2041 GTGCTGGGCTGGAAGATATCCACAGGGCTTGGCGCACTTCTGTGCTGTGTGGGGCC 2100
Db 2094 GTGCTGGGCTGGAAGATATCCACAGGGCTTGGCGCACTTCTGTGCTGTGTGGGGCC 2153
QY 2101 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGGCGCTACACACC 2160
Db 2154 CAGGACCCGCGCTGAGCTGTACTTTGTCAAGGTGATGTGAAGGGCGCTACACACC 2213
QY 2161 ATCCCCCAGACAGGCTCAAGGAGTCAATCGGACATCAAAACCCCAAGACAGTAC 2220
Db 2214 ATCCCCCAGACAGGCTCAAGGAGTCAATCGGACATCAAAACCCCAAGACAGTAC 2273
QY 2221 TGGCTGCGTGTATGCTGT 2280
Db 2274 TGGCTGCGTGTATGCTGT 2333
QY 2281 AAGAGCCAGCTCTTACCTTGAAGACCTCCAGCGCTACATGCGACAGTTCTGTGCTCAC 2340

Db 2334 AAGAGCCAGCTCTTACCTTGAAGACCTCCAGCGCTACATGCGACAGTTCTGTGCTCAC 2393
QY 2341 CTGACAGAGACACAGCCCGCTGAGGGATGCGGCTGTCTATCGACAGAGACTCTCTCTGAT 2400
Db 2394 CTGACAGAGACACAGCCCGCTGAGGGATGCGGCTGTCTATCGACAGAGACTCTCTCTGAT 2453
QY 2401 GAGGCCAGAGTGGCTCTTTCAGAGTCTTCTTCAAGCTTCTTCAAGCTTGTGCCACAGCCGCTGGC 2460
Db 2454 GAGGCCAGAGTGGCTCTTTCAGAGTCTTCTTCAAGCTTCTTCAAGCTTGTGCCACAGCCGCTGGC 2513
QY 2461 ATCAGGGGAGTCTTACCTTCAAGTCCAGTCCAGGGGATCCCGAGGGCTCCATCTCTCCAGC 2520
Db 2514 ATCAGGGGAGTCTTACCTTCAAGTCCAGTCCAGGGGATCCCGAGGGCTCCATCTCTCCAGC 2573
QY 2521 CTGCTCTGAGCCTGTGTCTACGCGGACATGAGAAACAGCTGTTTGGGGATTCGGCGG 2580
Db 2574 CTGCTCTGAGCCTGTGTCTACGCGGACATGAGAAACAGCTGTTTGGGGATTCGGCGG 2633
QY 2581 GACGGCTGCTCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACCTCACCCAC 2640
Db 2634 GACGGCTGCTCTGCGTTTGTGATGATTTCTTGTGTGACACCTCACCTCACCCAC 2693
QY 2641 GCGAAACCTTCTCAGACCTGTGTCCAGGTGTCCCTGAGTATGCTGCTGTGTGTGTGTGTGT 2700
Db 2694 GCGAAACCTTCTCAGACCTGTGTCCAGGTGTCCCTGAGTATGCTGCTGTGTGTGTGTGTGT 2753
QY 2701 TTGCGGAAGACAGTGTGAACTTCCCTGTAGAAGACAGGCGCTGGGTGCAAGGCTTTT 2760
Db 2754 TTGCGGAAGACAGTGTGAACTTCCCTGTAGAAGACAGGCGCTGGGTGCAAGGCTTTT 2813
QY 2761 GTTCAAGTCCGCGCCACCGGCTATTTCCCTGTGTGCGGCTGTGTGTGTGTGTGTGTGTGT 2820
Db 2814 GTTCAAGTCCGCGCCACCGGCTATTTCCCTGTGTGTGCGGCTGTGTGTGTGTGTGTGTGT 2873
QY 2821 CTGAGGTGAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCAC 2880
Db 2874 CTGAGGTGAGAGCGACTACTCCAGCTATGCCCCGGAACCTCCATCAGAGCCAGTCTCAC 2933
QY 2881 TTCAACCGCGGCTTCAAGGCTGGAGGAACATGCTCGCAACTCTTTGGGGCTTTGGCGG 2940
Db 2934 TTCAACCGCGGCTTCAAGGCTGGAGGAACATGCTCGCAACTCTTTGGGGCTTTGGCGG 2993
QY 2941 CTGAAGTGTCAAGCCTGTTTCTGGAATTTGCAAGTGAACAGCCTCCAGACGCTGTGCACC 3000
Db 2994 CTGAAGTGTCAAGCCTGTTTCTGGAATTTGCAAGTGAACAGCCTCCAGACGCTGTGCACC 3053
QY 3001 AACATCTACAGATCTCTCTGCTGCAAGGCTACAGGTTTCAAGCATGTGTGTGTGTGTGTGT 3060
Db 3054 AACATCTACAGATCTCTCTGCTGCAAGGCTACAGGTTTCAAGCATGTGTGTGTGTGTGTGT 3113
QY 3061 CCATTTTATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGTCTCTGACACG 3120
Db 3114 CCATTTTATCAGCAAGTTTGAAGAAACCCACATTTTCTGCGGTCTCTGACACG 3173
QY 3121 GCCTCTCTGCTACTCTCATCTGAAAGCCAAAGAACGAGGGATGTGCTGGGGGCCAAG 3180
Db 3174 GCCTCTCTGCTACTCTCATCTGAAAGCCAAAGAACGAGGGATGTGCTGGGGGCCAAG 3233
QY 3181 GCGCGCGCGGCTCTGCGCTTCCAGAGGCGGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3240
Db 3234 GCGCGCGCGGCTCTGCGCTTCCAGAGGCGGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3293
QY 3241 CTCAAGCTGACTGACACCGTGTCACTACGTGCGCACTCTGGGGTCACTCAGACAGCC 3300
Db 3294 CTCAAGCTGACTGACACCGTGTCACTACGTGCGCACTCTGGGGTCACTCAGACAGCC 3353
QY 3301 CAGACGAGCTGAGTGGAAAGTCCCGGGGACGACGCTGACTGCCCCGAGGCGCGAGCC 3360
Db 3354 CAGACGAGCTGAGTGGAAAGTCCCGGGGACGACGCTGACTGCCCCGAGGCGCGAGCC 3413
QY 3361 AACCGGACCTGCGCTCAGACTTCAAGACCATCTGAGCTGATGGCCACC 3411
Db 3414 AACCGGACCTGCGCTCAGACTTCAAGACCATCTGAGCTGATGGCCACC 3464

RESULT 13
US-10-205-629-1
; Sequence 1, Application US/10205629
; Publication No. US20030049236A1
; GENERAL INFORMATION:
; APPLICANT: Kassem, Moustapha
; APPLICANT: Jensen, Thomas
; APPLICANT: Rattan, Suresh
; TITLE OF INVENTION: Immortalized Stem Cells
; FILE REFERENCE: 006148.00002
; CURRENT APPLICATION NUMBER: US/10/205,629
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 60/315939
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: PA 2001 01148
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-629-1

Query Match 99.6%; Score 3397.6; DB 14; Length 3453;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3400; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGATGCCGCGCTCCCGCTGCGCGCGCTCCCTGCTGCGCGCGCTACCGCG 61
DB 8 CCATGCCGCGCTCCCGCTGCGCGCGCTCCCTGCTGCGCGCGCTACCGCG 67

QY 62 AGGTGCTGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCG 121
DB 68 AGGTGCTGCGCTGCGCGCGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCG 127

QY 122 AGCGCGCGCGCGCGCGCGCTTCCGCGCGCGCTGCGCGCGCGCGCGCGCG 181
DB 128 AGCGCGCGCGCGCGCGCGCTTCCGCGCGCGCTGCGCGCGCGCGCGCGCG 187

QY 182 GGGAGCGACG 241
DB 188 GGGAGCGACG 247

QY 242 TGGTGGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 301
DB 248 TGGTGGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307

QY 302 GCTTGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 361
DB 308 GCTTGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367

QY 362 GCAGCTACCTGCCCAACAGCGTGAACGCGCACTGCGGGGAGCGCGCGCGTGC 421
DB 368 GCAGCTACCTGCCCAACAGCGTGAACGCGCACTGCGGGGAGCGCGCGCGTGC 427

QY 422 TGGTGGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 481
DB 428 TGGTGGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487

QY 482 TGGTGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 541
DB 488 TGGTGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547

QY 542 CTGCCACTAGCG 601
DB 548 CTGCCACTAGCG 607

QY 602 AACGGGCTGGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 661
DB 608 AACGGGCTGGAACATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 667

QY 662 GTGCGAGAGCG 721
DB 668 GTGCGAGAGCG 727

QY 722 GTGCG 781
DB 728 GTGCG 787

QY 782 GCAGGACGCGTGAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 841
DB 788 GCAGGACGCGTGAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847

QY 842 AAGAGCCACCTCTTGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 901
DB 848 AAGAGCCACCTCTTGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 907

QY 902 GCCGCCAGCACCG 961
DB 908 GCCGCCAGCACCG 967

QY 962 CTTGTCCCGCGGTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1021
DB 968 CTTGTCCCGCGGTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027

QY 1022 AGCTGCG 1081
DB 1028 AGCTGCG 1087

QY 1082 TGGTGAAGACCATCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1141
DB 1088 TGGTGAAGACCATCTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1147

QY 1142 CCCG 1201
DB 1148 CCCG 1207

QY 1202 AGCGCAGTGCG 1261
DB 1208 AGCGCAGTGCG 1267

QY 1262 CCCAGCAGCG 1321
DB 1268 CCCAGCAGCG 1327

QY 1322 AGGAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1381
DB 1328 AGGAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1387

QY 1382 AGGTGTACG 1441
DB 1388 AGGTGTACG 1447

QY 1442 CCAAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1501
DB 1448 CCAAGGACACAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1507

QY 1502 ATGCCAAGCTCTGCG 1561
DB 1508 ATGCCAAGCTCTGCG 1567

QY 1562 TGGCAGAGAGCG 1621
DB 1568 TGGCAGAGAGCG 1627

QY 1622 TCCTGGCCAAAGTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1681
DB 1628 TCCTGGCCAAAGTTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1687

QY 1682 TCTTTATATGACGAGAGACCAAGTTCAAAAGAACAGAGCGCTCTTTTCTAACCG 1741
DB 1688 TCTTTATATGACGAGAGACCAAGTTCAAAAGAACAGAGCGCTCTTTTCTAACCG 1747

QY 1742 TCTGAGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGACGTGCGG 1801
Db 1748 TCTGAGCAAGTTGCAAGCATTTGAATCAGACAGCACTTGAAGAGGGTGACGTGCGG 1807
QY 1802 AGCTGTGGAAGAGAGAGTTCAGGAGCATTCGGGAAGCCAGGCCCCCTGTGACGTCCA 1861
Db 1808 AGCTGTGGAAGAGAGTTCAGGAGCATTCGGGAAGCCAGGCCCCCTGTGACGTCCA 1867
QY 1862 GACTCCGCTTCAATCCCCAAGCCTGACGGGCTGCGGCGATTGTGAACATGACTACGTG 1921
Db 1868 GACTCCGCTTCAATCCCCAAGCCTGACGGGCTGCGGCGATTGTGAACATGACTACGTG 1927
QY 1922 TGGAGCCAGAACGTTCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGTTGAAG 1981
Db 1928 TGGAGCCAGAACGTTCCGAGAGAAAGAGGGCCGAGCGTCTCACTCGAGGTTGAAG 1987
QY 1982 CACTGTTACGCTGCTCACTACGAGCGGGCGGGCGCCCCGCTCTGCGGCGCTCTG 2041
Db 1988 CACTGTTACGCTGCTCACTACGAGCGGGCGGGCGCCCCGCTCTGCGGCGCTCTG 2047
QY 2042 TGCTGGGCTTGAAGATATCCACAGGCGCTGCGCACCTTCTGCTGCTGCTGCGGCGG 2101
Db 2048 TGCTGGGCTTGAAGATATCCACAGGCGCTGCGCACCTTCTGCTGCTGCTGCGGCGG 2107
QY 2102 AGGACCCGCGCTGAGCTGTAATTTGCAAGGTGATGAGGCGCGCTACGACACCA 2161
Db 2108 AGGACCCGCGCTGAGCTGTAATTTGCAAGGTGATGAGGCGCGCTACGACACCA 2167
QY 2162 TCCCCAGAGAGAGGCTCACGAGAGTCAATCCGACATCATCAAAACCCAGAACAGTA 2221
Db 2168 TCCCCAGAGAGAGGCTCACGAGAGTCAATCCGACATCATCAAAACCCAGAACAGTA 2227
QY 2222 GCGTGGCTGGATGCGGTGATCCAGAGAGCGCCCATGGGCAAGTCCGCAAGGCTTCA 2281
Db 2228 GCGTGGCTGGATGCGGTGATCCAGAGAGCGCCCATGGGCAAGTCCGCAAGGCTTCA 2287
QY 2282 AGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTACC 2341
Db 2288 AGAGCCAGCTCTTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGCTACC 2347
QY 2342 TGCAGAGAGAGAGCGCCGCTGAGGGAGTCCGCTGCTCATGAGAGAGCTCCTCCTGA 2401
Db 2348 TGCAGAGAGAGAGCGCCGCTGAGGGAGTCCGCTGCTCATGAGAGAGCTCCTCCTGA 2407
QY 2402 AGGCCAGAGAGGCTCTTCCAGAGTCTTCTTCAAGCTTCAATGTCACACAGCGCGTGA 2461
Db 2408 AGGCCAGAGAGGCTCTTCCAGAGTCTTCTTCAAGCTTCAATGTCACACAGCGCGTGA 2467
QY 2462 TCAGGGGCAAGTCTTACGTCAGAGTCCAGGGGATCCCGCAGGCTCCATCCTTCCAGC 2521
Db 2468 TCAGGGGCAAGTCTTACGTCAGAGTCCAGGGGATCCCGCAGGCTCCATCCTTCCAGC 2527
QY 2522 TGCTGTGAGCTGTGCTACGCGGAGATGGAACAAGCTGTTTGGGGGATTGGCGGG 2581
Db 2528 TGCTGTGAGCTGTGCTACGCGGAGATGGAACAAGCTGTTTGGGGGATTGGCGGG 2587
QY 2582 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2641
Db 2588 ACGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2647
QY 2642 CGAAACCTTCTCAGAGACCCCTGTCGAGAGTTCCTCCTGAGTATGCTGCTGCTGCTG 2701
Db 2648 CGAAACCTTCTCAGAGACCCCTGTCGAGAGTTCCTCCTGAGTATGCTGCTGCTGCTG 2707
QY 2702 TCGGAGAGAGAGTGTGTAATTCCTGTGAAGAAGAGGCGCTGGGTGGCAGGCTTTG 2761
Db 2708 TCGGAGAGAGAGTGTGTAATTCCTGTGAAGAAGAGGCGCTGGGTGGCAGGCTTTG 2767
QY 2762 TTCAGATGCGGCGCCAGCGCTATTCCTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2821
Db 2768 TTCAGATGCGGCGCCAGCGCTATTCCTGTGCGGCTGCTGCTGCTGCTGCTGCTGCTG 2827
QY 2822 TGGAGGTGAGAGGAGTACTTCAAGTATGCGCGAGCTCCATCAGAGCAGTCTCACT 2881

Db 2828 TGGAGGTGAGAGGAGTACTTCAAGTATGCGCGAGCTCCATCAGAGCAGTGTCACT 2887
QY 2882 TCAACCGCGGCTTCAAGGCTGGAGAGACATGCGTGCAGAACTCTTGGGGTCTTGCGG 2941
Db 2888 TCAACCGCGGCTTCAAGGCTGGAGAGACATGCGTGCAGAACTCTTGGGGTCTTGCGG 2947
QY 2942 TGAAGTGTACAGCCTGTTCTGATTTGAGGTGAGACAGCTCCAGACGGTGTGACCA 3001
Db 2948 TGAAGTGTACAGCCTGTTCTGATTTGAGGTGAGACAGCTCCAGACGGTGTGACCA 3007
QY 3002 ACATCTACAGATTCCTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGACGTC 3061
Db 3008 ACATCTACAGATTCCTCCTGCTGAGGCGTACAGGTTTCAAGCATGTGTGCTGACGTC 3067
QY 3062 CATTTCATCAGAGTGTGGAAGAACCCACATTTTCTGCGGCTCATCTGTACACGG 3121
Db 3068 CATTTCATCAGAGTGTGGAAGAACCCACATTTTCTGCGGCTCATCTGTACACGG 3127
QY 3122 CTTCCCTCTGCTACTCCATCCTGTAAGAGCCAGAACGAGGAGTGTGCTGAGGCGCA 3181
Db 3128 CTTCCCTCTGCTACTCCATCCTGTAAGAGCCAGAACGAGGAGTGTGCTGAGGCGCA 3187
QY 3182 GCGCGCGCGGCTCTGCGCTCCGAGGCGGTGAGTGTGCTGAGGCGCAAGCATTCCTG 3241
Db 3188 GCGCGCGCGGCTCTGCGCTCCGAGGCGGTGAGTGTGCTGAGGCGCAAGCATTCCTG 3247
QY 3242 TCAAGTGTACAGACCGGTGCTACCTACGTGACACTCTGCGGTCACTCAGAGACAGCC 3301
Db 3248 TCAAGTGTACAGACCGGTGCTACCTACGTGACACTCTGCGGTCACTCAGAGACAGCC 3307
QY 3302 AGAGCAGCTGAGTCCGGAAGCTCCGAGGAGAGAGCGCTGACTGCTGAGGCGGAGCCA 3361
Db 3308 AGAGCAGCTGAGTCCGGAAGCTCCGAGGAGAGAGCGCTGACTGCTGAGGCGGAGCCA 3367
QY 3362 ACCCGGACTGCTCCTCAGACTTCAAGACCATCTGACTGATG 3405
Db 3368 ACCCGGACTGCTCCTCAGACTTCAAGACCATCTGACTGATG 3411

RESULT 14
US-10-105-616-1
; Sequence 1, Application US/10105616
; Publication No. US20030175967A1
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Clark, A. J.
; APPLICANT: Dunning, Chris
; APPLICANT: Cui, Wei
; APPLICANT: Zhao, Debbiao
; TITLE OF INVENTION: Vectors for telomere elongation in Nuclear Donor Cells and Improving the E
; FILE REFERENCE: 732/002
; CURRENT APPLICATION NUMBER: US/10/105,616
; PRIOR FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US Provisional Application 60/277,749
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 13766
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial construct comprising human TERT, myeloproliferatives
; OTHER INFORMATION: rcoma virus (MPSV) promoter, and vector components
US-10-105-616-1

Query Match 99.6%; Score 3397.6; DB 14; Length 13766;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3400; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 CGATGCGGCGGCTCCCGCTGCGAGCGCGTGGCTCCCTGCTGCGAGCAGCAGTACCGCG 61

Db 3987 CCATGCGCGCGCTCCCCGCTGCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCG 4046
QY 62 AGGTGCTGCGCTGCGCCACGTTGCTGCGCGCTGCGGCCCGCAGGGCTGCGCGCTGCTGCG 121
Db 4047 AGGTGCTGCGCTGCGCCACGTTGCTGCGCGCGCTGCGGCCCGCAGGGCTGCGCGCTGCTGCG 4106
QY 122 AGCGCGGGGACCCCGCGCGCTTCCGCGCGCTGCTGCGCCAGTGTGCTGCTGCTGCTGCT 181
Db 4107 AGCGCGGGGACCCCGCGCGCTTCCGCGCGCTGCTGCGCCAGTGTGCTGCTGCTGCTGCT 4166
QY 182 GGGACGACCG 241
Db 4167 GGGACGACCG 4226
QY 242 TGGTGGCGCGAGTGTGCTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 301
Db 4227 TGGTGGCGCGAGTGTGCTGACAGAGGCTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 4286
QY 302 GCTTGGCGCTGCTGCGAGCG 361
Db 4287 GCTTGGCGCTGCTGCGAGCG 4346
QY 362 GCAGCTACCTGCGCCCAACAGGCTGACCGCGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 421
Db 4347 GCAGCTACCTGCGCCCAACAGGCTGACCGCGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 4406
QY 422 TGGTGGCG 481
Db 4407 TGGTGGCG 4466
QY 482 TGGTGGCTGCTGCGAGCGCTGCGCGCTTACAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 541
Db 4467 TGGTGGCTGCTGCGAGCGCTGCGCGCTTACAGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 4526
QY 542 CTGCGCACTCAGCG 601
Db 4527 CTGCGCACTCAGCG 4586
QY 602 AACGGGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 661
Db 4587 AACGGGCTGGAACCATAGCGTCAAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4646
QY 662 GTGCGAGGAGCG 721
Db 4647 GTGCGAGGAGCG 4706
QY 722 GTGCGCGTGGCG 781
Db 4707 GTGCGCGTGGCG 4766
QY 782 GCAGAGCGCGTGGACCGAGTGAACCGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 841
Db 4767 GCAGAGCGCGTGGACCGAGTGAACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4826
QY 842 AAGAAGCCACTCTTTGGAGGGTGCCTGTGCGACCGCGCACTCCACCCATCCGCTG 901
Db 4827 AAGAAGCCACTCTTTGGAGGGTGCCTGTGCGACCGCGCACTCCACCCATCCGCTG 4886
QY 902 GCGCGCAGCACCACCG 961
Db 4887 GCGCGCAGCACCACCG 4946
QY 962 CTTGTCCCGCGGTGTACCGCGGAGACCAAGCACTTCTCTACTCTCTCAAGGCGACAGAGAGC 1021
Db 4947 CTTGTCCCGCGGTGTACCGCGGAGACCAAGCACTTCTCTACTCTCTCAAGGCGACAGAGAGC 5006
QY 1022 AGCTGCGCGCT 1081
Db 5007 AGCTGCGCGCT 5066
QY 1082 TCGTGAGACCACTTCTTCTGGGTTCCAGGCGCTGATGCCAGGGACTCCCGCAGGTTGC 1141

Db 5067 TCGTGAGACCACTTCTTCTGGGTTCCAGGCGCTGATGCCAGGGACTCCCGCAGGTTGC 5126
QY 1142 CCCGCTGCGCGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1201
Db 5127 CCCGCTGCGCGCGCTACTGCGCAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5186
QY 1202 ACGCGAGTGGCG 1261
Db 5187 ACGCGAGTGGCG 5246
QY 1262 CCCGAGCAGCGCGGTGTGTGCG 1321
Db 5247 CCCGAGCAGCGCGGTGTGTGCG 5306
QY 1322 AGAGGACACAGACCG 1381
Db 5307 AGAGGACACAGACCG 5366
QY 1382 AGGTGACGCGCTTGTGCG 1441
Db 5367 AGGTGACGCGCTTGTGCG 5426
QY 1442 CCAGGACCAACGAGCGCGCGCTTCTCTAGAGAACCAAGAACTTCTCTCTCTCTCTCTCTCTCTCT 1501
Db 5427 CCAGGACCAACGAGCGCGCGCTTCTCTAGAGAACCAAGAACTTCTCTCTCTCTCTCTCTCTCTCT 5486
QY 1502 ATGCCAAGCTTGTGCTGACGAGAGCTGAGTGAAGATGAGCGTGGCGGACTGCGCTTGC 1561
Db 5487 ATGCCAAGCTTGTGCTGACGAGAGCTGAGTGAAGATGAGCGTGGCGGACTGCGCTTGC 5546
QY 1562 TGGCAGAGAGCGCGCGGTGGCTGTGTCCGCGCGCAGAGCACCCTGCGTGAGAGAG 1621
Db 5547 TGGCAGAGAGCGCGCGGTGGCTGTGTCCGCGCGCAGAGCACCCTGCGTGAGAGAG 5606
QY 1622 TCCTGCGCAAGTTCCTGCACTGCGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1681
Db 5607 TCCTGCGCAAGTTCCTGCACTGCGTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5666
QY 1682 TCTTTATGTCAAGGAGACCAAGCTTCAAAAGAACAGAGCTTTTCTACCGGAAGAGTG 1741
Db 5667 TCTTTATGTCAAGGAGACCAAGCTTCAAAAGAACAGAGCTTTTCTACCGGAAGAGTG 5726
QY 1742 TCTGAGGCAAGTTCGAAGAGATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGG 1801
Db 5727 TCTGAGGCAAGTTCGAAGAGATTTGAATCAGACAGCACTTGAAGAGGTGACGTGCGG 5786
QY 1802 AGCTGTGGAAGAGAGGTGACGAGATCGGGAAGCCAGGCGCGCGCTGTAAGTCCA 1861
Db 5787 AGCTGTGGAAGAGAGGTGACGAGATCGGGAAGCCAGGCGCGCGCTGTAAGTCCA 5846
QY 1862 GACTCGCGCTTCAATCCCAAGCGTGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1921
Db 5847 GACTCGCGCTTCAATCCCAAGCGTGAAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5906
QY 1922 TGGAGCCAGAACGTTCCGACAGAAAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1981
Db 5907 TGGAGCCAGAACGTTCCGACAGAAAAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5966
QY 1982 CACTGTTCAGCGTGTCAACTACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2041
Db 5967 CACTGTTCAGCGTGTCAACTACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6026
QY 2042 TGGTGGCGCGAGATATCCAGAGCG 2101
Db 6027 TGGTGGCGCGAGATATCCAGAGCG 6086
QY 2102 AGGACCGCGCGCTGAGCTGTACTTGTCAAGTGTGATGTGAGCGCGCGCGCGCGCGCGCGCGCG 2161
Db 6087 AGGACCGCGCGCTGAGCTGTACTTGTCAAGTGTGATGTGAGCGCGCGCGCGCGCGCGCGCGCG 6146
QY 2162 TCCCGCAGAGAGGCTCAGGAGGTGATGCGCAGCATCATCAAAACCCAGAACAGCTACT 2221
Db 6147 TCCCGCAGAGAGGCTCAGGAGGTGATGCGCAGCATCATCAAAACCCAGAACAGCTACT 6206

QY 2222 GCGTGGCTGGTATGCGGTGCTCCAGAAAGCCGCCCATGGGCACTCCGCAAGGCTTTCA 2281
Db 6207 GCGTGGCTGGTATGCGGTGCTCCAGAAAGCCGCCCATGGGCACTCCGCAAGGCTTTCA 6266
QY 2282 AGAGCCAGCTCTTACCTTGACAGACTCCAGCCGTACATGGCAGAGTTGGTGGTCAAC 2341
Db 6267 AGAGCCAGCTCTTACCTTGACAGACTCCAGCCGTACATGGCAGAGTTGGTGGTCAAC 6326
QY 2342 TGCAGAGAGCAGCCCGCTGAGGAGTGGCTGCTCATGAGCAGAGCTCCTCTGAATG 2401
Db 6327 TGCAGAGAGCAGCCCGCTGAGGAGTGGCTGCTCATGAGCAGAGCTCCTCTGAATG 6386
QY 2402 AGGCCAGAGTGGCTCTTTCAGAGCTTCTTACGCTTATGTCACACGCGCTGGCA 2461
Db 6387 AGGCCAGAGTGGCTCTTTCAGAGCTTCTTACGCTTATGTCACACGCGCTGGCA 6446
QY 2462 TCAGGGGCAAGTCTTACCTGTCAGAGTGGCAGGGGATCCCGCAGGCTCCATCTCTGCA 2521
Db 6447 TCAGGGGCAAGTCTTACCTGTCAGAGTGGCAGGGGATCCCGCAGGCTCCATCTCTGCA 6506
QY 2522 TGCTGTGAGCTGTGCTACGCGCAGATGAGAACAGCTTTTGGGGATTCGGCGG 2581
Db 6507 TGCTGTGAGCTGTGCTACGCGCAGATGAGAACAGCTTTTGGGGATTCGGCGG 6566
QY 2582 ACGGCTGTCTGCTGCTGTTGGTGAATTTCTTGTGTGACACCTCACCCTCAACCA 2641
Db 6567 ACGGCTGTCTGCTGCTGTTGGTGAATTTCTTGTGTGACACCTCACCCTCAACCA 6626
QY 2642 CGAAACCTTCTCAGAGACCTGTCGAGGTGTCCCTGAGTATGCTGCTGGTGA 2701
Db 6627 CGAAACCTTCTCAGAGACCTGTCGAGGTGTCCCTGAGTATGCTGCTGGTGA 6686
QY 2702 TGCAGAGAGTGTGTAATTCCTGTAGAAGACGAGGCTGGTGGCAAGGCTTTG 2761
Db 6687 TGCAGAGAGTGTGTAATTCCTGTAGAAGACGAGGCTGGTGGCAAGGCTTTG 6746
QY 2762 TTTCAGATGCGGCGCCCAAGGCTTATCCCTGTGTGCGGCTGTCTGATACCGGAG 2821
Db 6747 TTTCAGATGCGGCGCCCAAGGCTTATCCCTGTGTGCGGCTGTCTGATACCGGAG 6806
QY 2822 TGGAGGTGAGAGCGGCTACTTCAAGCTATGCGGAGCTTCCATCAGAGCCAGTCTCA 2881
Db 6807 TGGAGGTGAGAGCGGCTACTTCAAGCTATGCGGAGCTTCCATCAGAGCCAGTCTCA 6866
QY 2882 TCAACCGGCTTCAAGGCTGGGAGAACATGCGTCAAACTTTGGGGTCTGCGG 2941
Db 6867 TCAACCGGCTTCAAGGCTGGGAGAACATGCGTCAAACTTTGGGGTCTGCGG 6926
QY 2942 TGAAGTGTACAGCCTGTTTGTGATTTGAGGTGAAGACCTCCAGAGGCTGACCA 3001
Db 6927 TGAAGTGTACAGCCTGTTTGTGATTTGAGGTGAAGACCTCCAGAGGCTGACCA 6986
QY 3002 ACATCTAAGATCTCTCTGCTGAGGCTGACAGGTTTCAAGCATGTGTGAGAGTCC 3061
Db 6987 ACATCTAAGATCTCTCTGCTGAGGCTGACAGGTTTCAAGCATGTGTGAGAGTCC 7046
QY 3062 CATTTCAAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACAGCG 3121
Db 7047 CATTTCAAGCAAGTTTGAAGAACCCCAATTTTCTGCGGCTCATCTGACAGCG 7106
QY 3122 CCTCCCTGCTACTCATCTCTGAAGAACCAAGAGGAGATGCTGGGGGCGCAAG 3181
Db 7107 CCTCCCTGCTACTCATCTCTGAAGAACCAAGAGGAGATGCTGGGGGCGCAAG 7166
QY 3182 GCGCGCGCGGCTCTGCGCTCGAGGCGCTGAGTGGCTGTGCGCAGCATCTCTGC 3241
Db 7167 GCGCGCGCGGCTCTGCGCTCGAGGCGCTGAGTGGCTGTGCGCAGCATCTCTGC 7226
QY 3242 TCAAGCTGACTGACACCGCTGTACCTAGTGGCTCTCTGGGGTCACTGAGAGAGCC 3301
Db 7227 TCAAGCTGACTGACACCGCTGTACCTAGTGGCTCTCTGGGGTCACTGAGAGAGCC 7286

QY 3302 AGACGAGCTGAGTCCGAAGCTCCCGGGAGACGAGCTGACTGCTTGAGAGCCGAGCCA 3361
Db 7287 AGACGAGCTGAGTCCGAAGCTCCCGGGAGACGAGCTGACTGCTTGAGAGCCGAGCCA 7346
QY 3362 ACCCGGACTGCTCCCTCAGACTTCAAGACCATCTGAGTGAATG 3405
Db 7347 ACCCGGACTGCTCCCTCAGACTTCAAGACCATCTGAGTGAATG 7390

RESULT 15

US-09-749-728B-32
; Sequence 32, Application US/09749728B
; Patent No. US20020142457A1
; GENERAL INFORMATION:
; APPLICANT: Umezawa, Akihiro
; APPLICANT: Hata, Jun-ichi
; APPLICANT: Fukuda, Keiichi
; APPLICANT: Ogawa, Satoshi
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Gojo, Satoshi
; APPLICANT: Yamada, Yoji
; TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOV
; FILE REFERENCE: 00766.000043
; CURRENT APPLICATION NUMBER: US/09/749, 728B
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-02-28
; PRIOR FILING DATE: 2000-02-28
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patentln Ver.2.0
; SEQ ID NO 32
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; OTHER INFORMATION: (1)..(3399)
US-09-749-728B-32

Query Match 99.6%; Score 3396; DB 9; Length 3396;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 ATGCGCGGCTCCCGCTGCGGAGCCGCTGCGCTCCTGCTGCGAGCCACTACCGGAG 63
Db 1 ATGCGCGGCTCCCGCTGCGGAGCCGCTGCGCTCCTGCTGCGAGCCACTACCGGAG 60
QY 64 GTGCTGCGGCTGCGGAGCTGCTGCGGAGCCGCTGCGGAGCCGCTGCGGAGCCGCTGCGGAG 123
Db 61 GTGCTGCGGCTGCGGAGCTGCTGCGGAGCCGCTGCGGAGCCGCTGCGGAGCCGCTGCGGAG 120
QY 124 CGCGGGAGCCCGGCTTTCGCGGCTGCTGCGGAGCTGCTGCGGAGCTGCTGCGGAGCTGCGGAG 183
Db 121 CGCGGGAGCCCGGCTTTCGCGGCTGCTGCGGAGCTGCTGCGGAGCTGCTGCGGAGCTGCGGAG 180
QY 184 GACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 243
Db 181 GACGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 244 GTGCGCGAGTGTGAGAGGCTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 303
Db 241 GTGCGCGAGTGTGAGAGGCTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 304 TTGCGGCTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 363
Db 301 TTGCGGCTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 364 AGCTAAGTCCCAACAGGAGTGAAG 423
Db 361 AGCTAAGTCCCAACAGGAGTGAAG 420

QY	424	CTGCGCCGCGTGGGCGCAGCGTGTGTTTCACTGCTGGCAGCGTGGCGCTTTGTG	483
Db	421	CTGCGCCGCGTGGGCGCAGCGTGTGTTTCACTGCTGGCAGCGTGGCGCTTTGTG	480
QY	484	CTGCTGGCTCCCACTGCGCTACCAAGTGTGCGGGCCGCGCTGTATCCAGCTCGCGCT	543
Db	481	CTGCTGGCTCCCACTGCGCTACCAAGTGTGCGGGCCGCGCTGTATCCAGCTCGCGCT	540
QYA	544	GCCACTCAGGCCCCCGCCCCCGCCACAACGCTAGTGGACCCCGAAGCGCTCTGGATGCGAA	603
Db	541	GCCACTCAGGCCCCCGCCCCCGCCACAACGCTAGTGGACCCCGAAGCGCTCTGGATGCGAA	600
QY	604	CGGGCTTGAACCATATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTTGCCAGCCCCGGGT	663
Db	601	CGGGCTTGAACCATATAGCGTCAAGGAGGCGGGGTCCCCCTGGGCTTGCCAGCCCCGGGT	660
QY	664	GCGAGGAGGCGCGGGGCGAGTGCACGCCGAAGTCTGCCGTTGCCCCAAGAGGCCAGCGT	723
Db	661	GCGAGGAGGCGCGGGGCGAGTGCACGCCGAAGTCTGCCGTTGCCCCAAGAGGCCAGCGT	720
QY	724	GCGCGTGCCTCTGAGCCGAGCGCAGCCCCCTTGAGCAGGGGTCTGCGGCCACCCGGGC	783
Db	721	GCGCGTGCCTCTGAGCCGAGCGCAGCCCCCTTGAGCAGGGGTCTGCGGCCACCCGGGC	780
QY	784	AGGACGCGTGGAACCGAGTGACCGGTGTTTCTGTGTGTATCACTGCCAGACCCGCCGA	843
Db	781	AGGACGCGTGGAACCGAGTGACCGGTGTTTCTGTGTGTATCACTGCCAGACCCGCCGA	840
QY	844	GAAGCCACTCTTTGGAGGGTGCCTCTCTGGACGCGCCACTCCCACCATCCGTGGC	903
Db	841	GAAGCCACTCTTTGGAGGGTGCCTCTCTGGACGCGCCACTCCCACCATCCGTGGC	900
QY	904	CGCCAGCACCAACGCGGGGCCCATCCACATCGCGGCCACCAAGTCCCTGGAGACGCT	963
Db	901	CGCCAGCACCAACGCGGGGCCCATCCACATCGCGGCCACCAAGTCCCTGGAGACGCT	960
QY	964	TGTCCCCCGGTAGCGCCGAGACCAAGCACTTCTCTACTCTTCAAGCGACAAGAGCAG	1023
Db	961	TGTCCCCCGGTAGCGCCGAGACCAAGCACTTCTCTACTCTTCAAGCGACAAGAGCAG	1020
QY	1024	CTGCGGCCCTCTTCTCTACTCAGCTCTCTGAGGCCCAAGCTGACTGGCGCTCGAGGCTC	1083
Db	1021	CTGCGGCCCTCTTCTCTACTCAGCTCTCTGAGGCCCAAGCTGACTGGCGCTCGAGGCTC	1080
QY	1084	GTGAGAGCCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGCAAGTTGCC	1143
Db	1081	GTGAGAGCCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGCAAGTTGCC	1140
QY	1144	CGCCTGCCCCAAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAAGCTGCTTGGGAACAC	1203
Db	1141	CGCCTGCCCCAAGCGCTACTGGCAATGCGGCCCTGTCTTCTGAAGCTGCTTGGGAACAC	1200
QY	1204	GCGCAGTGCCCTACCGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGTGCCTCAAC	1263
Db	1201	GCGCAGTGCCCTACCGGGTGTCTCTCAAGACGCACTGCCGCTGCGAGTGCCTCAAC	1260
QY	1264	CCAGCAGCCGTTGTCTGTGCCCGGAGAGACCCCAAGGCTCTGTGGCGGCCCGAGAG	1323
Db	1261	CCAGCAGCCGTTGTCTGTGCCCGGAGAGACCCCAAGGCTCTGTGGCGGCCCGAGAG	1320
QY	1324	GAGGACACAGACCCCGCTGCGCTGTGACAGTGTCCGACAGACAGCAGCCCTGGCAG	1383
Db	1321	GAGGACACAGACCCCGCTGCGCTGTGACAGTGTCCGACAGACAGCAGCCCTGGCAG	1380
QY	1384	GTGTACGCTTGTGTGGGCTGTCTGCGCGGCTGTGTGCCCCAGGCTCTGGGCTCC	1443
Db	1381	GTGTACGCTTGTGTGGGCTGTCTGCGCGGCTGTGTGCCCCAGGCTCTGGGCTCC	1440
QY	1444	AGGCACAACGAACGCGCTTCTCAGGAACACCAAGAATTCTCTCCCTGGGGAAGCAT	1503
Db	1441	AGGCACAACGAACGCGCTTCTCAGGAACACCAAGAATTCTCTCCCTGGGGAAGCAT	1500

QY	1504	GCCAAGCTCTCGCTGACGAGACTGACGTGGAAGATGACCGTCCGGGACTCGCCTTGCTG	1563
Db	1501	GCCAAGCTCTCGCTGACGAGACTGACGTGGAAGATGACCGTCCGGGACTCGCCTTGCTG	1560
QY	1564	CGCAGAGAGCCCAAGGGGTGGCTGTGTTCGCCGCCGACAGACACCGTCTGCGTGAGAGATC	1623
Db	1561	CGCAGAGAGCCCAAGGGGTGGCTGTGTTCGCCGCCGACAGACACCGTCTGCGTGAGAGATC	1620
QY	1624	CTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTAACGTCTGAGAGCTGCTCAGGTCTTTC	1683
Db	1621	CTGGCCAAAGTTCCTGCACTGGCTGATGAGTGTGTAACGTCTGAGAGCTGCTCAGGTCTTTC	1680
QY	1684	TTTTATGTCAACGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTTC	1743
Db	1681	TTTTATGTCAACGAGACCAAGCTTCAAAAGAACAGGCTCTTTTCTACCGGAAGAGTGTTC	1740
QY	1744	TGAGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAG	1803
Db	1741	TGAGCAAGTTGCAAGCATTTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGAG	1800
QY	1804	CTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGA	1863
Db	1801	CTGTGGAAGCAGAGGTCAAGCAGCATCGGGAAGCCAGGCCCGCCCTGTGACGTCCAGA	1860
QY	1864	CTCCGCTTCATCCCCAAGCCTGACGAGCTGCGCGCGAATTGTGAACATGACTACGTCTG	1923
Db	1861	CTCCGCTTCATCCCCAAGCCTGACGAGCTGCGCGCGAATTGTGAACATGACTACGTCTG	1920
QY	1924	GGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTACCTCGAGGTTGAAGCA	1983
Db	1921	GGAGCCAGAACGTTCCGACAGAAAGAGGGCCGAGCGTCTACCTCGAGGTTGAAGCA	1980
QY	1984	CTGTTACGCTGCTCAACTACGAGCGGGCGCGCCCCCGGCTCTGCGCGCTCTGTG	2043
Db	1981	CTGTTACGCTGCTCAACTACGAGCGGGCGCGCCCCCGGCTCTGCGCGCTCTGTG	2040
QY	2044	CTGGGCTTGACGATATCCACAGGGCCTGGCGCACTTCGTCTGCTGTGCGGGCCAG	2103
Db	2041	CTGGGCTTGACGATATCCACAGGGCCTGGCGCACTTCGTCTGCTGTGCGGGCCAG	2100
QY	2104	GACCCGCCGCTGAGCTGTACTTTGTCAAGGTGGAATGTGACGGGCGCGTACGACCATC	2163
Db	2101	GACCCGCCGCTGAGCTGTACTTTGTCAAGGTGGAATGTGACGGGCGCGTACGACCATC	2160
QY	2164	CCCCAGGACAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTACTGC	2223
Db	2161	CCCCAGGACAGGCTCACGGAGGTCAATCGCCAGCATCATCAAAACCCAGAACACGTACTGC	2220
QY	2224	GTGCGTGGTATGCCGTGGTCCAGAAAGGCCGCCATGGGCACGTCCGCAAGGCTTCAAG	2283
Db	2221	GTGCGTGGTATGCCGTGGTCCAGAAAGGCCGCCATGGGCACGTCCGCAAGGCTTCAAG	2280
QY	2284	AGCCACGTCTTAACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGACTCACTG	2343
Db	2281	AGCCACGTCTTAACCTTGACAGACCTCCAGCGGTACATGCGACAGTTCGTGACTCACTG	2340
QY	2344	CAGGAGACCAAGCCGCTGAGGAGTGCCTGTGTCATGAGCAGAGAGTCTCTCCTGAATGAG	2403
Db	2341	CAGGAGACCAAGCCGCTGAGGAGTGCCTGTGTCATGAGCAGAGAGTCTCTCCTGAATGAG	2400
QY	2404	GCCAGCAGTGGCTCTTGACAGTCTTCTTAAGCTTTCATGTGCCACACGCGTGCATC	2463
Db	2401	GCCAGCAGTGGCTCTTGACAGTCTTCTTAAGCTTTCATGTGCCACACGCGTGCATC	2460
QY	2464	AGGGCAAGTTCCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCAATCCTCCACGCTG	2523
Db	2461	AGGGCAAGTTCCTACGTCCAGTGCAGGGGATCCCGCAGGGCTCAATCCTCCACGCTG	2520
QY	2524	CTCTGCAGCTGTGCTACGCGCATGAGAAACAAGCTGTTTGCGGGGATTCGGCGGGAC	2583
Db	2521	CTCTGCAGCTGTGCTACGCGCATGAGAAACAAGCTGTTTGCGGGGATTCGGCGGGAC	2580
QY	2584	GGGCTGCTCTGCGTTTGTGATGATTTCTGTGTTGTGACACCTCACTCAACCCACGCG	2643


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Db 2581 GGGCTGCTCCTGCGTTGGTGGATGATTTCTTGTGGTGAACACCTCACTCACCCACGCG 2640
QY 2644 AAAACCTTCTCAGACACCCCTGTGCCAGGTGCTCCGTAGTATGGCTGCGTGAACCTG 2703
Db 2641 AAAACCTTCTCAGACACCCCTGTGCCAGGTGCTCCGTAGTATGGCTGCGTGAACCTG 2700
QY 2704 CGGAAGACAGTGTGAACCTTCCCTGTAGAGAAGAGCCCTGGGTGCAACGCTTTGTT 2763
Db 2701 CGGAAGACAGTGTGAACCTTCCCTGTAGAGAAGAGCCCTGGGTGCAACGCTTTGTT 2760
QY 2764 CAGATGCCGCGCCACGCGCTATTTCCCTGTGGTGGCGCTGTGCTGGATACCCGACCTG 2823
Db 2761 CAGATGCCGCGCCACGCGCTATTTCCCTGTGGTGGCGCTGTGCTGGATACCCGACCTG 2820
QY 2824 GAGGTGACAGCGACTACTCCAGCTATGCCCGGACTCCATCAGAGCCAGTCTACCTTC 2883
Db 2821 GAGGTGACAGCGACTACTCCAGCTATGCCCGGACTCCATCAGAGCCAGTCTACCTTC 2880
QY 2884 AACCGCGGCTTCAAGGTGGGAGGAGACATGCGTCCGAACCTCTTGGGGTCTTGCGGCTG 2943
Db 2881 AACCGCGGCTTCAAGGTGGGAGGAGACATGCGTCCGAACCTCTTGGGGTCTTGCGGCTG 2940
QY 2944 AAGTGTACAGCCTGTTTCTGGATTGTGACAGTGAACAGCCTCCAGACGGTGTGACCAAC 3003
Db 2941 AAGTGTACAGCCTGTTTCTGGATTGTGACAGTGAACAGCCTCCAGACGGTGTGACCAAC 3000
QY 3004 ATCTACAAGATCCTCTGCTGCTGACAGGCGTACAGTTCACGCATGTGTGCTGACGCTCCA 3063
Db 3001 ATCTACAAGATCCTCTGCTGCTGACAGGCGTACAGTTCACGCATGTGTGCTGACGCTCCA 3060
QY 3064 TTTCATCAGCAAGTTTGAAGAAGACCCCAATTTTCTGCGCGTCACTCTGACACGGCC 3123
Db 3061 TTTCATCAGCAAGTTTGAAGAAGACCCCAATTTTCTGCGCGTCACTCTGACACGGCC 3120
QY 3124 TCCCTCTGCTACTCCATCTCTGAAGCAAGCAAGGATGTGCTGGGGGCCAAGGGC 3183
Db 3121 TCCCTCTGCTACTCCATCTCTGAAGCAAGCAAGGATGTGCTGGGGGCCAAGGGC 3180
QY 3184 GCCGCCGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTC 3243
Db 3181 GCCGCCGCGCTCTGCGCTCCGAGGCGGTGAGTGGCTGTGCCACCAAGCATTCCTGCTC 3240
QY 3244 AAGCTGACTGACACCGGTGTCACTTACGTGCCACTCTGGGGTCACTCAGGACAGCCAG 3303
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QY 3304 ACGCAGCTGAGTGGAGAGCTCCCGGGGACGAGCTGACTGCCCTGAGGCGCAGCCAAAC 3363
Db 3301 ACGCAGCTGAGTGGAGAGCTCCCGGGGACGAGCTGACTGCCCTGAGGCGCAGCCAAAC 3360
QY 3364 CCGGCACTGCCCTCAGACTTCAAGACCATCTTGAC 3399
Db 3361 CCGGCACTGCCCTCAGACTTCAAGACCATCTTGAC 3396
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